

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 9, 2004, 07:07:47 ; Search time 1236.96 Seconds
(without alignments)

6326.134 Million cell updates/sec

Title: US-09-977-053-6

Perfect score: 10219
Sequence: 1 MWPRFAFCWGLALVSGWAT.....GVTKITCLSGEWNHLPYC 1842

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/US09977053/runat.06052004.075942.18178/app.query.fasta.1.5710
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=100 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=25
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09977053 @CNG 1.1.4042 @runat.06052004.075942.18178 -NCFU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04.*

1: geneseq1980s.*
2: geneseq1990s.*
3: geneseq2000s.*
4: geneseq2001as.*
5: geneseq2001bs.*
6: geneseq2002s.*
7: geneseq2003as.*
8: geneseq2003bs.*
9: geneseq2003cs.*
10: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10214	100.0	11546	8	AAD57253 Human CGD
2	10208	99.9	10878	6	AAD32025 Human C3b
3	9862	96.5	11152	6	ABT08491 Human nov
4	9812	96.0	11158	6	ABT08490 Human nov
5	8652.5	84.7	11230	6	AAD32026 Mouse C3b
6	7537	73.8	5124	4	AAD16667 Human C3b
7	5485	53.7	3448	6	ABZ11152 Human pol
8	4730	46.3	3128	6	ABK54124 CDNA enco

C	9	3133	30.7	2064	6	ABK35664	ADK35664	CDNA sequ
	10	3073	30.1	1969	4	AAH16567	Aah16567	Human cDN
	11	2479	24.3	1696	6	ABK54146	Abk54146	CDNA enco
	12	2374	23.2	1760	3	AZ294659	Aaz294659	Human EGF
	13	1977	19.3	1408	6	ABK35663	ADK35663	CDNA sequ
	14	1498	14.7	1892	4	AAS26857	Aas26857	Human cDN
	15	1447	14.2	1765	4	AAH08402	Aah08402	Human cDN
	16	1354	13.2	10489	4	ABL14889	Ab114889	Drosophil
	17	1341	13.1	706	7	ACA57318	Aca57318	Human adi
C	18	1328	13.0	13484	4	ABL14888	Ab114888	Drosophil
	19	1304	12.8	801	4	AAH07752	Aah07752	Human cDN
	20	1278	12.5	680	4	AAS28962	Aas28962	CDNA enco
	21	1278	12.5	680	4	AAS26930	Aas26930	Human cDN
	22	1278	12.5	680	4	ABA06507	AbA06507	Human cDN
	23	1278	12.5	680	4	AAS31580	Aas31580	CDNA enco
	24	1278	12.5	680	6	ABT07797	AbT07797	Novel hum
	25	1278	12.5	680	6	ABV83844	Abv83844	Human pol
	26	1237	12.1	3262	6	ABS51807	Abs51807	Human mdd
	27	998	9.8	598	2	AAV87221	Aav87221	EST clone
C	28	983	9.6	675	5	AAD02459	Aad02459	Mouse P10
	29	975	9.5	2697	7	ABX34482	Abx34482	Human mdd
	30	914.5	8.9	6728	6	ADD28942	Add28942	Human MOL
	31	914.5	8.9	6728	9	ADD18193	Add18193	Human mol
	32	914.5	8.9	9723	2	AAL55430	Aal55430	Human Not
	33	914	8.9	8113	4	ABL06899	Ab106899	Drosophil
	34	893.5	8.7	7410	6	AAD28941	Aad28941	Human MOL
	35	893.5	8.7	7410	9	ADD18191	Add18191	Human mol
	36	872	8.5	7596	7	AAD56128	Aad56128	Mouse Not
	37	872	8.5	7596	8	ADA02491	Ada02491	Mouse Not
	38	872	8.5	7596	9	ADB72229	Adb72229	Mouse Not
	39	872	8.5	8064	7	AAD56127	Aad56127	Mouse Not
	40	872	8.5	8064	8	ADA02490	Ada02490	Mouse Not
	41	872	8.5	8064	9	ADB72228	Adb72228	Mouse Not
	42	869.5	8.5	8221	7	ABT42465	Abt42465	Toxicity
	43	860	8.4	7673	7	ABS55875	AbS55875	Human pol
	44	853	8.3	7332	6	ABL40768	Ab140768	Constitut
C	45	847	8.3	37322	6	ABL06898	Ab106898	Drosophil
	46	838	8.2	763	6	ABS70453	AbS70453	Human bon
	47	837.5	8.2	2460	6	AAD28494	Aad28494	Human ext
	48	831.5	8.1	7615	6	AAD56130	Aad56130	Human NOT
	49	831.5	8.1	7615	8	ADA02493	Ada02493	Human NOT
	50	831.5	8.1	7615	9	ADB72231	Adb72231	Human NOT
	51	829	8.1	8091	2	AAV57001	Aav57001	Human Not
	52	829	8.1	8091	6	ABZ34974	Abz34974	Human gen
	53	829	8.1	8257	6	ABS70408	AbS70408	Human bon
	54	764.5	7.5	6677	2	AAH00989	Aah00989	Mus muscu
	55	764.5	7.5	6677	6	AAI72830	Aai72830	Mouse Not
	56	762	7.3	5617	2	AAV57163	Aav57163	Partial h
	57	745	7.3	3974	7	ABX75297	Abx75297	Mouse not
	58	745	7.3	3974	7	AAD52524	Aad52524	Murine no
	59	745	7.3	3974	7	ABZ81794	Abz81794	Mouse not
	60	745	7.3	4855	6	ABK35564	AbK35564	Gene JAG1
	61	745	7.3	6464	2	AAT40090	Aat40090	Human Ser
	62	745	7.3	6464	3	AZA49096	Aaz49096	Human Ser
	63	744	7.3	4208	2	AAV15201	Aav15201	Human ser
	64	744	7.3	5590	2	AAV63753	Aav63753	Human JAG
	65	744	7.3	5590	8	ACD06196	Acd06196	Human cDN
	66	744	7.3	5896	7	ABZ34802	Abz34802	Coding se
	67	744	7.3	5929	7	ACA04012	Aca04012	CDNA down
	68	743	7.3	4208	2	AAT70175	Aat70175	Prolifera
	69	739.5	7.2	4146	9	AAD60679	Aad60679	Human CRU
	70	739.5	7.2	4361	7	AAD60677	Aad60677	Human CRU
	71	739.5	7.2	4413	9	ACD05903	Acd05903	Novel hum
	72	739.5	7.2	4950	9	AAD60678	Aad60678	Human CRU
	73	739	7.2	5942	9	ADD14711	Add14711	Human 8rc
	74	737	7.2	5458	2	AAV03674	Aav03674	Human Jag
	75	733	7.2	4200	6	ABV99395	Abv99395	Human NOV
	76	727	7.1	3825	9	AAD60686	Aad60686	Human CRU
	77	727	7.1	3921	9	AAD60683	Aad60683	Human CRU
	78	721	7.0	4200	6	ABV99396	Abv99396	Human NOV
	79	716.5	7.0	3786	9	AAD60684	Aad60684	Human CRU
	80	714.5	7.0	2757	4	AAS26875	Aas26875	Human cDN
C	81	713	7.0	462	4	AAS26893	Aas26893	Human cDN

181 LeuHisAlaArgGluAsnSerThrIleValValPheLeuIleThrAspGlyTyrSerAsn 200
Db CTTTCATGCTAGAGAAACTCAAAAGATGTATTTCTCATCACTGATGGATATCCAAAT 897
201 GlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThr 220
Db GGGGGAGACCCCTAGACCAATTCAGCGTCACTGCGAGATTCAGGAGTGGAGATCTTCAC 957
221 PheGlyIleThrGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProIleGlu 240
Db TTTGGCATATGGCAAGGGAACATTCGAGAGCTGAATGACATGGCTTCCACCCCAAGGAG 1017
241 GluHisCysValTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeu 260
Db GAGCACTGTTTACCTCTACACAGTTTTTGAAGAAATTTGAGGCTTTAGCTCGCGGCAATG 1077
261 HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu 280
Db CATGAAGATCTACCTTCTGGGAGTTTTTATTCAGATGATATGGTCCACTGCTCATATCTT 1137
281 CysAspGluGlyAspCysCysAspArgMetGlySerCysIleCysGlyThrHisThr 300
Db TGTGATGAAGGCAAGGACTGCTGTGACCGAATGGGAAGCTGCMAATGTGGGACACACACA 1197
301 GlyHisPheGluCysIleCysGluCysGlyTyrTyrGlyGlyLeuGlnTyrGluCys 320
Db GGCCTATTTGAGTGATCTGTGAAAGGGGTATTCGGGAAAGGCTGCAGTATGATGTC 1257
321 ThrAlaCysProSerGlyThrTyrIleCysProGluGlySerProGlyIleSerCys 340
Db ACAGCTTGCCCATCGGGACATACAAACCTGGAAGCTCACAGGAGGATCAGCAGTTGC 1317
341 IleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCys 360
Db ATTCCATGCTCTGATCAAAATACACACTCTCCACCTGGGAAGCACATCCCTCGAAGACTGT 1377
361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
Db GTCTGAGAGAGGATACAGGGCATCTGGCCAGACCTGTGAACCTGTGCCACTGCCCTGCC 1437
381 LeuIleProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla 400
Db CTGAAGCTCCCGAANAATGGTTACTTTATCCAAACACTTGCACAAACCACTTCATGCA 1497
401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys 420
Db GCCTGTGGGTCCGATGTCCACCTCGAATTTGATCTTTGTGGGAAGCAGCATCATCTTATGT 1557
421 LeuProAsnGlyLeuThrSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
Db CTACCAATGGTTTGTGGTCCGGTTACAGAGACTACTCGAGAGTAAGAACATGTCTCTCAT 1617
441 LeuArgGlnProIleHisGlyHisIleSerCysSerThrArgGluMetLeuTyrIleThr 460
Db CTCCGCCAGCGAACAATGGCCACATCAGCTGTTCTCAAGGGGAATGTTATATAAGACA 1677
461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspIleLeuThrCys 480
Db ACATGTTTGGTTCCTGTGATGAAGGTACAGACTAGAGGCGAGTGAATAGCTTACTTGT 1737
481 GlnGlyAsnSerGlnThrAspGlyProGluProArgCysValGluArgHisCysSerThr 500
Db CAAGAAACAGCCATGTGGGATGGGCGAAGAACCCGGTGTGTGGAGCGCCACTGTTCCACC 1797
501 PheGlnMetProIleAspValIleIleSerProHisAsnCysGlyIleGlnProAlaIle 520
Db TTTTCAGATGCCAAGAGTGTATCATATCCCCCACACTGTGGCAAGCAGCAGCCAAA 1857
521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValIleGlu 540
Db TTTGGACGATCTGCTATGTAAGTTGGCCGCAAGGGTTCAATTTTATCTGGAGTCAAGAA 1917

541 MetLeuArgCysThrThrSerGlyIleThrAsnValGlyValGlnAlaAlaValCysIle 560
Db ATGCTGAGATGTACCACTTCTGGAAATGGAATGTGGAGTTCAGGCAGCTGTGTGTAAA 1977
561 AspValGluAlaProGlnIleAsnCysProIleAspIleGluAlaIleThrLeuGluGln 580
Db GAGCTGGAGGCTCTCNAATCAACTGTCTTAAGCAGATAGAGGCTAAGACTCTGGAACAG 2037
581 GlnAspSerAlaAsnValThrTyrGlnIleProThrAlaIleAspAsnSerGlyGluIle 600
Db CAGATCTTGCCCAATGTTTACCTGGCAGATTCACACAGCTAAGACAACTCTGGTGAAGA 2097
601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620
Db GTGTCACTCCAGCTTCATCCAGCTTTCACCCCACTTACCTTTTCCCAATGGAGATGTT 2157
621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
Db GCTATCTGTATACACGGCAACTGACCTATTCGGCAACACAGCCAGCTGCATTTTCCATATC 2217
641 LysValIleAspAlaGluProProValIleAspTyrCysArgSerProProValGln 660
Db AAGGTTATTTGATGCAAGAACCTCTGTATAGACTGGTGCAAGATCTCCACCTCCCGTCCAG 2277
661 ValSerGluIleValHisAlaAlaSerTyrAspGluProGlnPheSerAspAsnSerGly 680
Db GTCTCGAGAGGATCATACGCCAGCTGGGATGAGCTCAGTTCTCAGACAACTCAGGG 2337
681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
Db GCTGAATGCTCATTAACCAAGACTCATACAAAGGAGACCTTTTCCCTCAAGGGGAGACT 2397
701 IleValGlyTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
Db ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATTAACAGGACATGTGATATCCATAT 2457
721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
Db GTCATANAAGTTTCTCCCTGTGAATTCATTCACACTGTAAATGGGATTTATATGTC 2517
741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
Db ACTCCAGATAATACTGGAGTCAACTGTATTAACCTTGTGGAGGCTATGATTTTCAACA 2577
761 GluGlySerThrAspIleTyrTyrCysAlaTyrGluAspGlyValTyrIleProThrTyr 780
Db GAAGGTCCTACTGACAAAGTATTTATTTGTCTTATGAAGATGGCGTCTGGAACCAACATAT 2637
781 ThrThrGluTyrProAspCysAlaIleLysArgPheAlaAsnHisGlyPheLysSerPhe 800
Db ACCACTGAATGGCCAGACTGTGCCAANAACGTTTTTGCACCAACCCAGGTTCAAGTCTTT 2697
801 GluMetPheTyrIleAlaAlaArgCysAspAspThrAspLeuMetIleLysPheSerGlu 820
Db GAGATGTTCTCAAAAGCAGCTCGTTGTGTATGACACAGATCTGATGAAGAAGTTTTCTGAA 2757
821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
Db GCATTTGACAGCAGCCCTGGGAAAAATGGTCCCATCATTTTGTAGTATGACAGAGACAT 2817
841 AspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
Db GACTGCAGACTGGAGGAGAACCTGACCAANAATATTGCTAGATATATAATTATGACTAT 2877
861 GluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSer 880
Db GAAATGCTTTTGCAATTTGCAATTCGAGCCAGGTGCTGGGTGTCAGCTAATAGGCTGGATCTCT 2937
881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 900
Db TACGATGACTTCTCGACACTGTGCAAGAAACAGCCACAGCATCGGCAATGCCAAGTCC 2997
901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920

Db 2998 TCACGGATTAAAGAGTGCCTTATCTGACTATATAAATAAGTTAAATTTTAAATC 3057
Qy 921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluIrrpGluAsnGln 940
Db 3058 ACAGCTAGTGTGCCATTACCCGATGAAGAATAATGATCCCTTGAATGGAAATCAGCAA 3117
Qy 941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
Db 3118 CGACTCTCTCAGACATTGGAACTATCACAAATAAATGAAAGGACTCTCAACAAAGAC 3177
Qy 961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuLeuAlaAspSerAsnSerLeuGlu 980
Db 3178 CCCATGTATCTCTTACCTTTCAGCTTGCATCAGAAATCTTATAGCCGACAGCAATTCATTAGNA 3237
Qy 981 ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal 1000
Db 3238 ACAAAAAGAGCTTCCCTCTCTGACAGACAGCCCTCAGTGTCTGAGAGGCGTATGTGTGTC 3297
Qy 1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
Db 3298 AATTCGCCCTTTGGGAACCTATTATAATCTGGAACATTTTCACTCTGTAAGCTGCGGATC 3357
Qy 1021 GlySerTyrGlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr 1040
Db 3358 GGATCCTATCAAGATGAAGAGGGCACTTGAGTGCAGAGCTTTGCCCTCTGGGATGTAC 3417
Qy 1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr 1060
Db 3418 ACGGAATATATCCATTCAAGAAACATCTCTGAATGTAAAGCTCAGTGTAAACAGGACACC 3477
Qy 1061 TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLys 1080
Db 3478 TACTCATACAGTGGACTTGAAGTGTGAATCGTGTCCACTGGGCACCTTATCAGCCAAA 3537
Qy 1081 PheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAla 1100
Db 3538 TTTGGTTCCCGAGCTGCTCTCTGTGTCCAGAAACACCTCACTGTGTGAAAGAGGAGGCC 3597
Qy 1101 ValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeu 1120
Db 3598 GTGAACATTTCTGCTATGTGGAGTCTCTGTGTCCAGAAAGAAATTTCTCGCGTCTCTGGGTTA 3657
Qy 1121 MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
Db 3658 ATGCCCTGTACCCATGTCTCTGACTATTACCAACCTTAATGAGGAGGAGCCCTTCGC 3717
Qy 1141 LeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCys 1160
Db 3718 CTGGCCCTGTCTCTTTATGGAACTACCCCATTCGCTGCTGCATTCGATCCGTCACGAATGT 3777
Qy 1161 SerSerPheSerThrPheSerAlaAlaGluGluSerValProProAlaSerLeu 1180
Db 3778 TCAAGTTTATAGTTCACATTTCTCAGCGCAGAGGAAAGTGTGTGCGCCCTCTCTCTT 3837
Qy 1181 GlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPheAsn 1200
Db 3838 GGACATATATAAAGAGCGCATGAATCAGCAGTCAAGTGTTCCTCCATGAATGCTCTTTAAC 3897
Qy 1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
Db 3898 CTTTGCACCAATAGTGGAACTCTGCAGCACTTGGCGTGGTATGTATGTCTCTGTCCA 3957
Qy 1221 LeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCys 1240
Db 3958 CTTGGATATA CAGGCTTAAAGTGTGAACAGACATCGATGAGTGCAGCCCATCTGCTTGC 4017
Qy 1241 LeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGly 1260
Db 4018 CTCACCAATGAGTGTGTAAAGACTTATGTGGGAAATTCATTGTGAGTGCCTCATCAGGT 4077
Qy 1261 TyrThrGlyGlnArgCysGluAlaAsnIleAsnGluCysSerSerProCysLeuAsn 1280

Db 4078 TACACAGGTGACGCGTGTGAAGAAAATATAAATGAGTGTAGTCCAGTCTCTTGTTTAAAT 4137
Qy 1281 LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal 1300
Db 4138 AAAGGAATCTGTGTGTGATGGTGTGCTATCGTTGCACATGTGTGAAGGATTTGTA 4197
Qy 1301 GlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAla 1320
Db 4198 GGCCTGCATTGTGAACAGAGAGTCAATGATGCCAGTCAACCCATGCTTAATAATGCA 4257
Qy 1321 ValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThr 1340
Db 4258 GTCTGTGAAGACCAAGTGTGGGGATTCTTGTGCAAAATGCCACCTGGATTTTGGGTACC 4317
Qy 1341 ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCys 1360
Db 4318 CGATGTGAAGAAAGCTCGATGAGTGTCTCAGTCAGCCATGCAAAATGGAGCTACCTGT 4377
Qy 1361 LysAspGlyAlaAsnSerPheArgCysAlaAlaGlyPheThrGlySerHisCys 1380
Db 4378 AAGACGGTGCATAGCTTCAATGCCCTGTGTGAGCTGGCTTACAGGATCACACTGT 4437
Qy 1381 GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp 1400
Db 4438 GAATTTGAACATCAATGAATGTCAATTAATCAGTGTAGAAATCAGGCCACCTGTGTGGAT 4497
Qy 1401 GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr 1420
Db 4498 GAATTTAAATTCATACAGTTGTAAATGTCAAGCAGGATTTTTCAGGCAAAAGGTGTGAACA 4557
Qy 1421 GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet 1440
Db 4558 GACAGTCTACAGGCTTTAACTGTGATTTTGAAGTTTCTGGCATCTATGGATATGTCTATG 4617
Qy 1441 LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSer 1460
Db 4618 CTAGATGGCATGCTCCCATCTCTCAATGCTTAACCTGTACCTTCTGGATGAATCCTCT 4677
Qy 1461 AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr 1480
Db 4678 GACGACATGAATCTATGGAAACCAATCTCTATGAGTTGATTAACGGCAGGACCAATACC 4737
Qy 1481 LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGlyLysIleThr 1500
Db 4738 TTGCTCTGACTGATTAACGGCTGGGTCTTATGTGATGATGGCAGGGAAGATAACA 4797
Qy 1501 AsnCysProSerValAsnAspGlyArgTyrHisIleAlaIleThrTrpThrSerAla 1520
Db 4798 AACTGTCTCTCGTGAATGATGGCAGATGGCATCATATTGCAATCACTTGGCAAGTGCC 4857
Qy 1521 AsnGlyIleThrLysValTyrIleAspGlyLysLeuSerAspGlyValAlaGlyLeuSer 1540
Db 4858 AATGGCATCTGGAAGTCTATATCGAATGGGAAATATTCTGACGGTGGTGTCTGCTCTCT 4917
Qy 1541 ValGlyLeuProIleProGlyGlyValAlaLeuValLeuGlyGlnGlnAspLysLys 1560
Db 4918 GTTGTGTTGCCATACCTGTGTGGTGGTGTAGTCTCTGGGCAAGAGCAAGCAAAAA 4977
Qy 1561 GlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrp 1580
Db 4978 GGAGAGGGAATTCAGCCAGCTGAGTCTTTTGTGGGCTCCATGAAGCCAGCTCAACCTCTGG 5037
Qy 1581 AspTyrValLeuSerProGlnValLysSerLeuAlaThrSerCysProGluGluLeu 1600
Db 5038 GACTATGTCTGTCTCCACAGAGGTGAAGTCACTGGCTTACCTCTCTGCCAGAGGAACTC 5097
Qy 1601 SerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLys 1620
Db 5098 AGTAAAGGAACGTGTAGCATGGCTGATTTCTTGTGAGGAATTTGTGGGAAAGTGAAG 5157
Qy 1621 IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis 1640
Db 5158 ATCGATTTCTAGAGCATATTTTGTCTGATTTGCCCAACGCTTAGGAGGGGTCAAGTCCCTCAT 5217

Db 371 CGCGTGGCCATCGTGACCTTCTGTCCAAAGAACTACGTGGTCCGCCGCGTCATTACATC 430
Qy 141 SerThrArgArgAlaAargGlnHisLysCysAlaLeuLeuGlnGluLeuProAlaIle 160
Db 431 TCCACCGCGCGCGCGCCAGCACCAAGTGGCGTCTCTCCAAAGAGATCCCTGCCATC 490
Qy 161 SerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaGlnIleLeu 180
Db 491 TCCTACCGAGGTGGCGGCACCTACACCAAGGCGCTTCCAGCAAGCGCGCCAAATCTT 550
Qy 181 LeuHisAlaAargGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn 200
Db 551 CTTCAATGCTAGAGAAACTCAACAAAGTTGATTCTTCATCACTGATGATATTCCAAT 610
Qy 201 GlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThr 220
Db 611 GGGGGAGACCCCTAGACCAATTCAGCGCTCACTGCCGAGATTTCAGGAGTGGAGATCTTCACT 670
Qy 221 PheGlyIleThrGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu 240
Db 671 TTTGGCATATGGCAAGGGAACATTCGAGAGCTGAATGATGCTTCCACCCCAAGGAG 730
Qy 241 GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaAargArgAlaLeu 260
Db 731 GAGCACTGTACTCTCTACACAGTTTGAAGAAATTGAGGCTTTAGCTCGCCGGGCATTG 790
Qy 261 HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu 280
Db 791 CATGAAGATCTACCTTCTGGGAGTTTATTTCAGATGATATGCTCCACTGCTCTTATCTT 850
Qy 281 CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr 300
Db 851 TGTGATGAAGCGAGGACTGCTGTGACCGAATGGGAAGCTGCAAAATGGGGACACACACA 910
Qy 301 GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys 320
Db 911 GGCCATTTTGAAGTGCATCTGTGAAAAGGGGTATTACGGGAAGGTTCTGCAATGATGTC 970
Qy 321 ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyLysSerSerCys 340
Db 971 ACAGCTTCCCATCGGGACATACAAACCTGAAGGCTCACAGGAGGAATCAGCAGTTGC 1030
Qy 341 IleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCys 360
Db 1031 ATTCCATGTCTCTGATGAATAATCACACCTCTCCACCTGGGAAGCACATCCCTCAAGACTGT 1090
Qy 361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
Db 1091 GTCTGCAGAGAGGGATACGGGCATCTGGCCAGACTGTGAACCTGTGAACCTGCCCTGCC 1150
Qy 381 LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla 400
Db 1151 CTGAAGCCCTCCGAAAAATGGTTACTTTATCCAAAAACACTTGCACCAACCACTTCAATGCA 1210
Qy 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys 420
Db 1211 GCCTGTGGGTCCGATGTCAACCTGATTTGATCTTGTGGGAAGCAGCATCATCTATGT 1270
Qy 421 LeuProAsnGlyLeuTyrSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
Db 1271 CTACCCCATGTTTGTGGTCCGGTTCCAGAGACTACTGCAGAGTAAGAATGTTCTCAT 1330
Qy 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
Db 1331 CTCCGCCAGCCGAAACATGCCACATCAGCTGTCTTCAAGGGAATGTTATATAGACA 1390
Qy 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
Db 1391 ACATGTTTGGTTCCTGTGATGAAGGGTACAGCTAGAGAGGAGTGTATAGCTTACTTGT 1450
Qy 481 GlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGluArgHisCysSerThr 500

Db 1451 CAAGGAAACAGCCAGTGGGATGGCCAGAAACCCCGTGTGTGGAGCGCCACTGTGTTCCACC 1510
Qy 501 PheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys 520
Db 1511 TTTTCAGATGCCCAAGATATCAT 1570
Qy 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
Db 1571 TTTGGAGCAATCTGCTATGTAAGTTGCCGCCAAGGGTTCATTTTATCTGGAGTCAAGAA 1630
Qy 541 MetLeuArgCysThrThrSerGlyLysTyrAsnValGlyValGlnAlaAlaValCysLys 560
Db 1631 ATGCTGAGATGTACCACTTCTGGAAAAATGGAATGTCGAGTTTCAGGAGCTGTGTGTAA 1690
Qy 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln 580
Db 1691 GACGTGGAGGCTCTCTCAAAATCAACTGCTTAAGGACATAGAGGCTTAAGACTCTGGAAAC 1750
Qy 581 GlnAspSerAlaAsnValThrTyrGlnIleProThrAlaLysAspAsnSerGlyGluLys 600
Db 1751 CAAAGATTCTGCCAATGTTTACCTGGCAGATTCCACAGCTTAAGACAACCTCTGCTGAAAG 1810
Qy 601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620
Db 1811 GTGTCACTCCAGCTTCATCCAGCTTTCACCCCACTTACCTTTTCCCACTGGAGATGTT 1870
Qy 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
Db 1871 GCTATCGTATACACGGCAACTGACCTATCCGGCAACAGCCAGCTGCATTTTCCATATC 1930
Qy 641 LysValIleAspAlaGluProProValIleAspTyrCysArgSerProProValGln 660
Db 1931 AAGGTTATTGATGCAGAACCACTGTGCATAGACTGGTGCAGATCTCCACCTCCCGTCCAG 1990
Qy 661 ValSerGluLysValHisAlaIleSerThrAspGluProGlnPheSerAspAsnSerGly 680
Db 1991 GTCTCGGAGAGGTACATGCCCAAGCTGGGATGAGCCTCAGTTCTCAGACAACCTCAGGG 2050
Qy 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
Db 2051 GCTGAATTTGGTCAATTACCAAGAGTGCATACACAGGAGACTTTTCCCTCAGGGAGACT 2110
Qy 701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
Db 2111 ATAGTACAGTATACAGGCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATAT 2170
Qy 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
Db 2171 GTCATAAAAGGTTCTCCCTGTGAAATTCATTCACACCTGTAAATGGGATTTTATATGC 2230
Qy 741 ThrProAspAsnThrGlyValAlaAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
Db 2231 ACTCAGATAATACCTGGAGTCACTGTATTAACCTTGTCTGGAGGGCTATGATTTCA 2290
Qy 761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyr 780
Db 2291 GAAGGCTCTACTGACAGATATTATTGTCTTATGAAGATGGCGCTCTGGAACCAACATAT 2350
Qy 781 ThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
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Qy 801 GluMetPheTyrLeuAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGlu 820
Db 2411 GAGATGTTCTACAAAGCACTCGTGTGATGACACAGACTGTGATGAAGAGATTTTCTGAA 2470
Qy 821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
Db 2471 GCATTTGACAGCAGCCCTGGGAAAAATGGTCCCATCTTTTGTAGTGAAGAGATTTCTGAA 2530
Qy 841 AspCysArgLeuGluGlnAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
Db 2531 GACTGCAGACTGGAGGAGAACCTGACCAAAAAATATTGCTCTAGATATATATTATGACTAT 2590

QY 861 GluAenGlyPheAlaIleGlyProGlyGlyTTPGlyAlaAlaAenArgLeuAspTyrSer 880
DB 2591 GAAATGGCTTTGCAATTGGACACAGGTGGCTGGGGTGCAGCTAAATAGGGCTGGATTACTCT 2650
QY 881 TyrAspAspPheLeuAspThrValGlnGlnThrAlaThrSerIleGlyAsnAlaLysSer 900
DB 2651 TACGATGACTTCTGGACACTGTGCAGAAACAGCCACACAGCATCGGCATGCCAAGTCC 2710
QY 901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920
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QY 921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTTPGluAenGlnGln 940
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QY 941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
DB 2831 CGACTCTTTCAGACATGGAACTATCACAAATAACTGAAAGGACTTCAACAAGAC 2890
QY 961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGlu 980
DB 2891 CCCATGATTCTTTCAGCTTGCATCAGAAATACTTATAGCCGACAGCAATTCATTAGAA 2950
QY 981 ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal 1000
DB 2951 ACAAAAGAGGCTTCCCTCTTCGACAGCAGGCTCAGTGTGAGAGGGCTATGTGTGC 3010
QY 1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
DB 3011 AATGTCCCTTTGGGAACCTTATTATATCTGGAACTTTTACCTGTGAAAGCTGCCGATC 3070
QY 1021 GlySerTyrGlnAspGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr 1040
DB 3071 GGTATCTATCAAGATGAAGAGGCACTTGTAGTCAAGCTTTGCCCTCTGGGATGTAC 3130
QY 1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr 1060
DB 3131 ACGGAATATATTCATTCAAGAAACATCTCTGATTTGTAAGCTCAGTGTAAACAGGACCC 3190
QY 1061 TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLys 1080
DB 3191 TACTCAATACGTGGACTTGAGACTTGTGATCTGTCTCCACTGGGCACTTATCAGCCAAA 3250
QY 1081 PheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAla 1100
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QY 1101 ValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeu 1120
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QY 1121 MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
DB 3371 ATGGCTGTACCCATGCTCTGTGACTATTTACCACTTAATGCAGGAGGAGGCTTCTGC 3430
QY 1141 LeuAlaCysProPheTyrGlyThrProPheAlaGlySerArgSerIleThrGluCys 1160
DB 3431 CTGGCTGTCCCTTTTATGGAATACCCCATTCGCTGCTTCCAGATCCATCAGAAATGT 3490
QY 1161 SerSerPheSerSerThrPheSerAlaAlaGluGluSerValProProAlaSerLeu 1180
DB 3491 TCAAGTTTTAGTTCAACTTCTCAGCGGAGGAGGAAAGTGTGGTGGCCCCCTGCTCTCTT 3550
QY 1181 GlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn 1200
DB 3551 GGACATATTAAAGAGGAGCATGAAATCAGCAGTCAAGTTTTCCATGAATGCTTCTTTAAC 3610
QY 1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
DB 3611 CCTTCCCAATAGTGAACCTGCCAGCAACTTGGGGGTGTTATGTGTTGTCTCTGTCCA 3670

QY 1221 LeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCys 1240
DB 3671 CTTGGATATACAGGCTTAAAGTGTGAACACGACATCGATGAGTGCACCCACCTGCTTGC 3730
QY 1241 LeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGly 1260
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QY 1281 LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal 1300
DB 3851 AAAGGAATCTGTGTGATGGTGTGGCTGCTATCGTGCACATGTGTGAAAGGATTTGTA 3910
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QY 1321 ValCysGluAspGlnValGlyPheLeuCysLysCysProProGlyPheLeuGlyThr 1340
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QY 1361 LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys 1380
DB 4091 AAAGACGTTGCCAATAGCTTCAGATGCTGTGTGCAGCTGCTTCAAGGATCACACTGT 4150
QY 1381 GluLeuAsnIleAsnGlnCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp 1400
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DB 4271 GAACAGCTACAGGCTTTAACTTGGATTTTGAAGATTTCTGSCATCTATGGATATGTGTCATG 4330
QY 1441 LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetLysSerSer 1460
DB 4331 CTAGATGGCATGTCTCCATCTCTCCATGCTTCAACCTGTACCTTCTGGATGAATTCCTCT 4390
QY 1461 AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr 1480
DB 4391 GACGACATGAACTATGGAAACCCANCTCTATTCAGTTGNTAAAGCGACGACACATACC 4450
QY 1481 LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThr 1500
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QY 1521 AsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer 1540
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 Db 4811 AGTAAGGAACAGTGTAGCATGGCTGATTTCTTGTTCAGGATTTGGGGAAAGTGAAG 4870
 Qy IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis 1640
 Db 4871 ATCGATTCTAAGAGCATATTTGTTCTGATTGCCACCGCTTAGGAGGGTCAGTGGCTCAT 4930
 Qy LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro 1660
 Db 4931 CTGAGAACTGCAATCTGAAGATTTAAAGCCAGGTTCCAAAGTCAATCTGTTCTGTGATCCA 4990
 Qy GlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGln 1680
 Db 4991 GGCTTCAGCTGGTGGGAAACCTGTGTCAGTACTGTCTGATCAAGACAGTGGACACA 5050
 Qy ProLeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPhe 1700
 Db 5051 CCACCTTCCTCACTGTGAACGCAATAGCTGTGGGTGCCACCTCTCTTGGAGAAATGGCTTC 5110
 Qy HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr 1720
 Db 5111 CATTCAGCCGATGACTTCTATGCTGTCGACAGTAACTTACCAGTGCACAAATGGCTTAC 5170
 Qy TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTyrAsnGlyValSer 1740
 Db 5171 TATCTATTGGGTGACTCAGGATGTTCTGTACAGATATGGAGCTGGACGGCGTTTCA 5230
 Qy ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer 1760
 Db 5231 CCATCTCGCTTGTATGTCGATGAGTGCAGTTCGATTCAGATTTGATGAGCATGCTTCT 5290
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 Db 5291 TGCTTGAACTGAGTGAATCTTACATATGTTCTATGTGTCACCGTCCAGGATGGG 5350
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 Db 5351 AAAAATCTGTCAGAACTTATAAATGTAAGTCTCAGGAATCCGAAATGGCCACTCC 5410
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 Db 5411 TCAGGTGAGATTTATACAGTAGTGTCCGAAAGTCAATTTTGTGTGTCAGGAGGATACCAG 5470
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 Db 5471 TTGATGGAGTAAACCAAAATACATGTTTGGAGTCTGGAGATGGAAATCACTAATACCA 5530
 Qy TyrCys 1842
 Db 5531 TATTGT 5536
 RESULT 3
 ID ABT08491 standard; cDNA; 11152 BP.
 AC ABT08491;
 XX 28-NOV-2002 (first entry)
 DT Human novel protein NOV2b coding sequence SEQ ID NO: 7.
 DE Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;
 KW antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory;
 KW haemostatic; hypotensive; neuroprotective; anorectic; nootropic;
 KW antidepressant; immunosuppressive; antibacterial; antiparasitic;
 KW viricide; tranquilizer; anticonvulsant; osteopathic; analgesic;
 KW antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
 KW antiaddictive; gene; ss.

OS Homo sapiens.
 PN WO200259315-A2.
 XX 01-AUG-2002.
 XX 19-DEC-2001; 2001WO-US050076.
 XX 19-DEC-2000; 2000US-0256619P.
 PR 19-JAN-2001; 2001US-0262959P.
 PR 28-FEB-2001; 2001US-0272408P.
 PR 20-APR-2001; 2001US-0285189P.
 PR 26-JUL-2001; 2001US-0308039P.
 PR 09-AUG-2001; 2001US-0311266P.
 XX (CURA-) CURAGEN CORP.
 PA Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U;
 PI Shenoy S, Spytek KA, Gangolli E, Miller C, Boldog P, Li L;
 PI Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD;
 PI Thernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
 PI Rothenberg M;
 XX WPI: 2002-666903/71.
 DR P-PSDB; ABJ10590.
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
 PT or Alzheimer's disease.
 XX Claim 8; Page 43-45; 363pp; English.
 PS The present invention provides the protein and coding sequences of
 CC several novel human proteins, designated NOVX. These can be used in the
 CC treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-
 CC Lindau syndrome, Alzheimer's disease, stroke, tuberculous sclerosis,
 CC hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral
 CC palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia
 CC telangiectasia, leukodystrophies, addiction, anxiety, depression, pain,
 CC obesity, Crohn's disease, osteoporosis, inflammatory bowel disease,
 CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,
 CC diabetes, pancreatitis, autoimmune disease, asthma, arthritis,
 CC immunodeficiencies, HIV, viral, bacterial or parasitic infections, or
 CC graft-versus-host disease. The present sequence is a coding sequence of
 CC the invention
 SQ Sequence 11152 BP; 2951 A; 2606 C; 2711 G; 2884 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 11152
 Score: 9862.00 Matches: 1781
 Percent Similarity: 97.72% Conservative: 16
 Best Local Similarity: 96.85% Mismatches: 40
 Query Match: 96.51% Indels: 2
 DB: 6 Gaps: 1
 US-09-977-053-6 (1-1842) x ABT08491 (1-11152)
 Qy 4 ArgLeuAlaPheCysCysTrpGlyLeuAlaLeuValSerGlyTrpAlaThrPheGln 23
 Db 83 AGAATTTGCGGGCTTGTGGGTCTGGGCTCTGCTTTCGGGCTGGGCGACCTTTCAGCAG 142
 Qy 24 MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro 43
 Db 143 ATGTCCCGTCGCAATTTTCAGCTTCCGCTCTTCCCGGAGACCGCGCGGGGCCCC 202
 Qy 44 GlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArgValGluArg 63
 Db 203 GGGAGTATCCCGCGCGCGCTCTCTGCGGAGAAAGCGCGGAGAGGTGGAGCGG 262
 Qy 64 LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu 83

Db 263 CTGGCCAGGCGCTC-----CGCGTCGGCTGCTCGGGAGCTCAGCGAGCGCTCGGAG 316
Qy 84 LeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArgSerGluLeu 103
Db 317 CTTGCTCTCTCGTGGATGATTTGCTCAGCGTGGCGGAAGTCAACTTCCGCGAGCGAGCTC 376
Qy 104 MetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThrArgValAla 123
Db 377 ATGTTCTGTCGCGAAGCTGCTGTCGACTTCCCGTGGTCCCAAGCGCAAGCGCGTGGCC 436
Qy 124 IleValThrPheSerSerLysAsnThrValValProArgValAspTyrIleSerThrArg 143
Db 437 ATCTGTGACCTTCTCTGTCCAAGAACTACGTGGTGGCGGCTGCAATTACATCTCCACCGC 496
Qy 144 ArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIlePheProAlaIleSerTyrArg 163
Db 497 CGCGCGCGCCAGCACAAAGTGGCGCTGCTCTCCAAAGAGATCTCTCCCATCTCTACCGA 556
Qy 164 GlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAla 183
Db 557 GTGGCGGACCTTACNCCAAAGGGCGCTTCCAGCAAGCGCGCAAAATCTCTTTCATGCT 616
Qy 184 ArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAsp 203
Db 617 AGAGAAAACTCAACAAAGTTGTAATTTCTCATCTGATGATATTTCCAAATGGGGGAGAC 676
Qy 204 ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle 223
Db 677 CCTAGACCAATTCAGCGCTCAGTGGAGATTCAGGAGTGGAGATCTTTCATCTTTTGGCATA 736
Qy 224 TrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCys 243
Db 737 TGGCAAGGAGACATTCGAGAGCTGAATGACATGGCTTCCACCCCAAGGAGGAGCACTGT 796
Qy 244 TyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeuHisGluAsp 263
Db 797 TACCTGCTACACAGATTTTGAAGAAATTTAGGCTTTAGCTCGCGGGCAATTTGCATGAAGAT 856
Qy 264 LeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeuCysAspGlu 283
Db 857 CTACCTTCTGGAGATTTTATTTCAAGATGATATGCTCCACTGCTCATATCTTTGTGAGAG 916
Qy 284 GlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThrGlyHisPhe 303
Db 917 GCGAGAGACTGCTGTGACCGAATGGAGACTGCAATGCGGACACACACAGGCCCATTTT 976
Qy 304 GluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCysThrAlaCys 323
Db 977 GAGTGCATCTGTGAAAGGGGTATTACGGGAAAGTCTGCAGTATGAATGCACAGCTTGC 1036
Qy 324 ProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCysIleProCys 343
Db 1037 CCATCGGGGACATACAAACCTTGAAGCCTCACCAGGAGGAATCAGCAGTTGCATTCATGT 1096
Qy 344 ProAspGluAsnHisThrSerProGlySerThrSerProGluAspCysValCysArg 363
Db 1097 CCGATGAAATATCACACCTCTCCACTCGAGAGACATCCCTCGAAGACTGTGTCTGCAGA 1156
Qy 364 GluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuLysPro 383
Db 1157 GAGGGATACAGGGCATCTGGCCAGACTGTGAACTTTGTCTCACTGCTGCGCTTGAAGCCT 1216
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Db 1217 CCGCAAAATTTGTTACTTTTATCCAAACACTTGCACCAACCACTTCAATGAGCCTGTGG 1276
Qy 404 ValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuProAsn 423
Db 1277 GTCCGATGTACCTCGATTTGATCTTTGGGAGAGAGATCATCTTATGTCTACCCAAAT 1336
Qy 424 GlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHisLeuArgGln 443
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Qy 484 SerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThrPheGluMet 503
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Db 1637 ATCTGCTATGTAAGTTGCCCAAGGGTTCTATTTATCTGGAGTCAAGAAATGCTGAGA 1696
Qy 544 CysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLysAspValGlu 563
Db 1697 TGTACCACCTTCTGGAAATGGAATGTCGGAGTTTCAGGACCTGTGTGTAAGACGTGGAG 1756
Qy 564 AlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGlnAspSer 583
Db 1757 GCTCTCAATCAACTGCTCTAAGGACATAGAGCTTAAGACTCTGGAAACAGCAAGATTCT 1816
Qy 584 AlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysValSerVal 603
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Qy 604 HisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspValAlaIleVal 623
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Qy 624 TyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIle 643
Db 1937 TACACGGCAACTGACCTATCCGGCAACCCAGCCAGCTGCATTTTCCATATCAGGTTATT 1996
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Db 2057 AAGGTACATGCCCAAGCTGGGATGAGCCTCAGTTCTCAGACCACTCAGGGGCTGAATTG 2116
Qy 684 ValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGln 703
Db 2117 GTCATTTCCAGAACTCATACAGAGGAGACTTTTCCCTCAGGGGAGACTATAGTACAG 2176
Qy 704 TyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLys 723
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 QY 984 AlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysPro 1003
 DB 3017 GCTTCCCTCTTCGACAGACAGGCTCAGTGTGTGAGAGGGCGTATGTGTGATCAATTTGCCCT 3076
 QY 1004 LeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyr 1023
 DB 3077 TTGGGAACCTATTAATCTGAAACATTTACCTGTGAAAGCTGCGGATCGATGCCCTAT 3136
 QY 1024 GlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyr 1043
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 QY 1044 IleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyr 1063
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 QY 1064 SerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySer 1083
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 QY 1084 ArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIle 1103
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RESULT 4
ABT08490
ID ABT08490 standard; cDNA; 11158 BP.
XX
AC ABT08490;
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DT 28-NOV-2002 (first entry)
XX
DE Human novel protein NOV2a coding sequence SEQ ID NO: 5.
XX
KW Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;

KW antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory;
KW haemostatic; hypotensive; neuroprotective; anorectic; nootropic;
KW antidepressant; immunosuppressive; antibacterial; antiparasitic;
KW virucide; tranquilizer; anticonvulsant; osteopathic; analgesic;
KW antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
KW antiaddictive; gene; ss.
XX Homo sapiens.
XX
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PH Key Location/Qualifiers
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FT variation /*tag= b
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FT variation replace(9551,A)
FT variation /*tag= h
FT variation replace(9790,T)
FT variation /*tag= i
FT variation replace(10025,G)
FT variation /*tag= j
XX W0200259315-A2.
XX
XX 01-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050076.
XX
XX 19-DEC-2001; 2000US-0256619P.
PR 19-JAN-2001; 2001US-0262959P.
PR 28-FEB-2001; 2001US-0272408P.
PR 20-APR-2001; 2001US-0285189P.
PR 26-JUL-2001; 2001US-0308039P.
PR 09-AUG-2001; 2001US-0311266P.
XX
XX (CURA-) CURAGEN CORP.
XX Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U;
PI Shenoy S, Spytek KA, Gangolli E, Miller C, Boldog F, Li L;
PI Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD;
PI Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
PI Rothenberg M;
XX
XX WPI; 2002-666903/71.
DR P-PSDB; ABJ10589.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
PT or Alzheimer's disease.
XX
XX
PS Claim 8; Page 38-41; 363pp; English.
XX
XX The present invention provides the protein and coding sequences of
CC several novel human proteins, designated NOVX. These can be used in the
CC treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-
CC Lindau syndrome, Alzheimer's disease, stroke, tuberosus sclerosis,
CC hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral
CC palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia,
CC telangiectasia, leukodystrophies, addiction, anxiety, depression, pain,
CC obesity, Crohn's disease, osteoporosis, inflammatory bowel disease,
CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,
CC diabetes, pancreatitis, autoimmune disease, asthma, arthritis,
CC immunodeficiencies, HIV, viral, bacterial or parasitic infections, or

CC graft-versus-host disease. The present sequence is a coding sequence of
XX the invention
SQ Sequence 11158 BP; 2952 A; 2603 C; 2710 G; 2893 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	11158
Score:	9812.00	Matches:	1774
Percent Similarity:	97.23%	Conservative:	16
Best Local Similarity:	96.36%	Mismatches:	47
Query Match:	96.02%	Indels:	4
DB:	6	Gaps:	2

US-09-977-053-6 (1-1842) x ABT08490 (1-11158)

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Qy	24	MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro	43
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Qy	44	GlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArgValGluArg	63
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Qy	64	LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu	83
Db	263	CTGGCCACGCGCTTC-----CGGTGGCGGTCTGGCGGAGCTCAGCGAGCGCTGGAG	316
Qy	84	LeuValPheLeuValAspAspSerSerValGlyGluValAlaAsnPheArgSerGluLeu	103
Db	317	CTTGCTCTTCTGGTGGATGATTCGTCCAGCGTGGCGGAGTCAACTTCCGACGAGCTC	376
Qy	104	MetPheValArgLeuLeuSerAspPheProValValProThrAlaThrArgValAla	123
Db	377	ATGTTCGTCCGACGCTCTGTCGACTTCCCGTGGTGGCCGACCGCCGCGCGTGGCC	436
Qy	124	IleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIleSerThrArg	143
Db	437	ATCGTGACCTTCTCGTCCAGAACTACGTGTGGCGCGCTCGATTACATCTCCACCCGC	496
Qy	144	ArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIleProAlaIleSerThrArg	163
Db	497	CGCGCGCCACGACAGTGGCGCTGCTCTCCAGAGATCTCCCTGCCATCTCTTACCGA	556
Qy	164	GlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAla	183
Db	557	GGTGGCGGACCTACACGAGGCGCTTCCAGCGAGCGCGGCAAAATCTTCTTCATGCT	616
Qy	184	ArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAsp	203
Db	617	AGAGAAACTCAACAAAGTTGTATTTCTCTCACTGATGATATTCATATGGGGAGAC	676
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Db	677	CCTAGACCAATTCAGCGCTCATCTCGAGATTCAGAGTGGAGATCTTCACATTTTGGCATA	736
Qy	224	TrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCys	243
Db	737	TGGCAGGGAACTTCGAGACTGATGACATGCGCTTCACCCCAAGAGAGGAGCACTGT	796
Qy	244	TyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArg-----ArgAlaLeuHis	261
Db	797	TACCTGTACACAGTTTTTGAAGAAATTCAGGCTTTAGTGGCGCTCTGTGCATATGTTATT	856
Qy	262	GluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeuCys	281
Db	857	GTAGATCTACCTTCCTGGGAGTTTATTCAGATGATATGGTCCACTGCTCATATCTTTGT	916
Qy	282	AspGluGlyLysAspCysAspArgMetGlySerCysLysCysGlyThrHisThrGly	301

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Db	977	CATTTTGAGTGCACTGTGTGAAAAGGGGTATAACGGGAAAGGTCTGACGATGATGCAACA	1036
Qy	322	AlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCysIle	341
Db	1037	GTTTGGCCATCGGGACATACAACTGAAAGCTCACAGGAGGATCAGCAGTTGCATT	1096
Qy	342	ProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAspCysVal	361
Db	1097	CCATGTCTCTGATGAAATCATCACCTCTCCACTGGAGCACATCCCTCTGAAGCTGTGTC	1156
Qy	362	CysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeu	381
Db	1157	TGCAGAGGGATACAGGGCATCTGGCCAGACCTGTGAAGTTGTCCACTGCCCTGCCCTG	1216
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Db	1217	AAGCTTCCGGAATGTTACTTTATCCAAAACACTTGCACACACCACTTCAATGCAGCC	1276
Qy	402	CysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeu	421
Db	1277	TGTGGGGTCCGATGTCACCTCTGATCTGTGGGAAGCAGCATCATCTTATGTCTTA	1336
Qy	422	ProAsnGlyLeuThrSerGlySerGluSerTyrCysArgValArgThrCysProHisLeu	441
Db	1337	CCCAATGGTTTGTGGTCCGGTTCAGAGAGCTACTGCAGAGTAAGAACATGCTCTCATCTC	1396
Qy	442	ArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThrThr	461
Db	1397	CGCCAGCGGAAACATGGCCACATCAGCTGTCTACAGGGGAAATGTTATATAGACACA	1456
Qy	462	CysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCysGln	481
Db	1457	TGTTTGGTGGCTGTGATGAAGGGTACAGGCTAGAAAGCAGTGATAAGCTTACTTGTCAA	1516
Qy	482	GlyAsnSerGlnThrAspGlyProGluProArgCysValGluArgHisCysSerThrPhe	501
Db	1517	GGAAACAGCCAGTGGGATGGGCCAGAACCCCGGTGTGTGGAGCGCCACTGTTCACCTTT	1576
Qy	502	GlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPhe	521
Db	1577	CAGATGCCCAAGATGTCTATCATATCCCCCACAACCTGTGGCAAGCAGCCAGCAATTT	1636
Qy	522	GlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGluMet	541
Db	1637	GGGACGATCTGCTATGTAAGTTGCGCCCAAGGGTTTCATTTTATCTGGAGTCAAGAAATG	1696
Qy	542	LeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLysAsp	561
Db	1697	CTGAGTGTACCCCTCTCGGAAATGGAAATGTGGAGTTTCAGGCAGCTGTGTGTAAGAC	1756
Qy	562	ValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGlnGln	581
Db	1757	GTGAGGCTCTCAANTCAACTGTCTTAAGGACATAGAGGCTAAGACTCTGGAACAGCAA	1816
Qy	582	AspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyLysVal	601
Db	1817	GATTCTGCCAATGTATCTGGCAGATTCCAACAGCTAAAGACAACTCTGTGTGAAAGGTG	1876
Qy	602	SerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspValAla	621
Db	1877	TCAGTCCACGTTTCATCCAGCTTTTCCACCTTACCTTTCCTTTCCTTTCCTTTCCTT	1936
Qy	622	IleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLys	641
Db	1937	ATCGTATACAGGCACATGACCTATCCGCAACCCAGCCAGCTGCAATTTTCCATATCAAG	1996
Qy	642	ValIleAspAlaGluProProValIleAspTrpCysArgSerProProProValGlnVal	661
Db	1997	GTTATTTGATGCAGAACCACTGTCTATAGACTGGTGCAGATCTCCACCTCCCTCCAGGTC	2056

QY 662 SerGluYsValHisAlaSerTrpAspGluProGlnPheSerAspAsnSerGlyAla 681
DB 2057 TCGGAGAGGTACATGCGCAAGCTGGATGAGCCTCAGTTCTCAGACAACCTCAGGTGCT 2116
QY 682 GluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIle 701
DB 2117 GAATTTGGTCATTAACCAAGAGTATACACAGGAGACCTTTTCCCTCAAGGGGAGACTATA 2176
QY 702 ValGlnTrpThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleVal 721
DB 2177 GTACAGTATACAGCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATTGTC 2236
QY 722 IleIysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThr 741
DB 2237 ATAAAAGGTTCTCCCTGTGAAATTCATTCACACCTGTAAATGGGAATTTTATATGCAC 2296
QY 742 ProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGlu 761
DB 2297 CAGATATATCTGGAGTCAACTGTACATTAACTTGTCTGGAGGGCTATGATTTTCAGAA 2356
QY 762 GlySerThrAspIysTyrCysAlaTyrGluAspGlyValTrpIysProThrTyrThr 781
DB 2357 GGGTCTACTGCAAGTATTATTTGCTTATGAGATGGCGTCTGGAACCAACATATACC 2416
QY 782 ThrGluTrpProAspCysAlaIysLysArgPheAlaAsnHisGlyPheLysSerPheGlu 801
DB 2417 ACTGAATGGCCAGACTGTGCGTAAGCGTTTTCACAAACCAACCGGTTTCAAGTCTCTTGAG 2476
QY 802 MetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAla 821
DB 2477 ATGTTCTACAAAGCGCTCGTTGTGTATGATGACACAGATCTGATGAAGAATTTTCTGAAGCA 2536
QY 822 PheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAsp 841
DB 2537 TTTGAGACGACCTCGGAAAAATGGTCCCATCATTTTGTAGTGTATGACAGGACATTTGAC 2596
QY 842 CysArgLeuGluGluAsnLeuThrLysLysCysLeuGluTyrAsnTyrAspTyrGlu 861
DB 2597 TGCAGACTGGAGAGAACCTTGACCAAAAAATATTTGCTTGAATATAATTTATGACTATGAA 2656
QY 862 AsnGlyPheAlaIleGlyProGlyGlyTrpGlyAlaAlaAsnArgLeuAspTyrSerTyr 881
DB 2657 AATGGCTTTGCAATTTGTCAGGTGGCTGGGTGCGAGTAAAGCTGGATTAATCTCTTAC 2716
QY 882 AspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSerSer 901
DB 2717 GATGACTTCTCGACACTGTGCAAGAAACAGCCACAGCATCGGCAATGCCAAGTCCCTCA 2776
QY 902 ArgIleIysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIleThr 921
DB 2777 CGGATTAAGAAGAGTGGCCCATTTATCTGACTATAAATAATTAAGTTAAATTTTAAACATCA 2836
QY 922 AlaSerValProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGlnArg 941
DB 2837 GCTAGTGTGCCATTACCGATGAAGAAATGATACCTTGAATGGGAAAAATCAGCAAGCA 2896
QY 942 LeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspPro 961
DB 2897 CTCCTTCAGACATTTGGAACATATACAAATAAACTGAAAAAGGACTCTCTCAACAAAGACCCC 2956
QY 962 MetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThr 981
DB 2957 ATGTATTCTCTTTCAGCTTGCATCAGAAATATCTATTATAGCCGACAGCAATTCATTAGAAACA 3016
QY 982 LysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsn 1001
DB 3017 AAAAAGGCTTCCCTTCTGCAGACCGAGCTCAGTGTGTGAGAGGGCGTATGTGTGTCAT 3076
QY 1002 CysProLeuGlyThrTyrThrAsnLeuGluHisPheThrCysGluSerCysArgIleGly 1021
DB 3077 TGGCCCTTTGGGAACCTATTATATCTGGAACATTTTACCTGTGAAAGCTGCCGGATCGGA 3136

QY 1022 SerTyrGlnAspGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThr 1041
DB 3137 TCCATTCAGATGAAGAGAGGCAACTTGAATGCGAGCTTTGCCCTCTGGGATGACAGC 3196
QY 1042 GluTyrIleHisArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
DB 3197 GAATATATCCATTCAAGAAACATCTCTGATTGTAAGCTCAGTGTATAACAAGGACCTAC 3256
QY 1062 SerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPhe 1081
DB 3257 TCATACAGTGGACTTGAGACTTGTGAATCGTGTCCACTGGGCACCTATTACGCCAAAAATTT 3316
QY 1082 GlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaVal 1101
DB 3317 GGTTCGCCGAGCTCCCTCTCTGTCTCAGAAAAACCTCACTGTGAAAAAGAGGCCGTG 3376
QY 1102 AsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMet 1121
DB 3377 AACATTTCTGCATGTGGAGTTCTTGTCCAGAGGAAAAATTTCTGCGTTCTGGGTAAATG 3436
QY 1122 ProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeu 1141
DB 3437 CCCTGTCAACCATGTCTCGTGAATATTACCAACCTAATGAGGAGAGCCCTTCTGCCTG 3496
QY 1142 AlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSer 1161
DB 3497 GCCGTCCCTTTATGAACTTACCCCATTCCTGTGTTCCAGATCCATCAGAGATGTTCA 3556
QY 1162 SerPheSerThrPheSerAlaAlaGluSerValValProProAlaSerLeuGly 1181
DB 3557 AGTTTATAGTTCACTTTCTCAGCGGAGAGGAAAGTGTGTGTCGCCCTCTCTTGA 3616
QY 1182 HisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnPro 1201
DB 3617 CATATTAAAGAGGACATGAATCAGCAGTCAGGCAAGTCATGAATGCTTCTTTAAACCT 3676
QY 1202 CysHisAsnSerGlyThrCysGlnGluLeuGlyArgGlyTyrValCysLeuCysProLeu 1221
DB 3677 TGCACACATAGTGNACCTGCCAGCACTTGGGCGTGGTATGTTTGTCTCTGTCCACTT 3736
QY 1222 GlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeu 1241
DB 3737 GGAATACAGGTTTAAAGTGTGAAACAGACATCGATGATGTCAGCCACCTGCTTGCCTC 3796
QY 1242 AsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyr 1261
DB 3797 AACAAATGGAGTTTGTAAAGACCTAGTTGGGGAATTCATTTGTGAGTCCCATCAGGTAC 3856
QY 1262 ThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLys 1281
DB 3857 ACAGGTAAACACTGTGAAATTCAGATCAATGAATGTCACTCAATCCATGTAGAATCAG 3916
QY 1282 GlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGly 1301
DB 3917 GCCACCTGTGTGGATGAATTAATTCATACATGTTGTAATGTGAGCCAGGATTTTCAGGC 3976
QY 1302 LeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaVal 1321
DB 3977 AAAAGGTGTGAACAGGTATGTATCAACTCAGTGTGTTATTAATACCTTTAATATGAGCTC 4036
QY 1322 CysGluAspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThrArg 1341
DB 4037 TGTGAAGACCAAGTTGGGGGATCTTGTGCAAAATGCCCACTGGATTTTGGGTACCGCA 4096
QY 1342 CysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLys 1361
DB 4097 TGTGGAAGAACCTGCGATGATGCTCTCAGTCAGCCATGCAAAAATGGAGCTACCTGTATA 4156
QY 1362 AspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGlu 1381
DB 4157 GAGGGTCCCAATAGCTTCAGGTGCTGTGTGACGTGCTTTCAGAGATCACTGTGAA 4216
QY 1382 LeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu 1401

Claim 1; Fig 2A-2H; 20pp; English.

The invention relates to C3b/C4b complement receptor (CR)-like protein and its corresponding nucleic acid sequence. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, graft versus host disease, nervous system disorders (e.g. stroke, Alzheimer's disease), ischaemic conditions (e.g. atherosclerosis, stenosis, myocardial infarction, and ischaemia), metabolic disorders (e.g. obesity and diabetes); and reproductive disorders and infertility. The C3b/C4b CR-like nucleic acid molecules are used in gene therapy. The present sequence is mouse C3b/c4b CR-like cDNA

Sequence 11230 Bp: 2714 A; 2981 C; 2886 G; 2648 T; 0 U; 1 Other:

Db 1913 CAGCAGGACTCTGCTTAATGCCACCTGGGAGTCCCAACAGCTTAAGACCACTCTGTGTGA 1972
 Qy LysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp 619
 Db 1973 AAGGTGTCACTGCTCCAGCTCCAGCCAGCTTTACCCCACTTACCTCTTCCCAATTGGAGAC 2032
 Qy 620 ValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHis 639
 Db 2033 GTGGCCATCACCTACAGCGCAACCCAGCTCATCCGTAACCAAGCCAGCTGCACTTCTTAC 2092
 Qy 640 IleLysValIleAspAlaGluProProValIleAspTyrCysArgSerProProVal 659
 Db 2093 ATTAAAGTCATTGATGTGGAAACCGCTGTCATAGATTGTGTGCGATCTCCACCTCCATC 2152
 Qy 660 GlnValSerGluLysValHisAlaIleAspIleAspGluProGlnPheSerAspAsnSer 679
 Db 2153 CAGGTGCTAGAGAGAGCACCCTGCAAGCTGGGATGAGCCTCAGTCTCTCAGACCACTCC 2212
 Qy 680 GlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGlu 699
 Db 2213 GGGGCTGAATTGCTCAATACCAAGCAGTGCACACAGGGCGCATGTTTCTCATGGGGAA 2272
 Qy 700 ThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHis 719
 Db 2273 ACGGTGCTGTGTACACAGCCACTGACCCCTCAGGCAACACAGGACCTGTGACATCCAC 2332
 Qy 720 IleValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIle 739
 Db 2333 ATTGTCAATAAAGTTCTCCCTGTGAGTCCCTTCACCCCTGTAAACGGGACCTTTATC 2392
 Qy 740 CysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPhe 759
 Db 2393 TGTGCCAGGATAGTGTCTGGAGTAACTGTAGCTGAGCTGCAAGGAGGCTATGATTTTC 2452
 Qy 760 ThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThr 779
 Db 2453 ACAGAAAGGTCACTCAGAGAGTACTACTGTCTTTTGAAGTGTATCTGGAGACCAACA 2512
 Qy 780 TyrThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSer 799
 Db 2513 TACTCTACAGAAATGCCAGACTGTGTATATAAACGTTTTCACAAACCATGTTTCAAGTCC 2572
 Qy 800 PheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSer 819
 Db 2573 TTTGAAATGCTATACAAAACCACTCGCTGTGATGACATGATCTGTTTGAAGATTTCCT 2632
 Qy 820 GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
 Db 2633 GCAGCAATTTGAGACTACCTTGGGGAACATGTCCTCCCTTTTGTAAACGATGCTGATGAC 2692
 Qy 840 IleAspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAsp 859
 Db 2693 ATTGACTGCAGACTGGAGGAC---CTGACCAAAATACTGTCATCGATATATATACAC 2749
 Qy 860 TyrGluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyAlaAlaAsnArgLeuAspTyr 879
 Db 2750 TATGAAATGGCTTTGCAATTGGACAGAGGCTGGGGTGCAGGCAACAGGCTGGATTAT 2809
 Qy 880 SerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLys 899
 Db 2810 TCTACGATCACTTCTCGATGTTGTACAGAAACACCCACCGATGTGGGCAAGGCCAGA 2869
 Qy 900 SerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsn 919
 Db 2870 TCGTCACGGATTAAGAAAGTGTCCCATGTCGTGACCCCAAAATTCAGCTAATTTTAAAC 2929
 Qy 920 IleThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGln 939
 Db 2930 ATCAGAGCTAGCGTGCCTCCAGAGGAAAGAACGATACCCCTGAAATTGGAGAAATCAG 2989
 Qy 940 GlnArgLeuGlnThrLeuGluThrIleThrAsnLysLysLysArgThrLeuAsnLys 959

Db 2990 CAGCGACTCATTTAAGACATTGGAAAACAAATCAACCAATCGCTGAAAAGCACCTTTGAATAAA 3049
 Qy 960 AspProMetTyrSerPheGlnLeuAlaSerGluIleLeuAlaAspSerAsnSerLeu 979
 Db 3050 GAGCCCAATGATATCTTTTCAGCTCGCCTCGAAAACAGTGTGGTGTGACAGCAATTCCTC 3109
 Qy 980 GluThrLysLeuAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCys 999
 Db 3110 GAAAACAGAAAGGCTTTTCTCTCTGCAGACAGGCTCTGTGCTGAGGGGGCGCATGTGT 3169
 Qy 1000 ValAsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArg 1019
 Db 3170 GTCAACTGCCCTCGGAACTCTTACTCTCTGAGCAATTCACCTGTGTGAAGCTGCCTC 3229
 Qy 1020 IleGlySerTyrGlnAspGluGlyGlnLeuGluCysLysLeuCysProSerGlyMet 1039
 Db 3230 ATGGGATCTTACCAAGATGAAGAGGCGAGCTGGAATGCAAGCTCTGTCTCCCAAGACT 3289
 Qy 1040 TyrThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGly 1059
 Db 3290 CACCGGATATCTCCATTCAGAGAGGCTCTCTGAATGCAAGCTCAGTGTAAAGCAAGGC 3349
 Qy 1060 ThrTyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnPro 1079
 Db 3350 ACTACTCTTCCAGTGGGCTGGAGACTTGCATCGTGTCCGCTGGGTACTTATCAACCG 3409
 Qy 1080 LysPheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGly 1099
 Db 3410 GAATTTGGATCCCGAGCTGCCCTCTATGCCCCAGAAACCAACCAAGCGTGAAGAGGA 3469
 Qy 1100 AlaValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGly 1119
 Db 3470 GCGGTGACATCTCTCTGTGTGGAGTCCCTGTGCCAGTAGAGAGATTTCTCCGTTCTGG 3529
 Qy 1120 LeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPhe 1139
 Db 3530 CTAAACCCCTGCTACCTTGCCTCGAGACTATTACCAACCCCAATGACGAGAGTCTCTTC 3589
 Qy 1140 CysLeuAlaCysProPheTyrGlyThrProPheAlaGlySerArgSerIleThrGlu 1159
 Db 3590 TGCCTCGCTGTCTCTTTATGGAACCTACAAACCATCTCTGCGCCAGCTCTCTCATCAGAC 3649
 Qy 1160 CysSerSerPheSerThrPheSerAlaAlaGluSerValValProProAlaSer 1179
 Db 3650 TGTCTCAAGTTTACTCTTCTCAGCAGCAGAGAGAAAGCATAGTGCCTCTGTCGCC 3709
 Qy 1180 LeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePhe 1199
 Db 3710 CCTGAGCATTTCCAGAACCAAGTACGAAGTCAGCAGTCAGGTCTTTTCAAGATGCTTCTTA 3769
 Qy 1200 AsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCys 1219
 Db 3770 AACCCCTGCCAACACAGTGGAACTCTCCAAACAGCTTGGGGTGTGTATGTCTGTCTG 3829
 Qy 1220 ProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuPro 1239
 Db 3830 CCACCTGGATACAGGCTTAAGTGTGAACAGATATTGATGAATCAGCTCTCTGCTCT 3889
 Qy 1240 CysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheLysCysGluCysProSer 1259
 Db 3890 TGCCTCAATGTGGAATTTGTAGAGACCAAGTTGGGGGATTTACGCTGCGAATGTTCAATG 3949
 Qy 1260 GlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeu 1279
 Db 3950 GGCTATTTCAGGTCAATATGTGAAGAAATATTAATGAGTGTATCTCAGGCCCTTGTCTTA 4009
 Qy 1280 AsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPhe 1299
 Db 4010 AATAAGGAACTGCACTGACGCTGGCAAGCTTACCGCTGTACCTGTGTGAAAGGATAC 4069
 Qy 1300 ValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsn 1319
 Db 4070 ATGGGTGTGCACTGTGAAAACAGACGTCATGAATGACCAGTCAGTCCCTCTGTTAAACAA 4129

XX Claim 8; SEQ ID NO 15810; 2537pp + Sequence Listing; English.
 XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dr primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX

XX SQ Sequence 5124 BP; 1462 A; 1106 C; 1178 G; 1378 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 5124
 Score: 7537.00 Matches: 1347
 Percent Similarity: 99.63% Conservative: 1
 Best Local Similarity: 99.56% Mismatches: 5
 Query Match: 73.75% Indels: 0
 DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x AAH16667 (1-5124)

Qy 195 ThrAspGlyTyrSerAsnGlyGlyAspProArgProIleAlaAlaSerLeuArgAspSer 214
 Db 2 ACTGATGATATTCATATGGGGGAGACCTAGACCAATTCGACGCTCATCGAGATTCA 61
 Qy 215 GlyValGluIlePheThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMet 234
 Db 62 GGAGTGGAGATCTTCACATTTTGGCATATGGCAGGGAACATTCGAGAGCTGATGCATG 121
 Qy 235 AlaSerThrProLysGluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAla 254
 Db 122 GCTTCCACCCCAAGGAGGACCTGTTACCTGCTACACAGTATTTGAAGAATTCGAGGCT 181
 Qy 255 LeuAlaArgArgAlaLeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMet 274
 Db 182 TTAGCTCCGGGCAATTCGATGAGATCTACCTCTGGGAGTATTTATTTCAAGATGATATG 241
 Qy 275 ValHisCysSerTyrLeuCysAspGluGlyLysAspCysCysAspArgMetGlySerCys 294
 Db 242 GTCCACTGCTCATATCTTTTGATGATGAGCAGGAGTCTGCTGTGACCGAATGGGAAGCTGC 301
 Qy 295 LysCysGlyThrHisThrGlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLys 314
 Db 302 AAATGTGGGACACACACAGGCCATTTTGATGTCATCTGTGAAAGCGGTATTTACGGGAA 361
 Qy 315 GlyLeuGlnTyrGluCysThrAlaCysProSerGlyThrTyrLysProGluGlySerPro 334
 Db 362 GGTCTGCAGTATGATATGCACAGCTTGGCCATCGGGGACATACAAACCTCGAAGGCTCA 421
 Qy 335 GlyGlyIleSerSerCysIleProCysProAspGluAsnHisThrSerProGlySer 354
 Db 422 GGAGGATCAGCAGTTGATTCATGTTCTGATGAAATTCACACCTCTCCACCTGGGAAGC 481
 Qy 355 ThrSerProGluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGlu 374
 Db 482 ACATCCCTGAAGACTGTGCTGCAGAGGAGGATACAGGGCATCTGGCCAGACCTGTGAA 541

Qy 375 LeuValHisCysProAlaLeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCys 394
 Db 542 CTTGTCCACTGCTGCCCTGAAGCTCCGAAAATGGTTACTTTATCAAAACACTTGC 601
 Qy 395 AsnAsnHisPheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGly 414
 Db 602 AACCAACCACTTCAATGCAGCCCTGTGGGTCCGATGTCACTCGATTGATCTGTGGGA 661
 Qy 415 SerSerIleLeuLeuCysLeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArg 434
 Db 662 AGCAGCATCATTTATGTCTACCAATGGTTTGTGTCCGGTTTAGAGAGCTACTCGAGA 721
 Qy 435 ValArgThrCysProHisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArg 454
 Db 722 GTAAGAACATGTCTCATCTCCGCCAGCGAAACATGGCCATCATGCTGTTCTACAGG 781
 Qy 455 GluMetLeuTyrLysThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGly 474
 Db 782 GAATGTTATATACCAACCATGTTTGGTTGCTGTGTGATGAAGGGTACAGACTAGAGGC 841
 Qy 475 SerAspLysLeuThrCysGlnGlyAsnSerGlnTrpAspGlyProGluProArgCysVal 494
 Db 842 AGTCATAAGCTTACTTGTCAAGAAAACAGCCAGTGGGATGGGCCAGAACCCCGGTGTG 901
 Qy 495 GluArgHisCysSerThrPheGlnMetProLysAspValIleIleSerProHisAsnCys 514
 Db 902 GAGCCCACTGTTCCACCTTTTCAGATGCCCAAGATGTATCATATCCCCCAACTGT 961
 Qy 515 GlyLysGlnProAlaLysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIle 534
 Db 962 GCGAAGCAGCCAGCCAAATTTGGGACGATCTGCTATGTAAGTTGCCGCAAGGGTTCATT 1021
 Qy 535 LeuSerGlyValLysGluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyVal 554
 Db 1022 TTATCTGGAGTCAAAAGAAATGCTGAGATGTACCTCTCTGGAAAATGGAAATGTCGGAGTT 1081
 Qy 555 GlnAlaAlaValCysLysAspValGluAlaProGlnIleAsnCysProLysAspIleGlu 574
 Db 1082 CAGGCGCTGTGTGTAAAGACGTGGAGCTCTCTCAATCATCTGCTTAAGGCATAGAG 1141
 Qy 575 AlaTyrThrLeuGluGlnGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLys 594
 Db 1142 GCTAAGACTCTGGAAACAGCAGATTTCTGCCAATGTTACCTGCGAGATTCACACAGCTAA 1201
 Qy 595 AspAsnSerGlyLysValSerValHisValHisProAlaPheThrProProTyrLeu 614
 Db 1202 GACAACTCTGCTGTAAGAGGTGTCACTCCACGTTTCATCCAGCTTTCACCCCACTTACCTT 1261
 Qy 615 PheProIleGlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAla 634
 Db 1262 TTCCCAATTTGGAGATGTTGCTATCGTATACACGGCAACTGACTATTCGGCAACCAAGGCC 1321
 Qy 635 SerCysIlePheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArg 654
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 Qy 655 SerProProValGlnValSerGluLysValHisAlaAlaSerTrpAspGluProGln 674
 Db 1382 TCTCCACCTCCCGTCCAGGTCTCCGGAAGAGTACATGCGCGAGCTGGGATGAGCCTCAG 1441
 Qy 675 PheSerAspAsnSerGlyValGluLeuValIleThrArgSerHisThrGlnGlyAspLeu 694
 Db 1442 TTCTCAGCAACTCAGGGGCTGAATTTGTCATTATCCAGAGTTCATACAGAGGATACACAGAGGAGACCTT 1501
 Qy 695 PheProGlnGlyGluThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArg 714
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 Qy 715 ThrCysAspIleHisIleValIleLysGlySerProCysGluIleProPheThrProVal 734
 Db 1562 ACATGTGATATCCATATTTGTCAATAAAGGTTCTCCCTGTGAAATTCATTCACCTGTGA 1621

QY 735 AsnGlyAspPheIleCysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeu 754
DB 1622 AATGGGGATTTTATATGCACTCCAGATAAATACAGAGTCAACTGATCAATTAACCTTGCTTG 1681
QY 755 GluGlyTyrAspPheThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGly 774
DB 1682 GAGGGCTAGTATTCACAGAGGGTCTACTGACACAGTATTATTGCTTATGAAGATGGC 1741
QY 775 ValTyrIysBProThrTyrThrThrGluThrProAspCysAlaLysLysArgPheAlaAsn 794
DB 1742 GTCTGGAAACCAACATATACCACTGATGATGCCAGACTGTGCCAAAACGGTTTGCAAAC 1801
QY 795 HisGlyPheLysSerPheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeu 814
DB 1802 CACGGGTTCAGTCCCTTGTAGATGTTCTACAAAGCAGCTGGTGTGATGACACAGATCTG 1861
QY 815 MetLysLysPheSerGluAlaPheGluThrThrLeuGluLysMetValProSerPheCys 834
DB 1862 ATCAAGAAGTTTCTGAAGCATTTGAGACGACCTGGGAAAAATGGTCCCATCATTTTGT 1921
QY 835 SerAspAlaGluAspIleAspCysArgLeuGluAsnLeuThrLysLysTyrCysLeu 854
DB 1922 AGTGATCGACAGACATTCGCTGGAGACTGGAGGAGAACCTGCACAAAATAATTCGCTA 1981
QY 855 GluTyrAsnTyrAspTyrGluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyAlaAla 874
DB 1982 GAATATAATTTATGACTATGAAATATGGCTTTGCAATTTGGACAGGTGGCTGGGGTGCAGCT 2041
QY 875 AsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSer 894
DB 2042 AATAGGCTGGATTTACTTTAGACTGACTTCTTGGACACTGTGCAAGAAACAGCCACAAGC 2101
QY 895 IleGlyAsnAlaLysSerSerArgIleLysArgSerAlaProIleuSerAspTyrLysIle 914
DB 2102 ATCGCAATGCCAAGTCTCAAGGATTTAAAGAAAGTGGCCCCATTTATCTGACTATAAAAT 2161
QY 915 LysLeuIlePheAsnIleThrAlaSerValProLeuProAspGluArgAsnAspThrLeu 934
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QY 935 GluTyrGluAsnGlnGlnArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLys 954
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QY 1035 CysProSerGlyMetTyrThrGluTyrIleHisSerArgAsnIleSerAspCysLysAla 1054
DB 2522 TGCCCCCTCTGGGATGTACAGGAAATATATCCATTCAGAAACATCTCTGATTGTAAAGCT 2581
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QY 1075 GlyThrTyrGlnProLysPheGlySerArgSerCysLeuSerCysProGluAsnThrSer 1094
DB 2642 GGCACCTATCAGCCAAAATTTGGTTCGCGAGCTGCCCTCTCGTGTCCAGAAAACACCTCA 2701
QY 1095 ThrValLysArgGlyAlaValAsnIleSerAlaCysGlyValProCysProGluGlyLys 1114

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DB 2762 TTCTCGGTTCTGGGTTAATGCCCTGTCAACCATGTCTCGTACTATTATCAACACTAAT 2821
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DB 3362 CCATGCTTAAATTAATGCGTCTGTGAAGACAGGTTGGGGATTTCTGTGTCAAAATGCCCA 3421
QY 1335 ProGlyPheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCys 1354
DB 3422 CCTGGATTTTGGGTACCCGATGTGGAAGAACGTCGATGAGTGTCTCAGTCAGCCATGC 3481
QY 1355 LysAsnGlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGly 1374
DB 3482 AAAAATGGAGCTACTCTGTAAGACGCTGCAATAGCTTTCAGATGCTGTGTGTGCAAGTGGC 3541
QY 1375 PheThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsn 1394
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QY 1395 GlnAlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSer 1414
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QY 1415 GlyGlnArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGly 1434
DB 3662 GGCAAAAGGTGTGAAAACAGAACAGTCTACAGGCTTTAACTGGATTTTGAAGATTTCTGGC 3721
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DB 3722 ATCTATGATATGTATGTGTGGATGTCTCCATCTCTCCAGTCTTCAACCTGTATACC 3781
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3782 TTCTGGATGAATCTCTGACGACATGAACATATGGAACACCAATCTCTATGCAAGTGTAT 3841
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 3842 AACGGCAGGACAAATACCTTCTCTGATGATTAACGGCTGGGTCTTTATGTGAAT 3901
 1495 GlyArgGluLysIleThrAsnGlyProSerValAsnApsGlyArgTrpHisIleAala 1514
 3902 GCGAGGGAAGATGACAACTGTCTCTCGGTGAATGATGGCAGATGCATCATATTGCA 3961
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 3962 ATCACTTGGACAAGTGCCATGCTGGAAGTCTATATCGATGAGGGAATATTCTGAC 4021
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 4022 GGTGGTGTGGCTCTCTGTGGTTTGCCCATACCTGGT 4060

RESULT 7
 ABZ11152
 ID ABZ11152 standard; cDNA; 3448 BP.
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 AC ABZ11152;
 DT 20-JAN-2003 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 34.
 XX
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
 cell-proliferative disorder; neurodegenerative disease; bacterial;
 Parkinson's disease; Alzheimer's disease; autoimmune disease;
 multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 arthritis; cystostatic; immunomodulator; nootropic; neuroprotective;
 antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
 antiarthritic; gene; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200270539-A2.
 FN
 XX 12-SEP-2002.
 PD
 XX 05-MAR-2002; 2002WO-US005095.
 PP
 XX 05-MAR-2001; 2001US-00799451.
 PR
 XX (HYSE-) HYSEQ INC.
 XX
 PA Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 DR WPI; 2002-759812/82.
 DR P-PSDB; ABP68935.
 XX
 XX New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX
 PS Claim 1; SEQ ID NO 34; 1012pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated polynucleotide (1) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ1119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,

CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 3448 BP; 1014 A; 754 C; 769 G; 911 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,15e-314 Length: 3448
 Score: 5485.00 Matches: 982
 Percent Similarity: 99.90% Conservative: 1
 Best Local Similarity: 99.80% Mismatches: 1
 Query Match: 53.67% Indels: 0
 DB: 6 Gaps: 0
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 QY 318 TyrGluCysThrAlaCysProSerGlyThrTrpLysProGluGlySerProGlyGly 337
 DB 1 TATGAATGCACAGCTTGCCCATCGGGGACATACAACTGAGCCTCACCAGGGAATC 60
 QY 338 SerSerCysIleProCysProApsGluAsnHisThrSerProGlySerThrSerPro 357
 DB 61 AGCAGTTGCATTCCATGTCCTCCGATGAAATACACCTCTCCACCTGGAAGCACATCCCT 120
 QY 358 GluApsCysValCysArgGluGlyTrpArgAlaSerGlyGlnThrCysGluLeuValHis 377
 DB 121 GAAGACTGTGTCTGACAGAGGGATACAGGCATCTGGCAGACCTGTGAACTTGTCCAC 180
 QY 378 CysProAlaLeuLysProGluAsnGlyTrpPheIleGlnAsnThrCysAsnAsnHis 397
 DB 181 TGCCCTGCTCGAGCCTCCGAAATGTTACTTTATCCAAACACTTGCACCAACAC 240
 QY 398 PheAsnAlaAlaCysGlyValArgCysHisProGlyPheApsLeuValGlySerSerIle 417
 DB 241 TTCAATGCAGCCTCTGGGGTCCGATGTCACCTCGGATTTGATCTTGTGGGAAGCAGCATC 300
 QY 418 IleLeuCysLeuProApsGlyLeuTrpSerGlySerGluSerTrpCysArgValArgThr 437
 DB 301 ATCTTATGCTACCAATGGTTGTGTCGGTTCAGAGAGCTACTGCAGAGTAGANACA 360
 QY 438 CysProHisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeu 457
 DB 361 TGTCTCTCATCTCGCCAGCCGGAACATGCCACATCAGCTGTTCTACAGGGAATGTTA 420
 QY 458 TyrLysThrThrCysLeuValAlaCysApsGluGlyTrpArgLeuGluGlySerApsLys 477
 DB 421 TATAAGACAAACATGTTGGTTCCTGTGATGAAGGGTACAGACTAGAGGCGATGAAG 480
 QY 478 LeuThrCysGlnGlyApsSerGlnTrpApsGlyProGluProArgCysValGluArgHis 497
 DB 481 CTTACTTGTCAAGGAACAGCCAGCTGGATGGCCAGAAACCCCGGTGTGTGGAGCCGAC 540
 QY 498 CysSerThrPheGlnMetProLysApsValIleIleSerProHisAenCysGlyLysGln 517
 DB 541 TGTTCACCTTTTCAGATGCCAAAGATGTCATCATATCCCCCACAACCTGTGGCAAGCAG 600
 QY 518 ProAlaLysPheGlyThrIleCysTrpValSerCysArgGlnGlyPheIleLeuSerGly 537
 DB 601 CCAGCCAAATTTGGGACGATCTGCTATGTAAGTTGCCCGCAAGGGTTTCATTTATCTGGA 660
 QY 538 ValLysGluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAala 557
 DB 661 GTCAAGAAATGCTGAGATGTTACCACTTGTGNAATGGAATGTCGGAGTTCAGGCAGCT 720
 QY 558 ValCysLysApsValGluAlaProGlnIleAsnCysProLysApsIleGluAlaLysThr 577
 DB 721 GGTGTAAAGACGTGGAGGCTCTCTCAATCAACTGTCTTAAGGACATAGAGGCTAAGACT 780
 QY 578 LeuGluGlnGlnApsSerAlaAsnValThrTrpGlnIleProThrAlaLysApsAsnSer 597

Db 781 CTGGAACAGCAGACATCTTCTGCAATGTTTACCTGGCAGATTCACACAGCTAAAGACAACTCT 840
Qy 598 GlyGluValSerValHisValHisProAlaPheThrProTyrLeuPheProIle 617
Db 841 GGTGAAGAAGGTGTCAGTCCAGTTCATCCAGCTTTTACCCCACTTACCTTTTCCCAATT 900
Qy 618 GlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIle 637
Db 901 GGGAGATGTTGCTATCGTATACACGGCACTGACCTATCCGGCAACCCAGCCAGCTGCATT 960
Qy 638 PheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArgSerProPro 657
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Qy 678 AsnSerGlyValAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGln 697
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Qy 718 IleHisIleValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAsp 737
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Qy 738 PheIleCysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyr 757
Db 1261 TTTATATGCACTCCAGATAATACTGAGAGTCACTGTATCATTAATCTGCTTGGAGGCTAT 1320
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Qy 778 ProThrTyrThrThrGluTrpProAspCysAlaIleLysArgPheAlaAsnHisGlyPhe 797
Db 1381 CCAACATATACCACTGAATGGCCAGACTGTGCCAAAAAAGCTTTTGCAACACCCAGGGTTC 1440
Qy 798 LysSerPheGluMetPheTyrLysAlaAlaAraCysAspAspThrAspLeuMetLysLys 817
Db 1441 AAGTCTTTTGAGATGTTCTACAAAGCAGCTCGTTGTGTATGATGACACAGATCTGTAGAGAAG 1500
Qy 818 PheSerGluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAla 837
Db 1501 TTTTCTGAAGCATTTGAGACGACCTCGGGAATAATGGTCCCATCATTTTGTAGTGATGCA 1560
Qy 838 GluAspIleAspCysArgLeuGluGluAsnLeuThrIleLysLysTyrCysLeuGluTyrAsn 857
Db 1561 GAGGACATTTGACTGCGAGCTGGAGGAGAACCTGACCAAAAAAATATTGCCCTAGAGATATAAT 1620
Qy 858 TyrAspTyrGluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyAlaAlaAsnArgLeu 877
Db 1621 TATGACTATGAANAATGCTTTGCAATTTGACACAGGTGGCTGGGGTGCAGCTAATAGGCTG 1680
Qy 878 AspTyrSerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsn 897
Db 1681 GATTTACTTCTTACGATGCTTCTGGACACTGTGCAAGNAACAGCCACAGCATCGGCAAT 1740
Qy 898 AlaLysSerSerArgIleLysArgSerAlaProLeuSerSerAspTyrIleLysLeuIle 917
Db 1741 GCCAGGTCTCTCAGGATTAAGAAGTGGCCCAATATCTGACTATATAAATAAGTTAAT 1800
Qy 918 PheAsnIleThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTrpGlu 937
Db 1801 TTTAACATCACAGCTAGTGTGCCATTACCCGATGAAGAANAATGATACCTTTGAATGGGAA 1860
Qy 938 AsnGlnGluArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeu 957
Db 1861 AATCAGCAAGACTCTCTCAGACATTTGGAACCTATACAAATAAATCTGAAAAAGACTCTC 1920

Qy 958 AsnLysAspProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsn 977
Db 1921 AACAAAGACCCCATGATTTCTTTTTCAGTTGCATCAGAAATACATTATAGCCGACAGCAAT 1980
Qy 978 SerLeuGluThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArg 997
Db 1981 TCATTAGAAAACAAAAAGGCTTCCCTTCTGCAGACAGGCTCAGTGTCTGAGAGGGGT 2040
Qy 998 MetCysValAsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSer 1017
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Qy 1018 CysArgIleGlySerTyrGlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSer 1037
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Qy 1038 GlyMetTyrThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLys 1057
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Db 2701 CTCTGTCCACTTGGATATACAGGCTTAAAGTGTGAAGTGAACATCGATGAGTGCAGCCCA 2760
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Qy 1298 GlyPheValGly 1301
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 DB 1385 AGCCTGTGGGGTCCGATGTCACCTTGGATTGATCTTGTGGAGACGACATCATCTTATG 1444
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 QY 440 sLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrlsTh 460
 DB 1505 TCTCCGCGAGCCGAAACATGCGCACATCAGCTGTTCTACAGGGAATGTTATATAAGAC 1564
 QY 460 rThrCysLeuValAlaCysAspGluGlyTyArgLeuGluGlySerAspLysLeuThrCy 480
 DB 1565 AACATGTTGGTTGGTCTGTGATGAAGGGTACAGACTAGAAAGCAGGATGAAGCTTACTTG 1624
 QY 480 sGlnGlyAenSerGlnTyrAspGlyProGluProArgCysValGluArgHisCysSerTh 500
 DB 1625 TCAAGGAACACGACGAGTGGATGGCCAGAACCCCGGTGTGTGGAGCGCCACTGTTCAC 1684
 QY 500 rPheGlnMetProLysAspValIleIleSerProHisAenCysGlyLysGlnProAlaly 520
 DB 1685 CTTTCAGATGCCCAAGATATCATCATATATATATATATATATATATATATATATATAT 1744
 QY 520 sPheGlyThrIleCysTyTyValSerCysArgGlnGlyPheIleLeuSerGlyValysG 540
 DB 1745 ATTTGGGACGATCTGCTATGATGTAAGTTGGCCGCAAGGGTCAATTTTATCTGGAGTCAAGA 1804
 QY 540 uMetLeuArgCysThrThrSerGlyLysTrpAenValGlyValGlnAlaAlaValCysLy 560
 DB 1805 AATGCTGAGATGTACCACTTCTGGAATGGATGTGGAGTTCAAGGAGCTGTGTGTAA 1864
 QY 560 sPheValGluAlaProGlnIleAenCysProLysAspIleGluAlaLysThrLeuGlu 580
 DB 1865 AGACGTGGAGGCTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1924
 QY 580 nGlnAspSerAlaAenValThrTrpGlnIleProThrAlaLysAspAenSerClyGluLy 600
 DB 1925 GCNAGATTCTGCCAATGTTTACCTGGCAGATTCACACAGCTAAAGCACTCTGGTGAA 1984
 QY 600 sValSerValHisValHisProAlaPheThrProProTyLeuPheProIleGlyAspVa 620
 DB 1985 GGTGTGAGTCCAGCTTCATCCAGCTTTTCCACCACTTACCTTTTCCCAATGGAGATGT 2044
 QY 620 lAlaIleValTyThrAlaThrAspLeuSerGlyAenGlnAlaSerCysIlePheHisil 640
 DB 2045 TGTATGATATACAGGCACTGACCTATCCGCAACCAAGCCAGCTGCAATTTTCCATAT 2104
 QY 640 eLysValIleAspAlaGluProProValIleAspTyrCysArgSerProProValG 660
 DB 2105 CAAGGTATTTGATGCAAGAACCACTGTCTATAGACTGGTGCAGATCTCCACCTCCCGTCCA 2164
 QY 660 nValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAenSerG 680
 DB 2165 GGTCTCGAGAGATACATGCGCCAGCTGGATGAGCTTCTCTCAGCAACTCAGG 2224
 QY 680 yAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluTh 700
 DB 2225 GGCTGAATTTGGTCAATACAGAGATCATACAGGAGAGACTTTTCCCTCAAGGGGAGAC 2284
 QY 700 rIleValGlnTyThrAlaThrAspProSerGlyAenAenArgThrCysAspIleHisil 720

DB 2285 TATAGTACAGTATACAGCCACTGACCCCTCAGCAATAACAGGACATGTGATATCCATAT 2344
 QY 720 eValIleLysGlySerProCysGluIleProPheThrProValAenGlyAspPheIleCy 740
 DB 2345 TGTCTATAAAGGTTCTCCCTGTGAATTCATTCACACCTGTAAATGGGGATTTTATATG 2404
 QY 740 sThrProAspAenThrGlyValAenCysThrLeuThrCysLeuGluGlyTyArgPheTh 760
 DB 2405 CACTCCAGATTAATCTGGAGTCACTGTACATTAATCTTCTGGAGGGCTATGATTTTCC 2464
 QY 760 rGluGlySerThrAspLysTyTyCysAlaTyArgGluAspGlyValTrpLysProThrTy 780
 DB 2465 AGAAGGGTCTACTGACCAAGTATTTATGCTTATGAAGATGGCTCTCGAAACCAACATA 2524
 QY 780 rThrThrGluTrpProAspCysAlaLysLysArgPheAlaAenHisGlyPheLysSerPh 800
 DB 2525 TACCACCTGAATGCCAGACTGTGCCAAAAAAGCTTTTGAACACACCGGTTCAGTCCCT 2584
 QY 800 eGluMetPheTyLeuAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGl 820
 DB 2585 TGAGATGTTCTACAAAGCAGCTCGTTGTGATGACACAGATCTGATGAAGAAGTTTCTGA 2644
 QY 820 uAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIl 840
 DB 2645 AGCATTTGAGACGACCTCGGAAAAAATGGTCCCATCATTTTGTAGTATGCAGAGGACAT 2704
 QY 840 eAspCysArgLeuGluGluAenLeuThrLysLysTyTyCysLeuGluTyArgPheThrAspTy 860
 DB 2705 TGACTGCAGACTGGAGGAGAACCTGACCAAAAAAATATTCCTAGATATATATATATGACTA 2764
 QY 860 rGluAenGlyPheAlaIleGly 867
 DB 2765 TGAATAATGGCTTTGCAATTGGT 2786

RESULT 9
 ABK35664/c
 ID ABK35664 standard; cDNA; 2064 BP.
 XX AC ABK35664;
 XX DT 08-MAY-2002 (first entry)
 XX DE cDNA sequence #55 encoding novel human secreted protein.
 XX KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
 XX KW immune deficiency disorder; blood disorder; inflammatory disorder;
 XX KW infectious disorder; allergic condition; neurodegenerative disorder;
 XX KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
 XX KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
 OS Homo sapiens.
 XX WO200177289-A2.
 XX PD 18-OCT-2001.
 XX PF 29-MAR-2001; 2001WO-US010232.
 XX PR 06-APR-2000; 2000US-0195605P.
 XX (GEM) GENETICS INST INC.
 XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 XX PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
 XX PI Clark HF, Pechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
 XX DR WPI; 2002-179322/23.
 XX Six hundred and twenty three polynucleotides derived from a variety of
 XX human tissue sources which encode secreted proteins, useful for treating
 XX immune deficiencies and disorders such as autoimmune disorders.

XX AAH16567;
 XX 26-JUN-2001 (first entry)
 XX DE Human cDNA sequence SEQ ID NO:15640.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN BP1074617-A2.
 XX PD 07-FEB-2001.
 XX PF 28-JUL-2000; 2000BP-00116126.
 XX PR 29-JUL-1999; 99JP-00248036.
 XX PR 27-AUG-1999; 99JP-00300253.
 XX PR 11-JAN-2000; 2000JP-00118776.
 XX PR 02-MAY-2000; 2000JP-00183767.
 XX PR 09-JUN-2000; 2000JP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX PI WPI; 2001-318749/34.
 XX DR
 XX DX
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 XX PS Claim 8; SEQ ID NO 15640; 2537pp + Sequence Listing; English.
 XX CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention
 XX SQ Sequence 1969 BP; 603 A; 434 C; 430 G; 502 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,07e-172 Length: 1969
 Score: 3073.00 Matches: 547
 Percent Similarity: 99.45% Conservative: 0
 Best Local Similarity: 99.45% Mismatches: 3
 Query Match: 30.07% Indels: 0
 DB: 4 Gaps: 0
 US-09-977-053-6 (1-1842) x AAH16567 (1-1969)
 QY 318 TyrGluCysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIle 337

1	TATGATGCACAGCTTGCCCATCGGGACATACAACTCAGGCTCACCAGGAGGATC	60
338	SerSerCysIleProCysProAspGluAsnHisThrSerProGlySerThrSerPro	357
61	AGCAGTTGCATTCATGTCCTCCGATGAAATCACAACCTCTCCACCTGGAAGCACATCCCT	120
358	GluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHis	377
121	GAAGACTGTGTCGACAGAGAGGATACAGGGCATCTGGCCAGACTGTGAACCTTGTCAC	180
378	CysProAlaLeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHis	397
181	TGCCCTGCCCTGAGGCTCCGGAATGGTTACTTTATCCAAACACTTGCACACACAC	240
398	PheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIle	417
241	TTCAATGCAGCTGTGGGTCCGATGTCACCTCGATTGATCTGTGGGAAGCAGCATC	300
418	IleLeuCysLeuProAsnGlyLeuTyrSerGlySerGlnSerTyrCysArgValArgThr	437
301	ATCTTATGTCACCCCAATGGTTGTGGTCCGGTTCAGAGAGCTACTGCAGAGTAAGACA	360
438	CysProHisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeu	457
361	TGTCCTCACTCTCCGACGCGAACAACATGGCCACATCAGCTGTTCTACAGGGAATGTA	420
458	TyrLysThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLys	477
421	TATAAGACAACATGTTTGGTGGCTGTGATGAAGGGTACAGACTAGGAAGGCAGTAAAG	480
478	LeuThrCysGlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGluArgHis	497
481	CTTACTTGTCAAGGNAACAGCCAGTGGATGGGCGCAGAACCCCGGTGTGTGAGCGCCAC	540
498	CysSerThrPheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGln	517
541	TGTTCCACCTTCAGATGCCAAGATGTTCATCATATCCCCCACAACCTGTGGCAGCAG	600
518	ProAlaLysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGly	537
601	CCAGCCAAATTTGGGACGATCTGCTATGTAAAGTTGCCGCCAAGGGTTCATTTATCTGGA	660
538	ValLysGluMetLeuArgCysThrThrSerGlyTyrTrpAsnValGlyValGlnAlaAla	557
661	GTCAAGAAATGCTGAGATGTACCACTTCTGGAAATGGAAATGCGAGTTCAGGAGCT	720
558	ValCysLysAspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThr	577
721	GTGTGTAAAGCTGGAGGCTCTCTCAATCACTGTCTTAAGGACATAGAGGCTTAAGACT	780
578	LeuGluGlnGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSer	597
781	CTGGAACAGCAAGATCTTCCATGTTTACCTGGCAGATTCCACAGCTAAAGACAACCTCT	840
598	GlyGluLysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIle	617
841	GGTGAAGAGGTGTGTCAGTCGCGTTCATCCAGCTTTTCAACCCACCTTACCTTTTCCCAAT	900
618	GlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIle	637
901	GGAGATGTTGCTATCGTATACAGCGCACTGACATATCCGGCAACACAGGCGCAGTGCATT	960
638	PheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArgSerProPro	657
961	TTCCATATCAGGTTATTGATGTCAGAAACCACTGTCTATAGACTGGTGCAGACTCTCCACT	1020
658	ProValGlnValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAsp	677
1021	CCCGTCCAGTCTTCGGAAGGATGATGCGCAAGCTGGATGAGCTCTAGTCTCTAGAC	1080
678	AsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGln	697

Db 1081 AACTCAGGGGCTGATTTGGTCAATACACAGAGTCATACACAGAGACCTTTTCCCTCAA 1140
Qy 698 GlyGluThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAsp 717
Db 1141 GGGGAGACTATAGTACAGTATACAGGCACATGACCCCTCAGGCAATAACAGGACATGTGAT 1200
Qy 718 IleHisIleValIleGlySerProCysGluIleProPheThrProValAsnGlyAsp 737
Db 1201 ATCCATATTGCTATAAAGGTTCTCCCTGTGAATCCCATTTCCACACCTGTAAATGGGGAT 1260
Qy 738 PheIleCysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyr 757
Db 1261 TTTATATGCTCTCAGATATATCTGGAGTCACTGTATCACTTAATCTTCTGGAGGGCTAT 1320
Qy 758 AspPheThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLys 777
Db 1321 GATTTTCACAGAGGGTCTACTGACAGATATATTATTTGCTTATGAAGATGGCGTCTGGAAA 1380
Qy 778 ProThrTyrThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPhe 797
Db 1381 CCAACATATACCACTGAATGCCAGACTGTGCCAAAACGTTTTCGAACCCACGGGTTC 1440
Qy 798 LysSerPheGluMetPheTyrLysAlaArgCysAspAspThrAspLeuMetLysLys 817
Db 1441 AGTCTCTTGAGATGTTCTACAGACAGCTGCTGTGTATGACACAGATCTGATGAAGAAG 1500
Qy 818 PheSerGluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAla 837
Db 1501 TTTTCTGAAGCATTGGAGACGACCCCTGGGAAAATGGTCCCATCATTTTGTAGTATGCA 1560
Qy 838 GluAspIleAspCysArgLysGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsn 857
Db 1561 GAGGACATTGACTGCAGACTGGAGAGAACCTGCACAAAATAATATGCTAGATAATAAT 1620
Qy 858 TyrAspTyrGluAsnGlyPheAlaIleGly 867
Db 1621 TATGACTATGAAAATGGCTTTGCAATTGGT 1650
RESULT 11
ABK54146
ID ABK54146 standard; cDNA; 1696 BP.
XX
AC ABK54146;
XX
DT 05-JUN-2002 (first entry)
XX
XX cDNA encoding human secreted protein sequence #28.
DE
XX Human secreted protein; autoimmune disease; hyperproliferative disorder;
KW cardiovascular disorder; cerebrovascular disorder; infection; cancer;
KW nervous system disorder; ocular disorder; epithelial cell proliferation;
KW wound healing; skin aging; sunburn; transplantation; chemotaxis;
KW tissue regeneration; food additive; preservative; cytostatic; cardiant;
KW antiviral; antiallergic; antiinflammatory; antibacterial; antifungal;
KW gene; ss.
XX
OS Homo sapiens.
XX
XX WO200218412-A1.
PN
XX
PD 07-MAR-2002.
XX
PF 17-JAN-2001; 2001WO-US001384.
XX
XX 28-AUG-2000; 2000US-0228086P.
PR
XX 04-JAN-2001; 2001US-0259516P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CB, Soppet DR;
PI Olsen HS, Moore PA, Wei P, Ebner R, Duan RD, Shi Y, Choi GH;
PI Fisciella M, Ni J;
XX

WPI; 2002-269525/31.
P-ESDB; AAU91108.

Seventeen nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.

Claim 4; Page 435-436; 505pp; English.

The present invention relates to the isolation of novel human secreted proteins, and the polynucleotide sequences encoding them. The secreted proteins are useful to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The secreted proteins are also useful in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the secreted proteins can also be used in alleviating symptoms associated with disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which can be diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cancer, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Parkinson's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. ABK54119-ABK54167 encode human secreted protein sequences

Sequence 1696 BP; 349 A; 489 C; 475 G; 369 T; 0 U; 14 Other;

Alignment Scores:

Pred. No.:	4e-137	Length:	1696
Score:	2479.00	Matches:	464
Percent Similarity:	97.68%	Conservative:	0
Best Local Similarity:	97.88%	Mismatches:	8
Query Match:	24.26%	Indels:	4
DB:	6	Gaps:	0

US-09-977-053-6 (1-1842) x ABK54146 (1-1696)

Qy	1	MetTrpProArgLeuAlaPheCysCysTrpGlyLeuAlaLeuValSerGlyTrpAlaThr	20
Db	238	ATGTGGCCCTCGCCCTGGCCCTTTGTGTCTGGGGCTCTGGGGCTCTGGGGCTGGGGC	297
Qy	21	PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro	40
Db	298	TTTCAGCAGATGTCCCGTCCGGCAATTTTCAGTTCCGCTCTTCCCGAGACCGCGCS	357
Qy	41	GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg	60
Db	358	GGGGCCCCGGGAGTATCCCGCGCCCGCTCTCTGGCGCAGAAAGCGCGGGGAGCAGA	417
Qy	61	ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu	80
Db	418	GTGAGCGCGCTGGGCCAGCGCTTCCGGCAGCGCTCTCGGGAGCTCAGCGAG	477
Qy	81	ArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGluValValAsnPheArg	100
Db	478	CGCCTGGAGCTTGTCTCTCTGTGTGATTTCTCCAGCGTGGCGGAGTCAACTTCCGC	537
Qy	101	SerGluLeuMetPheValArgLysLeuSerAspPheProValValProThrAlaThr	120
Db	538	AGCGAGCTCATGTTCTCGCAAGCTGTCTCCGACTTCCCGTGGTCCCGGCGCAG	597
Qy	121	ArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIle	140
Db	598	CGCGTGGCCATGTGTGACCTTCTCGTCCAAAGAACTACGTGGTGGCCCGCGCTCGATT	657
Qy	141	SerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluLeuProAlaIle	160

Db	658	TCCACCCGCGCGCGCGCCAGCAAGTGC	CGCGTGTCTCTCCAAGAGATCCCTCGCCATC	7117
Qy	161	SerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaGlnIleLeu	180	
Db	718	TCCTACCGAGGTGCGGCACCTACACCAAGGCGCTTCCAGCAAGCGCGCAATTCCT	777	
Qy	181	LeuHisAlaArgGluAAsnSerThrLysValValPheIleuIleThrAspGlyTyrSerAsn	200	
Db	778	CTTCATGCTAGAGAAACTCAACAAAGTTGTATTCTCATCTAGTGWTAATTCCAA-	836	
Qy	201	GlyGlyAspProArgProIleAlaSerLeuArgAspSerGlyValGluIlePheThr	220	
Db	837	GGGGAGACCTTAGCCCAATTCGAGCGTCACTCGCAGATTGAGGATGGAGATCTTCACT	896	
Qy	221	PheGlyIleTrpGlnGlnValAsnIleArgGluLeuAsnAspMetalSerThrProLysGlu	240	
Db	897	TTTGGCATATGCCAAGGGAACATTCGAGAGCTGAATGCATGGCTCCACCCCAAGGAG	956	
Qy	241	GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgArgAlaLeu	260	
Db	957	GAGCACTGTTACCTGCTCACTWTTTGTGAGAAATTTGAGGCTTTAGCTCGCGGCAATG	1016	
Qy	261	HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu	280	
Db	1017	CATCAAGATCTACCTCTCTGGGAGTTTATTCAGATGATATGGTCCACTGCTCATATCTT	1076	
Qy	281	CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr	300	
Db	1077	TGTGATGAAGGCAAGGACTGCTGTGACCGAATGGGAAGTGCAAATGTGGGACACACACA	1136	
Qy	301	GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys	320	
Db	1137	GGCCATTTTGAGTGCACTGTGAAAGAGGGTATTACGGAAAGGCTCTGCAGTATGAAATGC	1196	
Qy	321	ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys	340	
Db	1197	ACAGCTTCCCATCGGGACATACAAACCTGAAGGCTCACCGAGGAGNATCAGCAGTTGC	1256	
Qy	341	IleProCysProAspGluAAsnHisThrSerProGlySerThrSerProGluAspCys	360	
Db	1257	ATTCATGCTCTGATGAAATCACACCTCTCCACTCGAAGCACATCCCTCGAAGACTGT	1316	
Qy	361	ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla	380	
Db	1317	GTCTGCGAGAGGGATACAGGGCATCTGGCCAGACCTGTGAACTTGTCCACTGCCTCGCC	1376	
Qy	381	LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla	400	
Db	1377	CTGAAGCTCCCGAAATGGTTACTTTATCCAAAACACTTGCAACACACCACTTCAATGCA	1436	
Qy	401	AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys	420	
Db	1437	GCCTGTGGGGTCCGATGTCACTCCCTGGATTTGATCTTGTGGGAAGCAGCATCATCTTATGT	1496	
Qy	421	LeuProGlnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis	440	
Db	1497	YTACCCCAATGGTTGTGGTTCGGTTCAGAGAGCTACTGCGAGTAAGAACTATGCTCTCAT	1556	
Qy	441	LeuArgGlnProLysHis-GlyHisIleSerCysSer-ThrArgGluMetLeuTyrLys-	459	
Db	1557	CTCCGCCCGCAACATGGGCCACATCAGCTGTCTTCAAGGGAAATGTTATATAAGG	1616	
Qy	460	ThrThrCysLeuValAlaCysAspGluGlyTyrArgLeu	472	
Db	1617	ACAACATGTTTGGTTGGCTGTGATGAAGGGGTACAGATTA	1655	

RESULT 12

RESOL 12
AAZ94659

ID AAZ94659

XX

AC AA294659;

XX
DT 18-JUL-2000 (first entry)

XX Human EGF repeat-containing protein EGF-Hy1 cDNA.
DE
XX
XX EGF-Hy1; epidermal growth factor; human; cancer; immunomodulator;
KW neuroprotective; anti rheumatic; antiarthritic; antiallergic;
KW proliferative regulator; cytostatic; anticoagulant; thrombolytic;
KW antiinflammatory; diagnosis; ss.
XX
XX Homo sapiens.
OS

	Key	Location/Qualifiers
CD	CDS	4. .1407
FT		/*tag= a

AA PN WO200017357-A1.

XX
PD
30-MAR-2000.

20-SBP-1999: 99WO-US021812.

XX
PR 18-SEP-1998: 98US-00157308.XX
PA (HYSE-) HYSRO INC.

XX Ford JE. Mulero JJ. Yeung G. Montgomery J.

XX
DR WPI: 2000-292844/25.

DR WFI, 2000-232014/
DR P-PSDB; AAY79332.

Human EGF-Hy1 polypeptide and polynucleotide sequences, useful for diagnosis, prognosis and monitoring of cancer.

PS Claim 1; Page 131-133; 141pp; English.

The present sequence is that of human EGF-Hyl cDNA, as deduced from clones obtained by RACE using foetal brain cDNA. The encoded polypeptide (see Y79321) bears similarity to the epidermal growth factor (EGF) - repeat of Notch, a protein involved in cell fate control mechanisms regulating multicellular development. Of 18 human tissues tested, only foetal liver, foetal skin, foetal brain and adult lung expressed EGF-Hyl, suggesting expression mainly in developmental tissues. EGF-Hyl includes 3 EGF repeats, and polynucleotides encoding these EGF repeat regions, as well as the entire coding region, are also claimed (nucleotides 1048-1158, 1162-1270, 1276-1404 and 4-1407 of the present sequence). An additional sequence for EGF-Hyl (see AA294658) was obtained by PCR. The invention also provides methods for the use of EGF-Hyl polypeptides and polynucleotides as diagnostics, therapeutics and research reagents. In particular, they are used for diagnosis, prognosis or monitoring of cancer. They can also be used for stimulating and suppressing the immune system, and hence in treating immune deficiencies and disorders, including infections and autoimmune disorders such as connective tissue disease, multiple sclerosis, rheumatoid arthritis, myasthenia gravis and autoimmune inflammatory eye disease. They can also be used to treat allergic reactions and conditions, and to regulate haematopoiesis, tissue growth, activin/inhibin, chemotaxis/chemokinesis, haemostasis, thrombolysis, receptor/ligand binding, antiinflammatory responses, leukaemia and nervous system disorders.

Sequence 1760 BP: 515 A; 367 C; 398 G; 479 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	6.62e-121	Length:	1760
Score:	2374.00	Matches:	433
Percent Similarity:	96.07%	Conservative:	7
Best Local Similarity:	94.54%	Mismatches:	17
Query Match:	23.23%	Indels:	1
DB:	3	Gaps:	0

US-09-977-053-6 (1-1842) x AAZ94659 (1-1760)

Qy	845	GluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe	864
Db	3	GAGGAGCGCCGACCCCAATCTTCGACACTGCAGCTTACGACTTCCAGCTGGCTGG	62

Qy	865	AlaIleGlyProGlyGlyTrpGlyAlaAlaAsnArgLeuAspTyrSerTyrAspPhe	984
Db	63	GCgATGGGACcAGGGGGCTGGGGCGCAGCTCATAGGCTGGAGTACTTTCAGGATGACTTG	122
Qy	885	LeuAspThrValGlnGlnThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLys	904
Db	123	CTGACCGCTGAGCAAGAAACAGCCACAGCATCGGCAATGCCAAGTACTCACGGAGCTAT	182
Qy	905	ArgSerAla-ProLeuSerAspTyrIlyLysLeuIlePheAsnIleThrAlaSerVa	924
Db	183	AAGAGCGCAGCCATTATCTGACTATAAAATTAAGTTAAATTTTAACATCACAGCTAGTGT	242
Qy	924	LProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGlnArgLeuGlu	944
Db	243	GCCATTACCCGATGAAGAAATGATACCCCTTGAATGGGAAATCAGCAACGATCTCCTTCA	302
Qy	944	nThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyrSe	964
Db	303	GACATTTGGAACATATCAAAATAAATGAAAGAGCTCTCMAAAGACCCCATGTATTC	362
Qy	964	rPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrIlyLysAl	984
Db	363	CTTTTCAGCTTGGCATCAGAAATACTTATAGCGGACAGCAATTCATTAGAAACAAAAAGGC	422
Qy	984	aSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLe	1004
Db	423	TTCCCCCTCTCGACACcAGGCTCAGTGTCTGAGAGGGCGGTATGTGTGTCAATTTGCCCTTT	482
Qy	1004	uGlyThrTyrTrpAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGl	1024
Db	483	GGGAACCTATTATATCTCGAACAATTTCACTGTGAAGCTGCGGATCGGATCCTATCA	542
Qy	1024	nAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIl	1044
Db	543	AGATGAAGAAGGGCAACTTGAGTGCAAGCTTTTGCCCCCTCTGGGATGTATACAGGAATAT	602
Qy	1044	eHisSerArgAsnIleSerAspCysValLysAlaGlnCysLysGlnGlyThrTyrSerTyrSe	1064
Db	603	CCATTCAAGAAACATCTCTGATTGTGAAGCTCAGTGTAAACAGGCACTTACTCATACAG	662
Qy	1064	rGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySerAr	1084
Db	663	TGGACTTGAGACTTGTGWAATCGTCCACTGGGCATTTATCAGCCAAAAATTTGGTTCGCG	722
Qy	1084	gSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSe	1104
Db	723	GAGCTGCCTCTCGTGTCCAGAAAAACCTCAACTGTGAAAGAGAGCGCGTGAACATTTC	782
Qy	1104	rAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCysHi	1124
Db	783	TGCATGTGGAGTTCCTTGTCCAGAAGGAAATTCCTCGCGTTCTGGGTAAATGCCCTGTCA	842
Qy	1124	sProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysPr	1144
Db	843	CCCATGTCTCGTGACTATTACCAACCTTAATCGAGGGAAGGCCCTTCTGCGCTGGCCTGTC	902
Qy	1144	oPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSerSerPheSe	1164
Db	903	CTTTTATGGAATACTACCCCATTTGCGTGTCCAGATTCATACAGAAATGTTCCAGTTTATG	962
Qy	1164	rSerThrPheSerAlaAlaGluGluSerValProProAlaSerLeuGlyHisIleLys	1184
Db	963	TTCAACTTTCTCAGGGCGCAGAGGAAGTGTGTGTCGCCCTCTCTTGGACATATTA	1022
Qy	1184	sLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHisAs	1204
Db	1023	AAAGAGGCATGAAATCAGCAGCTAGGTTTTTCATGAATGCTTCTTTAAACCCCTTGCCCAA	1082
Qy	1204	nSerGlyThrCysGlnLeuGluValArgGlyTyrTrpValCysLeuCysProLeuGlyTyrTh	1224
Db	1083	TAGTGGAACTCTCCAGCAACTTGGCGGTGGTATGTTTGTCTCTGTCCACTTGGATATAC	1142

Qy	1224	gGlyLeuLysCysGluThrThrAspGluCysSerProLeuProCysLeuAsnGlnG	1244
Db	1143	AGGCTTAAAGTGTGAACACACATCATGATGAGTGCAGCCCACTGCCCTCTCAACATGG	1202
Qy	1244	YValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGlyG	1264
Db	1203	AGTTTGTAAAGACCTAGTTGGGGAATTCATTTGTGAGTGGCCATCAGGTTACACAGGTCA	1262
Qy	1264	nArGysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLysGlyIleCy	1284
Db	1263	GCGGTGTGAAGAAATATAAATCAGGTGTAGTCCAGTCCCTGTGTTTAAATAAAGGAATCTG	1322
Qy	1284	sValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGly	1301
Db	1323	TGTTGATGGTGTGGCTGGCTATCTTGACATGTTGTGAAGGATTTGTAGGT	1374
RESULT 13			
ABK35663			
ID	ABK35663	standard; cDNA; 1408 BP.	
AC	ABK35663;		
DT	08-MAY-2002	(first entry)	
XX		cDNA sequence #54 encoding novel human secreted protein.	
DE		Human secreted protein; hyperproliferative disorder; autoimmune disorder;	
KW		immune deficiency disorder; blood disorder; inflammatory disorder;	
KW		infectious disorder; allergic condition; neurodegenerative disorder;	
KW		liver fibrosis; coagulation disorder; gene therapy; antimicrobial;	
KW		tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.	
XX		Homo sapiens.	
OS			
XX		WO200177289-A2.	
FN		18-OCT-2001.	
PD		29-MAR-2001; 2001WO-US010232.	
XX		06-APR-2000; 2000US-0195605P.	
PF		(GENY) GENETICS INST INC.	
XX		Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;	
PI		Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;	
PI		Clark HP, Pechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;	
XX		WPI; 2002-179322/23.	
DR		Six hundred and twenty three polynucleotides derived from a variety of	
XX		human tissue sources which encode secreted proteins, useful for treating	
PT		immune deficiencies and disorders such as autoimmune disorders.	
PT		Claim 1; Page 101; 393pp; English.	
XX		The present invention relates to the isolation of novel cDNA sequences	
XX		which encode human secreted proteins. The cDNA sequences have been	
CC		derived from a variety of human tissues. The invention also provides a	
CC		method for producing proteins from these polynucleotide sequences. The	
CC		proteins are useful for identifying compounds that modulate their	
CC		activity and production. The sequences of the invention are useful for	
CC		treating diseases such as hyperproliferative disorders (e.g. cancer),	
CC		immune deficiency disorders (e.g. severe combined immunodeficiency	
CC		(SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders	
CC		(e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis),	
CC		infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma),	
CC		neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis,	
CC		coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide	
CC		sequences of the invention are also useful in gene therapy. ABK35610-	
CC		ABK36232 represent the cDNA sequences of the invention that encode for	
XX		novel human secreted proteins	

SQ Sequence 1408 BP; 456 A; 285 C; 291 G; 376 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.39e-107 Length: 1408
 Score: 1977.00 Matches: 362
 Percent Similarity: 99.72% Conservative: 0
 Best Local Similarity: 99.72% Mismatches: 1
 Query Match: 19.35% Indels: 1
 DB: 6 Gaps: 0

US-09-977-053-6 (1-1842) x ABK35663 (1-1408)

Qy 505 LysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPheGlyThrIle 524
 Db 2 AAGATGTCATCATATCCCCACATCTGTGGCAGCAGCCAGCCAAATTTGGAGCAGATC 61
 Qy 525 CysTyrValSerCysArgGlnGlnPheIleLeuSerGlyValLysGluMetLeuArgCys 544
 Db 62 TGCTATGTAAGTTGCCGCCAAGGGTTCATTTTATCTGGAGTCAAGAGAAATGCTGAGATGT 121
 Qy 545 ThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCysLysAspValGluAla 564
 Db 122 ACCACTTCTGGAAATGAATGTCGGAGTTCCAGGAGCTGTGTGTAAGAGCTGGAGCT 181
 Qy 565 ProGlnIleAsnCysProLysAspIleAlaLysThrLeuGluGlnAspSerAla 584
 Db 182 CCTCAATCACTGTCTTAGGACATAGAGCTAAGACTCTGGAAACAGCAGATTTCTGCC 241
 Qy 585 AsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysValSerValHis 604
 Db 242 AATGTTACTGGCAGATTTCCACACAGCTTAAGACCAACTCTGGTGAAGAGTGTCTAGTCCAC 301
 Qy 605 ValHisProAlaPheThrProProTyrIlePheProIleGlyAspValAlaIleValTyr 624
 Db 302 GTTTCATCCAGCTTTCCACCCCACTTACCTTTTCCCAATTGGAGATGTTGCTATCGTATAC 361
 Qy 625 ThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIleAsp 644
 Db 362 ACGGCACTGACCTATTCGGGACACAGCCAGCTGCAATTTTCCATATCAAGTTATTTGAT 421
 Qy 645 AlaGluProProValIleAspTrpCysArgSerProProValGlnValSerGluLys 664
 Db 422 GCAGAACCCCTGTCTAGATAGCTGTGTGTCAGATCTCCACTCCGCTCCAGGTTCTCGGAGAG 481
 Qy 665 ValHisAlaIleAspTrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeuVal 684
 Db 482 GTACATGCCGCAAGCTGGATGAGCTTCAGTTCTCAGACCACTCAGGGCT-GAATTTGGTC 540
 Qy 685 IleThrArgSerHisThrGlnGlnAspLeuPheProGlnGlyGluThrIleValGlnTyr 704
 Db 541 ATTACCAAGAGTCTATACACAGGAGAGCTTTTCCCTCAAGGGGAGACTATAGTACAGTAT 600
 Qy 705 ThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLysGly 724
 Db 601 ACAGCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATTTGTCATAAAGGT 660
 Qy 725 SerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAspAsn 744
 Db 661 TCTCCCTGTGAATTTCCATTCACACCTGTGAATGGGATTTTATATGCATCTCCAGATAT 720
 Qy 745 ThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySerThr 764
 Db 721 ACTGGAGTCACTGATCATATTAACCTTGTGGAGGGCTATGATTTTCAAGAGGGTCTACT 780
 Qy 765 AspLysTyrTyrCysAlaLysGluAspGlyValTrpLysProThrTyrThrThrIleTrp 784
 Db 781 GACAAGTATTTATTTGCTTATGAGATGGGCTCTGGAAACCAACATATACCACTGATATGG 840
 Qy 785 ProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGluMetPheTyr 804
 Db 841 CCAGACTGTGCCAAAACAGCTTTTGGCAACACAGGGTTCAAGGCTCTTTGAGATGTTCTAC 900
 Qy 805 LysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAlaPheGluThr 824

Db 901 AAGCAGCTCGTTCTGTGATGACACAGATCTGATGAAGAAGTTTCTTGAAGCATTTTCAGAGC 960
 Qy 825 ThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAspCysArgLeu 844
 Db 961 ACCCTGGGAAAAATGGTCCCATCATCTTTTGTAGTGTGACAGGACATTTGACTGCGAGCTG 1020
 Qy 845 GluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe 864
 Db 1021 GAGGAGAACCTGACCAAAAATATTTGCTAGATATATATTTATGACTATGAAAATGCTTT 1080
 Qy 865 AlaIleGly 867
 Db 1081 GCAATGCT 1089
 RESULT 14
 AAS26857
 ID AAS26857 standard; cDNA; 1892 BP.
 AC AAS26857;
 XX 07-NOV-2001 (first entry)
 DT
 DE Human cDNA encoding a novel secreted protein, SEQ ID 49.
 XX Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;
 XX cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective;
 XX antibacterial; virucide; fungicide; ophthalmological; vulnerary;
 XX secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 XX cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 XX cerebral ischaemia; angiogenesis; nervous system disorder;
 XX Alzheimer's disease; infection; ocular disorder; corneal infection;
 XX wound healing; epithelial cell proliferation; skin ageing; food additive;
 XX preservative; antiproliferative.
 OS Homo sapiens.
 PN WO200155441-A2.
 XX 02-AUG-2001.
 PD 17-JAN-2001; 2001WO-US001320.
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184684P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-019076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-020515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
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PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
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 PR 23-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
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 PR 02-OCT-2000; 2000US-0236802P.
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 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
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PR 08-NOV-2000; 2000US-0246613P.
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 PR 17-NOV-2000; 2000US-0249214P.
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 PR 17-NOV-2000; 2000US-0249216P.
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 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
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 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251858P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-476222/51.
 P-PSDB; AAU16952.

Novel polypeptides and polynucleotides useful as diagnostic reagents to
 diagnose diseases or disorders associated with aberrant expression or
 activity of polypeptides, for treating blood clotting disorder,
 hemophilia.

Claim 1; SEQ ID NO 49; 601pp; English.

The invention relates to isolated nucleic acid molecules and their
 encoded secreted proteins. The nucleic acids and proteins are used to
 prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 in diagnosing a pathological condition or susceptibility to a
 pathological condition. Antibodies to the proteins can also be used in
 alleviating symptoms associated with the disorders and in diagnostic
 immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
 (ELISA). Disorders which are diagnosed or treated include autoimmune
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
 neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
 arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysplasia,
 nervous system disorders e.g. Alzheimer's disease, infections caused by
 bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
 and many other disorders listed in the specification. The polypeptides
 can also be used to aid wound healing and epithelial cell proliferation,
 to prevent skin aging due to sunburn, to maintain organs before
 transplantation, for supporting cell culture of primary tissues, to
 regenerate tissues and in chemotaxis. The polypeptides can also be used
 as a food additive or preservative to increase or decrease storage
 capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 minerals, cofactors and other nutritional components. The present
 sequence encodes a novel secreted protein of the invention. Note: The

Alignment Scores:

Pred. No.: 3 81e-79 Length: 1892
 Score: 1498.00 Matches: 263
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.62% Mismatches: 0
 Query Match: 14.66% Indels: 0
 DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x AAS26857 (1-1892)

QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValAspGlyPheValGlyLeuHis 1303
 DB 2 TGTGTTGATGGTGGCTGCTATCGTGCACATGTGAAAGGATTTGTAGCGCTGCAT 61
 QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGlu 1323
 DB 62 TGTGAACAGAAAGTCAATGAATCCAGTCAAAACCCATGCTTAAATTAATGAGTCTGTGAA 131
 QY 1324 AspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThrArgCysGly 1343
 DB 122 GACCAGTTGGGGATTCATGTCMAATGCCACCTGGATTTTGGTACCCGATGTGA 181
 QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly 1363
 DB 182 AGAAGCTGCATGAGTGTCTCAGTCAGCCATGCAGAAATGGAGCTACCTGTAAAGACGGT 241
 QY 1364 AlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 DB 242 GCCAATAGCTTCAGATGCGCTGTGTGAGCTGGCTTCACAGATCACACTGTGAATGAAC 301
 QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
 DB 302 ATCAATGAATGTCAGTCTAATCATCATAGTAATCAGCCACCTGTGTGGATGAATTAAT 361
 QY 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer 1423
 DB 362 TCATACAGTTGTAATGTCAGCCAGGATTTTCAGGCCAAGGTCGAAACAGAACAGTCT 421
 QY 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyLysLeuGlyTyrValMetLeuAspGly 1443
 DB 422 ACAGGCTTTAACTGGATTTTGAAGTTCTGGCATCTATGGATATGTCATGTAGATGGC 481
 QY 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspMet 1463
 DB 482 ATGCTCCATCTCTCCATGCTTAACCTGTACCTTCTGGATGAATCTCTGACGACATG 541
 QY 1464 AsnTyrGlyThrProLeuSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
 DB 542 AACTATGGAACCAATCTCTATGCAATGATAACGGCAGCGACATACTTGCTCCTG 601
 QY 1484 ThrAspTyrAsnGlyTrpValLeuTyrValAsnGlyArgGluValIleThrAsnCysPro 1503
 DB 602 ACTGANTATAACGGCTGGGTTCTTTATGTGAATGGCAGGAAAGATAACAACTGTCCC 661
 QY 1504 SerValAsnAspGlyArgTrpHisHisIleAlaIleThrTrpThrSerAlaAsnGlyIle 1523
 DB 662 TCGGTGAATGATGGCAGATGGCATATATTCATCACTTGGACAGTGGCATGGCATC 721
 QY 1524 TrpLysValTyrIleAspGlyLysLeuSerAspGlyAlaGlyLeuSerValGlyLeu 1543
 DB 722 TGGAAAGTCTATATCATGATGGAAATATCTGACGGTGTGCTGCGCTCTCTGTGGTTG 781
 QY 1544 ProIleProGly 1547
 DB 782 CCCATACCTGGT 793

RESULT 15

AAH08402

ID AAH08402 standard; cDNA; 765 BP.

XX AC AAH08402;

XX DT 26-JUN-2001 (first entry)

XX

DE Human cDNA clone (5'-primer) SEQ ID NO:5237.
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX Homo sapiens.
 XX EF1074617-A2.
 XX 07-FEB-2001.
 XX 28-JUL-2000; 2000EP-00116126.
 XX 29-JUL-1999; 99JP-00248036.
 XX 27-AUG-1999; 99JP-00300253.
 XX 11-JAN-2000; 2000JP-00118776.
 XX 02-MAY-2000; 2000JP-00183767.
 XX 09-JUN-2000; 2000JP-00241899.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 1; SEQ ID NO 5237; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

Sequence 765 BP; 202 A; 182 C; 194 G; 183 T; 0 U; 4 Other;

Alignment Scores:

Pred. No.: 1.28e-76 Length: 765
 Score: 1447.00 Matches: 251
 Percent Similarity: 98.82% Conservative: 0
 Best Local Similarity: 98.82% Mismatches: 3
 Query Match: 14.16% Indels: 0
 DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x AAH08402 (1-765)

QY 195 ThrAspGlyTyrSerAsnGlyGlyAspProArgProIleAlaSerLeuArgAspSer 214

DB 2 ACTGATGATATTCCCAATGGGGAGACCCCTAGACCAATTGCGCGTCTACTCGAGATTCA 61

QY 215 GlyValGluIlePheThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMet 234

Db 62 GGAGTGGAGATCTTTCACCTTTTGGCATATGCGCAAGGACATTCGAGAGCTGAATGACATG 121
 Qy 235 AlaSerThrProGluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAla 254
 Db 122 GCTTCACCCCAAGGAGGAGCAGCTTTACCTGCTACACAGTTTGAAGAAATTTGAGGCT 181
 Qy 255 LeuAlaArgArgAlaLeuHisGluLeuLeuProSerGlySerPheIleGlnAspMet 274
 Db 182 TTAGTCTCCCGGCGCAATGATGAAGATCTTCTCGGAGTTTATTCAGATGATATG 241
 Qy 275 ValHisCysSerTyrLeuCysAspGluGlyLysAspCysCysAspArgMetGlySerCys 294
 Db 242 GTCCACTCTCATATCTTTGTGATGAGGACAGGACTCTGTGACCGAATGGAGAGCTG 301
 Qy 295 LysCysGlyThrHisThrGlyHisPheGluCysIleCysGluLysGlyTyrTrpGlyLys 314
 Db 302 AAATGTGGACACACACAGGCCATTTTGAAGTGCATCTGTGAAGAGGGGTATTACGGGAA 361
 Qy 315 GlyLeuGlnTyrGluCysThrAlaCysProSerGlyThrTyrLysProGluGlySerPro 334
 Db 362 GGTCTGCAGTATGAATGACAGCTTGCCCATCGGGACATACAAACCTGAAGGCTCACCA 421
 Qy 335 GlyGlyIleSerSerCysIleProCysProAspGluAsnHisThrSerProGlySer 354
 Db 422 GGAGGAATCAGCAGTTGCTCATTCATGCTCTGATGAATAATCACACCTCTCCACTGGAAGC 481
 Qy 355 ThrSerProGluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGlu 374
 Db 482 ACATCCCTCTGAAGCTGTCTGCAGAGAGGATACAGGGCATCTGGCCAGACCTGTGAA 541
 Qy 375 LeuValHisCysProAlaLeuLysProGluLysGlyTyrPheIleGlnAsnThrCys 394
 Db 542 CTTCGCCACTGCTCCCTGGAAGCTCTCCGAAATGGTTACTTTATCCAAACACTTGC 601
 Qy 395 AsnAsnHisPheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGly 414
 Db 602 AACACCACTTCATGACAGCTGTGGGTCCGATGTCAACCTGATTTGATCTTGGGA 661
 Qy 415 SerSerIleLeuLeuCysLeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArg 434
 Db 662 AGCAGCATCATCTTATGCTACCCAAATGTTTGTGTCGGTCCGNTTANAGAGCTACTGCAGA 721
 Qy 435 ValArgThrCysProHisLeuArgGlnProLysHisGlyHis 448
 Db 722 GTAAGAACATGCTCTCATCTTCGGCAGCGCAACATGNCAC 763

RESULT 16
 ABL14889

ID ABL14889 standard; cDNA; 10489 BP.

AC ABL14889;

XX ABL14889;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39149.

XX Drosophila melanogaster expressed polynucleotide; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

OS WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.
 DR P-PSDB; ABB70786.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Claim 1; SEQ ID NO 39149; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 10489 BP; 2233 A; 3116 C; 3060 G; 2080 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,93e-70 Length: 10489
 Score: 1354.00 Matches: 514
 Percent Similarity: 32.61% Conservative: 250
 Best Local Similarity: 21.94% Mismatches: 705
 Query Match: 13.25% Indels: 879
 DB: 4 Gaps: 87

US-09-977-053-6 (1-1842) x ABL14889 (1-10489)

Qy 6 AlaPheCysCysTyrGlyLeuAlaLeuValSerGlyTrpAlaThrPheGlnGlnMetSer 25
 Db 1417 GCACAATGCTGTGATGTGCGCCACATTCGCGC-----1452
 Qy 26 ProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaProGlySer 45
 Db 1453 -----CGATTGC--CGAGCTCGAACCCCGA-----1477
 Qy 46 IleProAlaProProAlaProGlyAspGluAlaAlaGlySerArgValGlu-----62
 Db 1478 ATTGGAGCTTGGCCCTCCAGTCGCGACCGCTTTTCGGTACGCTGCTCAGCTTTACATGT 1537
 Qy 63 ArgLeuGlyGlnAlaPheArgArg---ArgValArgLeuLeuArgGluLeuSerGluArg 81
 Db 1538 CCCATTGGACAGGAGTTTGCACCGCGCAAGACGCGACTGGTTACCGAATG-TCTGCGCG 1596
 Qy 82 LeuGluLeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArgSer 101
 Db 1597 TGGCAACTGGAGTGTCTCTCATATACC-----CAAGTGTGAGG-AGGTCT 1640
 Qy 102 GluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThrArg 121
 Db 1641 ACTGCGGTCTGTGCCACAATCGACACGGTTTCTCCATTGCTCTCTCGAACGTAACCT 1700
 Qy 122 ValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIleSer 141
 Db 1701 ATCGCGGTATAGCAATGTACCACTGTCTAGCGCGCTTTTCGCTCGCGTGCCTCGGA 1760
 Qy 142 ThrArgArgAla-----ArgGlnHisLysCys---Ala 151
 Db 1761 TCGAAGAGATC-TCTGTCTCGGATGGCCGTTGGAGCGAGACGCCCACTGATGGCC 1819
 Qy 152 LeuLeuLeuGlnGluIleProAlaIleSerTyr-----ArgGlyGly 165
 Db 1820 TCCAGTGGCAGCGCTGCGGAAGTGGCACACGCAACGTCACCTGCTGTAATGAGGT 1879
 Qy 166 GlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAlaArgGlu 185
 Db 1880 GGT-----CGCAGC 1888

186 AsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAspProArg 205
1889 TAGCGCACCATTTGTCAGTATGAGTGTGAGCCGGCTACGAGCGCATGCGCATCCC--- 1945
206 ProIleAlaLeuSerLeuArgAspSerGlyValIlePheThrPheGlyIleTyrGln 225
1946 -----GTGCTGACCTGTATGTTCGAACGGCAGCTCGAGT 1978
226 GlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCysTyrLeu 245
1979 GGTGATGTATACCAAGATGCACG-----CGCAAGCGGTGCTTC--- 2014
246 LeuHisSerPheGluGluPheGluAlaLeuAla-----Arg 257
2015 -----GAAATCCCGACCATTTGCCAACGGCTTTGTGTGGACTCGACCGGA 2059
258 ArgAlaLeuHisGluAsp-----LeuProSerGlySerPheIleGln 271
2060 GCCTACTCTTCGGCGATGAGGCGAGGTGCTGCTTCAAGGGCTACAAACTGATCGGC 2119
272 AspAspMetValHisCysSerTyr-----LeuCysAspGlu 283
2120 AGCAACATCATGCGCTGCACGAGCGAGGCCAGAGTTTCGAGCAGCGCGCGAGGAC 2179
284 GlyLysAspCys-----CysAspArgMetGlySerCysValCysGlyThrHis 299
2180 ATCAACAGTGCAGCTCTCTCGAGTGGAC-----CTAACACACCGAGTCCAGACAG 2236
300 ThrGlyHisPheGluCysIleCysGluLysGlyTyrProly----- 313
2237 AACGGCTCTCTCACTGCCAGTGCAGGACGCGGATTCAC-GGCTACCACCGAGTGTGGCC 2295
313 ----- 313
2296 CGTCGTGATTTGGGCTTGGGTAAATGAGGCGCATACCGGATGACAGCATCACCACTCGGT 2355
314 -----LysGlyLeuGlnTyrGluCysThrAla----- 322
2356 CAGTGAGCGGGCTACAGCAGGAGCAGCTGCGCTTGAACACGATGGCTGTGGGTGG 2415
323 -----CysProSerGlyThrTyrLysPProGluGlySer----- 333
2416 CTCTTCGGAGCTGTGTGCCAAGTCTGATCTACTGACCTGAGCGCACCCACCATTTCTGCG 2475
333 ----- 333
2476 TGGCTTCCGACCATGTCGTGAGCGTCCCGANGGCAATGTGGCTTCAGCTCGCGGT 2535
333 ----- 333
2536 GCGTCTGCGAGTACACCAACGATCTGACGGATGTGTTCAAGGATTATGCCAATCCCGACGG 2595
333 ----- 333
2596 CACTGCGTGAATTCGGCATCTCGGAGCCAGCTCTCCATCTTAAACCTGCGCCCTGCC 2655
334 -----ProGly----- 335
2656 CATCGAAGCTCGTATATTGCTTCGCGATCCAGGACTACGTGGGTGCGCCCTGTCTGGG 2715
336 ---Gly-IleSerSerCys-----IleProCysProAspGluAsnHisThrSerProPr 352
2716 CATGGAGCTGATGGGTGACGCGCTGTGGATTGCTGACATCAACGAGTGCAGCAAGAA 2775
352 oGlySerThrSerProGluAspCysVal-----CysAr 363
2776 CAATGGCGGTGTGACCAAGAGTGCATCACTCACCGGGGGATTTGCTGTGGCTGCA 2835
363 gGluGlyTyrArg----- 368
2836 CACTGGCTACCACTGTATACCTTCCAAACGCGAGGTGGCTATCACATCGAAGCGCTCGA 2895
368 aSerGlyGln-----ThrCysGluLeuValHisCy 378

2896 ATCCGCGAACAGTGTGAGTGTGACACCTATCAGCGCAACAGACCTGTGTCTCTCATGTG 2955
378 sProAlaLeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPh 398
2956 TCCCGAACTGGAGGCGCCGAGAATGTCACTCTCAGCGCAGCAAGAACATCATCTACT 3015
398 eAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleI 418
3016 TGGCGATGTGGTCCGCTTCCAGTGCCTTTGGCTACATCATGAGCGGCGAGCTCGGCGC 3075
418 eLeuCysLeuProAsnGlyLeuTyrPheSerGlySerGlySerTyrCysArgValArgThrCy 438
3076 CCGTGTGCTCTCCAGCGGTCACTGGAACGCCAGCGTACCGAGTGCATATTATGCCAATG 3135
438 sProHisLeu----- 441
3136 CGTTTCCCTGCCGATGACAAGTTGGAGGGTCTGACTGTGGGCCCGCCCGATCCCGAATC 3195
441 ----- 441
3196 CGTTCTAGTGCCTTCCGTGACAAATGTGACCAATTACGTGGGATCGCGGAGCGCCAACT 3255
441 ----- 441
3256 GAGAGCCACCGCTTCTCTGCTTCCGCGAGTGCCTGTAAGATCCCAAGCCCGGTCTGCC 3315
442 -----ArgGlnProLysHisGlyHisIleSerCys----- 451
3316 CGATTACTGCTATCCGAATGACGCGCTTGTGCCGAGTGGATGCTACTACCCCAT 3375
452 -----SerThrArgGluMetLeuTyrLysTh 460
3376 GCCAACGCCCGCGCAGAAATACGACAGTGTGTGACACTGCG-----TATCAGAG 3426
460 rThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGly-----Se 475
3427 CAGCTTCTTCTTGGCTGCCAGAACACCTTTAAGTTGGCTGACAGACGCGGTCTGCACGA 3486
475 rAspLysLeuThrCysGlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValG 495
3487 CAATGTGGTGTGTGTGGAGCCGATGTATCTGGGACTTTGGAGATCTTCTGCTGTGAGG 3546
495 uArgHisCysSerThrPheGlnMetProLysAsp----- 506
3547 ACCTGTGTGCGAGATCCGGAGACCGCGAGATGGTGCAGCATTCACCGCAGTATGA 3606
507 -----ValIleIleSerProHi 512
3607 GCAGAGCTCGGAGGTGTACTTCCGCTGCAATCGTCTGCTGATCATCTCTGATCAATCCGCG 3666
512 sAsn----- 513
3667 ACCCATTTACATACGAGCGAGCGAGTCCAAAGTTCATCAAGCTTTTGGATTAAGTTC 3726
513 ----- 513
3727 CGSCAGATTCGGATTCCGATTCGGCCATCAATGCCACTTCGAGCGACCCCAATTACGAGGCCAA 3786
514 -----CysGlyLysGln----- 517
3787 GAACATCCGTCTCAACTCGGCCACTGGCTGTGTGGCAAGCAGGAGGCGCTTCACCTATGT 3846
517 ----- 517
3847 GAGCGTGGATCTGGGTGCAGATCTATCGAGTCAAGCGGATTCGTGTGAAGGGGTGTGTTAC 3906
517 ----- 517
3907 CAACGACATTTGTGGGCGAGGCCCGACGAGATTCGGTCTTCTTACAAACAGCTGAGAGCGA 3966
518 -----ProAlaLysPheG 522
:::|

1188 uileSerSerGlnValPheHisGluCysPheAsnProCysHisAsnSerGlyThrCy 1208
 5876 -----TGTGGTGAAGGTGCTTGCAGCAGCGCGACTGTG 5910
 1208 sGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrThrGlyLeuLysCy 1228
 5911 TGTGCCCATGGCCATGACATCCAGTGTCTGTCCGCGCCGATCTCTGGACGTCGCTG 5970
 1228 sGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsnGlyValCysLysAs 1248
 5971 CGAACAGGACATGACGAGTGGCTCCAGCCCTGTGTACAAATGGTGTGATGCAAGGA 6030
 1248 pLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGlyGlnArgCysGluG 1268
 6031 TCTGCCGAGGGCTATCGCTGTGAGTGGCCGGCTGGATCTCGGGCATCAATTCGACGA 6090
 1268 uAsnIleAsnGluCysSerSerProCysLeuAsnLysGlyIleCysValAsp----- 1286
 6091 GGAGCCAGTGTACTGTGGCAACGACACTGTTCGGCCAGGGCCATGTGCAAGAACGAGCC 6150
 1287 -----GlyValAlaGly----- 1290
 6151 GGCGTACAGAACTGACTGTCTGTGCGCGAGTGGCTTACACCGCGGATCAGTGGCAGCT 6210
 1290 ----- 1290
 6211 GACCATCGATCCGTGCACGGCGAATGCATCCGTGGCGAAACGGAGCCAGCTCCAGGC 6270
 1291 -----TyrArgCysThrCysValLysGlyPheValGlyLeuHisCysG 1305
 6271 CTTGGAGCAGGTCGCTACAAAGTGCAGTGTGTCCCGGATGGGAGGCGCATCTGTGA 6330
 1305 uThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGluAspG 1325
 6331 GCAGAAATATCAATGACTGTTCGGAGATCCCTGCTGTGGCGCCCAACTGCACAGATCT 6390
 1325 nValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThrArgCysGlyLysAs 1345
 6391 GGTCAATGACTTCCAGTGGCCCTGTCCGCCAGGATTTACGGCGCAAGCGATCGAGCAAA 6450
 1345 nValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGlyAlaAs 1365
 6451 GATCGATCTCTGCCTATCCGAACCATGCAAGCATGGC-----ACCTGCGTGGATCTGTGT 6507
 1365 nSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAs 1385
 6508 CGATCAGCAGTGTGTTGGCCATCCGGCTGGACGGATCCGCTCGCACATCAACATCGA 6567
 1385 nGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTy 1405
 6568 CGACTGGAGAACCGACCTCGGCCAATGAGGNACTTGGTCGACCTGGTCGAGCGCTA 6627
 1405 rSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGlu-ThrGluGlnSerThrG 1425
 6628 TAGCTGCAACTGTGAACCCGGCTACACGGCGCAGAAATTCGCCGACACCATCGACGACTG 6687
 1425 lPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGlyMetL 1445
 6688 CG----- 6689
 1445 euProSerLeuHisAlaLeuThrCys-----ThrPheTrpMetLysSerSerA 1461
 6690 --CCTCGAATCCCTCCAGCAGCGCGCCACTGTGTGACCACTGGTGGATGGCTTCAGCTG 6747
 1461 spAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrL 1481
 6748 CAAATCGCGCCCTGGCTACGCTGGGTCTCTCTCGC----- 6782
 1481 euLeuLeuThrAspTyrAsnGlyTrpValLeuTyrValAsnGlyArgGluLysIleThrA 1501
 6783 -----AGCCCGAGATCGACGA 6798
 1501 enCysProSerValAsnAspGlyArgTrpHisIleAlaIleThrTrpThrSerAlaA 1521

6799 GTGTCTGAGCGACCCCTCGCAATCCGGTGGCGACGG-----AGCGCTG 6840
 1521 anGlyIleTrpLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer- 1540
 6841 CCTCGATCTGGACAAACAAT-----TCGAGTGGCTGTGTCGGGACGGGAT 6885
 1541 ValGlyLeuProIleProGlyGly-----GlyAlaLeuVal-Leu----- 1553
 6886 CAAGGACCCCTGTGCGCCACGACATCGATCGAGCGCGGCGCGCTGTCTGAACAA 5945
 1554 -GlyGlnGluGlnAspLysLysGlyGlu-----GlyPheSerProAlaGluSerPh 1570
 6946 CGGCATCTGTGCGATCGCTGGTGGCTTTGAGTGGCGCTCGCGAGCCAGGA----- 6997
 1570 eValGlySerIleSerGlnLeuAsnLeuTrpAspTyrValLeuSerProGlnGlnVally 1590
 6998 -----TGGAGTGGCATCGCTCGCGAGCAGCAGGTGAC 7029
 1590 sSerLeuAlaThrSerCysProGluLeuSerLysGlyAsnValLeuAlaTrpProAs 1610
 7030 CACGTGGAGCTCAGGCGCGTGGCAGAACGATCCGAGCTGCATCGACCTGTTCCAGGA 7089
 1610 pPheLeuSerGlyIleValGlyLysValLysValLysValLysValLysValLysVal 1630
 7090 CTAC-----TTCTCGGTG----- 7102
 1630 pCysProArgLeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysPr 1650
 7103 -TGTCCTCCAGC---GCGACCGATGGCAGACATGCGAGACCGCTCCGGA----- 7147
 1650 oGlySerLysValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProValG 1670
 7148 -----CGCTGCATCGCTGGATCTCT----- 7165
 1670 nTyrCysLeuAsnGlnGlyGlnTrpThrGlnProLeuProHisCysGlu----- 1686
 7166 ---TGATGACCGTGGCAAG-----TGCCAGGACTTTGGCTC 7200
 1687 -ArgIleSerCysGlyValProProProLeuGluAsnGlyPheHisSerAlaAspAspPh 1706
 7201 TGGTCTTTAACTGCACTGTCCT-----GCGGAT----- 7228
 1706 eTyrAlaGlySerThrValThrTyrGln-----CysAsnAs 1718
 7229 -TACTCGGCATTTGGTGTCTAGTACGAGTACGACGATCGCGAGGAGCATGCTGTGAGAA 7287
 1718 nGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnG 1738
 7288 TGGC-----GCCACTGTGTGGACAATGGTGTCT-----GG 7317
 1738 yValSerProSerCys-----LeuAspValAspG 1748
 7318 CTACAGCTGCCAGTGGCCACCTGCTCCACCGTGGCAATTCGGAACAGGACATCGTGA 7377
 1748 uCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAsnValAspGlySerTy 1768
 7378 CTGCAAGGACAACTCT---TGCCCAACCGGCGCCACGCTGGTGGATCTTAACCAACGGCTT 7434
 1768 rIleCysSerCysValProProTyrThrGlyAspGlyLysAsnCysAlaGluProIleLe 1788
 7435 CTACTGTCACTGC-----CCCTTCAATATACCGGAGACGATTCGCCGACGCGCATCCA 7488
 1788 s 1788
 7489 A 7489
 RESULT 17
 ACAS7318
 ID ACAS7318 standard; cDNA; 706 BP.
 XX
 AC ACAS7318;

DT	10-JUN-2003	(first entry)	
DE	Human adipocyte Selected Interacting domain, SID, cDNA #405.		
KW	Human; ss; gene; prey; adipocyte; SID; selected interacting domain;		
KW	anorectic; antidiabetic; protein-protein interaction; diabetes;		
KW	yeast 2-hybrid assay; metabolic disorder; obesity.		
XX	Homo sapiens.		
OS	WO200286122-A2.		
PN	31-OCT-2002.		
PD	14-MAR-2002; 2002WO-EP003768.		
PF	14-MAR-2001; 2001US-0275734P.		
PR	(HYBR-) HYBRIGENICS.		
PA	Legrain P, Daviet L;		
XX	WPI; 2003-103412/09.		
DR	P-PSDB; ABB070774.		
XX	New complex between two interacting proteins in adipocyte cells, useful		
PT	for identifying selected interacting domains that modulate protein		
PT	interactions, or for preventing or treating metabolic disorders such as		
PT	obesity or diabetes.		
XX	Claim 7; Page 244; 382pp; English.		
PS	The invention relates to a complex between two interacting proteins in		
CC	adipocyte cells, given in the specification. The proteins are identified		
CC	by selecting a bait protein from a known adipocyte marker and then		
CC	performing a yeast 2-hybrid selection to isolate prey proteins encoded by		
CC	members of an adipocyte cDNA library. The proteins are designated SID		
CC	(RTM) (selected interacting domains) proteins. Also included are a		
CC	polynucleotide encoding a polypeptide in the adipocyte cells, a		
CC	recombinant host cell expressing at least one of the interacting		
CC	polypeptides of the complex, selecting a modulating compound in acid		
CC	cells, a SID (RTM) polypeptide comprising any of the 738 amino acid		
CC	sequences given in the specification (including its fragment or variant),		
CC	a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences		
CC	given in the specification (including its fragment or variant), a vector		
CC	comprising the SID (RTM) polynucleotide, a recombinant host cell		
CC	comprising the vector, a protein chip comprising the polypeptides and a		
CC	record comprising all or part of the data, listed in the specification.		
CC	The complex, polypeptides, polynucleotides and compounds are useful for		
CC	preventing or treating metabolic disorders such as obesity or diabetes.		
CC	The polynucleotides are useful as probes or primers. The complex is		
CC	particularly useful for identifying selected interacting domains (SID		
CC	(RTM)) for screening drugs that modulate the protein interaction, thus		
CC	exhibiting the therapeutic effect. The present sequence encodes a SID		
CC	(prey) protein of the invention		
XX	Sequence 706 BP; 202 A; 137 C; 173 G; 194 T; 0 U; 0 Other;		
SQ	Alignment Scores:		
	Pred. No.: 2, 11e-70 Length: 706		
	Score: 1341.00 Matches: 234		
	Percent Similarity: 100.00% Conservative: 1		
	Best Local Similarity: 99.57% Mismatches: 0		
	Query Match: 13.12% Indels: 0		
	DB: 7 Gaps: 0		
US-09-977-053-6	(1-1842) x ACA57318 (1-706)		
QY	1242 AsnAsnGlyValCysGlyAspLeuValGluPheLeuCysGluCysProSerGlyTyr 1261		
DB	2 AACATGGAGTTGTAAAGACCTAGTTGGGAATTCATTGTGAGTGGCCCATCAGGTAC 61		
QY	1262 ThrGlyGlnArgCysGluGluAsnLeuAsnGluCysSerSerProCysLeuAsnLys 1281		
DB	62 ACAGGTGAGCGGTGTGAAGAAATATAAATGAGTGTAGCTCCAGTCTCTGTTTAAATAA 121		
QY	1282 GlyTleCysValAspGlyValAlaGlyTyrArgCysThrCysValGlyGlyPheValGly 1301		
DB	122 GGAATCTGTGTGTGATGGTGTGGCTGCTATCGTTGCACATGTGTGAAAGGATTTGTAGGC 181		
QY	1302 LeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaVal 1321		
DB	182 CTGATTGTGAAACAGAGTCAATGAATGCCAGTCAAAACCCATGCTTAAATTAATGAGTTC 241		
QY	1322 CysGluAspGlnValGlyPheLeuCysLysCysProGlyPheLeuGlyThrArg 1341		
DB	242 TGTGAGACCAAGTTGGGGGATTTCTTGTGCAATGCCACCTGGATTTTGGGTACCCGA 301		
QY	1342 CysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLys 1361		
DB	302 TGTGAAAGAAACGTGATGAGTGTCTCAGTCAGCCATGCAAAATGAGAGTACCTGTGAAA 361		
QY	1362 AspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGlu 1381		
DB	362 GACGGTGCCTAATAGCTTCTGATGCTGTGAGCTGGCTTTCACAGGATCACACTGTGAA 421		
QY	1382 LeuAsnLeuAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu 1401		
DB	422 TTGACATCAATGAATGTCTCAATCATGTAGAAATCAGGCCACCTGTGTGGATGAA 481		
QY	1402 LeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlu 1421		
DB	482 TTAATTCATACAGTTGTAAATGTCCAGCCAGGATTTTCAGGCAAAAGGTGTGAAACAGAA 541		
QY	1422 GlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeu 1441		
DB	542 CAGTCTACAGGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGGATATGTCTGCTA 601		
QY	1442 AspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAsp 1461		
DB	602 GATGGCATGCTCCCATCTCTCCATGCTTAACCTGTAACCTTCTGGATGAAATCTCTGAC 661		
QY	1462 AspMetAsnTyrGlyThrProLysSerTyrAlaValAspAsnGly 1476		
DB	662 GACATGAACATGGAACACCACTCTCTATGCAAGTTGATAACGGC 706		
RESULT 18			
ABL14888/c			
ID	ABL14888 standard; cDNA; 13484 BP.		
XX	AC ABL14888;		
XX	DT 26-MAR-2002 (first entry)		
XX	Drosophila melanogaster expressed polynucleotide SEQ ID NO 39146.		
DE	Drosophila; developmental biology; cell signalling; insecticide;		
KW	pharmaceutical; gene; ss.		
XX	Drosophila melanogaster.		
XX	WO200171042-A2.		
PN	27-SEP-2001.		
PD	23-MAR-2001; 2001WO-US009231.		
PF	23-MAR-2000; 2000US-0191637P.		
PR	11-JUL-2000; 2000US-00614150.		
PR	(PEKE) PE CORP NY.		
PA	Venter JC, Adams M, Li PWD, Myers BW;		
PI	WPI; 2001-656860/75.		
XX	P-PSDB; ABB70785.		

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX Claim 1; SEQ ID NO 39146; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins (AB857737-
CC AB872072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13484 BP; 2974 A; 3619 C; 3741 G; 3150 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.63e-68 Length: 13484
Score: 1328.00 Matches: 518
Percent Similarity: 32.44% Conservativity: 256
Best Local Similarity: 21.71% Mismatches: 718
Query Match: 13.00% Indels: 900
DB: 4 Gaps: 88

US-09-977-053-6 (1-1842) x AB114888 (1-13484)

Qy 6 AlaPheCysCysThrGlyLeuAlaLeuVal-----SerGlyTyrAla 19
Db 11068 GCACATCTGCTGGGTAAGTCTTTATATTGAGATTACATAGTTCAATCT 11009

Qy 20 ThrPheGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAla 39
Db 11008 TCAATCTTGATCTCTAGATGGTGGCCACATCTCTGGCCGATGTC-CCGAGCTGCAA 10950

Qy 40 ProGlyAlaProGlySerIleProAlaProAlaProAlaProGlyAspGluAlaGlySer 59
Db 10949 CCGCGA-----ATTGGAGCCTTGGCCTCCAGTCCGACACCGCTTTCCGTACG 10902

Qy 60 ArgValGlu-----ArgLeuGlyGlnAlaPheArgArg-----ArgValArgLeuLeu 75
Db 10901 CTGGTCAGCTTTACATGCTCCATTTGACAGAGTTTGCCACCGGCAAGACCGGCTGTT 10842

Qy 76 ArgGluLeuSerGluArgLeuGluLeuValPheLeuValAspSerSerSerValGly 95
Db 10841 ACCGAATG-TCTGGCGGTGGCACTGGAGTGTCTCTACATACCCCAAGTGTGAG--GGT 10785

Qy 96 GluValAsnPhe----- 99
Db 10784 GAGTGTGCTTACCTATTTCATAATTGGATTCCATAATGATATGCAATCCCTTCCA 10725

Qy 100 ---ArgSerGluLeuMetPheValArgGlyLeuLeuSerPheProValValProThr 118
Db 10724 CAGAGTCTACTCGGTCCTGTCGCCAACAATGCAACAGGTTTCTCATTTGGCTCTCGA 10665

Qy 119 AlaThrArgValAlaIleValThrPheSerSerSerSerSerSerValValProArgValAsp 138
Db 10664 ACCTAACCTATCCGGGTATAGCAATGATACCACTGCTAGCGCGGCTTTGCTTCCGCTCGG 10605

Qy 139 TyrIleSerThrArgAla-----ArgGlnHisLys 149
Db 10604 GTGCTCCGATCGAGAAGATC-TCTGTGTCGCCGATGGCGTGGAGCGACAGCCCCAC 10546

Qy 150 Cys---AlaLeuLeuGlnGluIleProAlaIleSerTyr----- 162
Db 10545 TGCATGGCTCCCGAGTGGCGAGCGCTGGCGAAGTGGCAGCCACGCCCAACGCTCCGCTG 10486

Qy 163 ArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHis 182
Db 10485 AATGGAGGTGGT----- 10474

Qy 183 AlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGly 202
Db 10473 ---CGCAGTACCGCACCATTTGTCAGTATGAGTGTGAGCGCGCTACGAGCGCAATGCG 10417

Qy 203 AspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGly 222
Db 10416 CATCCC-----GTGCTGACCTGTATGTTCGACAGCGC 10387

Qy 223 IleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHis 242
Db 10386 ACCTCGAGTGGTGTATGATACCAAGATGCAAG-----CGCAAGCGG 10348

Qy 243 CysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAla----- 256
Db 10347 TGTCTC-----GAATTCCGACCATTTGCCAACGGCTTTGTGTGTGAC 10306

Qy 257 ---ArgArgAlaLeuHisGluAsp-----LeuProSerGlySer 268
Db 10305 TCGACGGCGAGCTTACTCTTCGGCGATGAGCCAGGCTGCTTCAAGGGCTACAA 10246

Qy 269 PheIleGlnAspAspMetValHisCysSerTyr-----Leu 280
Db 10245 CTGATCGCGACCAACATCATGCGCTGCAGCGAGGCCAGAGTTTCGAGCAGCCGCGCAGC 10186

Qy 281 CysAspGluGlyLysAspCys-----CysAspArgMetGlySerCysLysCys 296
Db 10185 TGCAGGACATCAACGAGTGCAGCTCTCTGCGAGTGGCAG-----CTAACCCACCGCAGTGC 10129

Qy 297 GlyThrHisThrGlyHisPheGluCysIleCysGluLysGlyTyrTyrGly----- 313
Db 10128 CAGNACAGCAAGCGCTCTCTCCACTGCCAGTGCAGGCGGATTCAC--GGTACCACCGA 10070

Qy 313 ----- 313
Db 10069 GTGTGGCCCGCTCGGTGATTGGGCTTGGGTAATGAGGAGCATACCGATGACGATCAC 10010

Qy 314 -----LysGlyLeuGlnTyrGluCysThrAla----- 322
Db 10009 CACTCGGTGAGTGCAGCGCGCTTACGCAAGGAGCAGCTGCGCTTGAAACAGATGGGTG 9950

Qy 323 -----CysProSerGlyThrTyrLysProGluGlySer--- 333
Db 9949 GTGGGTGGCTCTCTCGAGCGCTGTGTGCCAACTGATGATCTCATCGACTGAGGACCCAC 9890

Qy 333 ----- 333
Db 9889 CATTCGTGGTGGCTTCCGACCATGTCCGTGCGAGCTCCCGATGSCAATGTGGCCTTCAG 9830

Qy 333 ----- 333
Db 9829 CTGGCGGTGGCTGTGTCAGTACACCAAGATCTGACGAGTGTTCAGAGGATATGCGAA 9770

Qy 333 ----- 333
Db 9769 TCCGACGGCACTGCGCTCGAATTCGCACTCTGAGGACCCAGCTCTCCATCTTAAACT 9710

Qy 334 -----ProGly----- 335
Db 9709 GCGCTGCCCATCGAAGCTCGCTATATTGCTTCGCGATCCAGGACTACGTGGGTGGCGCC 9650

Qy 336 -----Gly-IleSerSerCys-----IleProCysProAspGluAsnHisTh 349
Db 9649 CTGTCTGCGCATGAGCTGTGAGTGGCTGACGCGCTGTGATTTGGTGTGACATCAACAGAGT 9590

Qy 349 rSerProGlySerThrSerProGluAspCysVal----- 361
Db 9589 CAGCAAGAACATGGCGGCTGTGACCAAGATGATCAATCACTACCGGGCGGATTTGCTGTG 9530

Qy 362 ---CysArgGluGlyTyrArg----- 367
Db 9529 TGGCTGCAACACTGCTGCTTACCAGCTGTACACTCCCAACCGGACCGCTGGCTATCATCGA 9470

QY 368 -----AlaSerGlyGln-----ThrCysGluLe 375
DB 9469 AGCTCCGAAATCCGGGAGCTGATGGTGACACCTATCAGCCCAACAGACCTGTGTCC 9410
QY 375 uValHisCysProAlaLeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAs 395
DB 9409 TCTCATGTGTCCTCCGAATCTGGAGCGCCGAGAAATGGTCAACTCTCTGAGCGACAGAAAGCA 9350
QY 395 nAsnHisPheAsnAlaAlaCysGlyValArgCysPheHisProGlyPheAspLeuValGlySe 415
DB 9349 CTATCACTTTGGCGAGTGGTGGCTTCAGTGCCACATTTGGCTACATCATGAGCGGCGAG 9290
QY 415 rSerIleIleLeuLysLeuProAsnGlyLeuTrpSerGlySer-----GluSerTyrCy 433
DB 9289 CTCGGCGCCCTGTGGCTCTCCAGCGGTTCAGTGGAAAGCCAGCGTACCGAGTGCATTTG 9230
QY 433 sArgValArgThr----- 437
DB 9229 TAAAGTTTATACATTCTCAATGAATTCCTCAATTTTACTAAACAGAAATGGTCAC 9170
QY 437 ----- 437
DB 9169 TTTTCAGATGCCAAATGCGTTTCCCTGCCCGATGACAAAGTTGGAGGCTCTGACTGTGCC 9110
QY 438 -----CysProHisLeuArgGln----- 443
DB 9109 CGCCCCGATCCCGAATCCGTTCTAGTGGCTTTCGGTGACAAATGTGACCATTTAGTGGCGA 9050
QY 443 ----- 443
DB 9049 TCGCCGGGAGCCAACTGAGAGCCACCGCTTCTCTGTTTCGGGAGTGGCGTATCGAT 8990
QY 444 -----ProLysHisGlyHisIleSerCys----- 451
DB 8989 CCCAAGCCGGTCTGTGCCGATTAATCTAGTGGCTATCCGGAATCAGCCCTCTTGTCCCGAGTG 8930
QY 452 -----SerThrArgGluMetLe 457
DB 8929 GATTGCTACTACCATGCCAAAGCCCGCGGAGAAATACGGACAGTTTGTG-GACACTCG 8871
QY 457 uTyrLysThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGly----- 474
DB 8870 CTATCAGACGACTTCTTCTTTGGCTGCCAGAACACCTTTAAGTTGGCTGGCAGACGGG 8811
QY 475 -----SerAspLysLeuThrCysGlnGlyAsnSerGlnTrpAspGlyProGluProArg 492
DB 8810 TCGTCAACGACATGTGGTTGTGTGGAGCGATGTATCTGGGACTTTGGAGATCTTGG 8751
QY 492 gCysValGluArgHisCysSerThrPheGlnMetProLysAsp----- 506
DB 8750 CTGTGAGGACCTGTGTGCGAGGATCCGGGAAGACCGGCAGATGGTCCGACATTTGCAGG 8691
QY 507 -----ValIleIle 509
DB 8690 CAGCTATGACGAGCTCGGAGGTGTACTTGGCTGCAATCGTCTGCTGCTACATCTGAT 8631
QY 509 eSerProHisAsn----- 513
DB 8630 CAATCCGGCACCATTATCATATGATACCGGAGCCAGAGTGCAAGGTTCATCAAGCCTTTTGG 8571
QY 513 ----- 513
DB 8570 ATTAAGTTCCGCGAGGATTCGGGATTCGGCCATCAATGCCACTCGGAGCGACCAATTA 8511
QY 514 -----CysGlyLysGln----- 517
DB 8510 CGAGGCCAAGACATCCGCTCTCAATCGGCCCACTGGCTGGTGTGGCAAGCAGGAGCCCTT 8451
QY 517 ----- 517
DB 8450 CACCTATGTGAGCGTGGATCTGGGTGAGATCTATCGAGTCAAGGCGGATCTGTGAAAGG 8391
QY 517 ----- 517

DB 8390 TGTGTTTACCAACGACATTGTGGCAGGCCACCGAGATTGGTCTTCTTCTTCAACAACAGC 8331
QY 518 -----ProAl 519
DB 8330 TGAGAGCGAGAACTACGTGGTGTACTTCCCAATTTCAATCTGACCATCGAGATCCAGG 8271
QY 519 alyAspPheGlyThrIleCysTyrValSer-----CysArgGlnGlyPheIleLe 535
DB 8270 CMACTACGCGAGCTGGCCATGATCAGCTGCGCCAAAGTTCTGTCAGGCTCGCTTGTGAT 8211
QY 535 uSerGlyValLys-----GluMetLeuArgCysTh 545
DB 8210 CCTTGAATAGTGAGCTACATGACAAACGCTGTCTGAAGTTCTGAGTTCTGATGGCTGCCA 8151
QY 545 rThrSerGlyLys-----TrpAsnValGlyValGlnAlaAlaValCysLys 560
DB 8150 GGAGCCGAACAGGAACCACTCTCTGGCTACGACTACCGGTAC-----TCCCGGTGGT 8097
QY 560 sAspValGluAlaProGlnIle---AsnCysProLysAsp---IleGluAlaLysThrLe 578
DB 8096 GGCACACGACACCACTCTTCCAAACTGCGCGAGCAACCAATTTGGTGGCGACCGA 8037
QY 578 uGluGlnGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerG 598
DB 8036 TGAGATGGAGGAGTACTACCGCTTAACTTACCGAAACCCAGCGCGTGCACAACCTCCGG 7977
QY 598 yGluLysValSerValHisValHisProAla-----PheThrProProTyrLeuPhePr 616
DB 7976 ATCGATTGCGCCCTGGAGATCAAGCCACAGAACTTCCGACACCCAGCTACATTTTCAA 7917
QY 616 oileGlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCy 636
DB 7916 G-----GATACGGTTGTAAAGTACTGCGCTTTTACTACGATGGCAATGTGGCCATCTG 7863
QY 636 silePheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArgSerPr 656
DB 7862 CGAGATCAACATCAGGTGCGCGATGTAACACCCACTGCTGCAG---TGC----- 7814
QY 656 oProProValGlnValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSe 676
DB 7813 -CCCCAGAGCTATGTGATTGAGCTAGTGTGATCGCCAGGACAGCTACACTGTGTGAACCTCAA 7755
QY 676 rAspAsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeu----- 694
DB 7754 CGATCCCGGAAGAGG-----ATCAAGACCTCCGACGACACAGGAGATGTGAGTT 7704
QY 695 -----PheProGlnGlyGluThrIle-----ValGlnTyrTh 705
DB 7703 GCAGTTACGCCCGAGAGTGCCCAACATCAAGATCGGAAACTTCGACAACTGACCGCTAC 7644
QY 705 rAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLysGlySe 725
DB 7643 GGCACACGATAGTACACACACCGCGCCCTGCCACTTCCAGGCTCTGTGGAAGGCTTC 7584
QY 725 rProCys-----GluIleProPheThrProValAsnGlyAspPheIleCysThrPr 742
DB 7583 ACCCTGCTGGAGCTCCAG---CCGCGCGGAATGGTGCATCAATTCCTGCTGCC 7527
QY 742 oAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGl 762
DB 7526 TGGTATCGTGGTATCGAATGATTCGCCAGTGCAGCCAGGATTCGCTTTCACCGACGG 7467
QY 762 ySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyrThrTh 782
DB 7466 CGAACCACTGGAAGACCTTCTCTGCGAGACATCACTGTGTGGCGTCCACAGCTCGGTGT 7407
QY 782 rGluTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLys---SerPheGl 801
DB 7406 G-----CCGACTGGGTCCGAGAACACGAGGAGCGCGCTACACAGTGCAGCCCTC 7353
QY 801 uMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAl 821

7352 CATTACCTACCGCGCAATGGAGCAGTGGCCCAATCTCTGTCTGGGTCTAGTACCAAGAGGT 7293
821 aPheGluThrThrLeuGly-----LysMetValProSerPheCysSerAsp----- 836
7292 GCTGGCAGACGACTATGGCGGACTCAACAGTGTCTCTCGCAGCGCTCTCCGCGGTGAA 7233
837 -----AlaGluAspIleAspCysArgLeuGluGluAsnLeuTh 849
7232 TGTCAACATGAATGTGACCTTTGTGAAGTCTGTGCGCCATGCTGTGCGAGAGATGTGT 7173
849 rlyAspTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPheAlaIleGlyProG 869
7172 CAAGATG----- 7166
869 yGlyTrpGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrValG 889
7165 -----GACTTCATCTCTCCAT-- 7148
889 nGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaProLe 909
7147 -----CTGCCCGCTGTGGTTCAGCCCGACGCTGTACGACCT 7113
909 uSerAspTyrLysIleLysLeuIlePheAsnIleThrAlaSerValProLeuProAspG 929
7112 GTGGCGCTCCAGCTGAACCTGTATCTTTGATCTG-----AGTGTACCTATGCCAGTGC 7059
929 u---ArgAsnAspThrLeuGluTrpGluAsnGlnArgLeuLeuGlnThrLeuGluTh 948
7058 CGTGATGATGATGACCTTTGAACATTCGCAACATCGGTAAACAGTGTCTCCGCTACGCGC 6999
948 rIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyrSerPheGlnLeuAl 968
6998 CCTCAAGTCGCAATCTCGCGAGGATTTAACTGCAAT-----GT 6960
968 aSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSerProPheCy 988
6959 GGGCGAGGTACTGAACATGACACACCGACGATGCGG----- 6923
988 sArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThrTyrTy 1008
6922 -----CGTTCCTGCACTGTCCGCGCGGACGATGT 6891
1008 rAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAspGluGlu 1028
6890 GTGAGAGGTGACAGACGCTGACCTACTCCCGAGGGGTACTACAGAACCGTACCG 6831
1028 yGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAs 1048
6830 CCAGGGAACCTGCTGCGCTGCGCGCGGACCTACACCAAGGAGGAGGCGACCAAGTC 6771
1048 nIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyrSerGlyLeuGluTh 1068
6770 GCAGCGGAGTGCATTCCTGCTGCGGTTATGACCTACTACCCACCGGACTGTGGCC 6711
1068 rCysGluSerCysProLeuGlyThrTyr-----GlnProLysPheGlySerArgSe 1085
6710 GTGCTCGGAGTGTCGCGTAACCTATTCTACGCGGACCAACCAACCGGTGGATTACAGGA 6651
1085 rCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAl 1105
6650 TTGCGAGGCTGTCCGCGACAGAGCTTACCTACCGCGGCTGCCTCGAACAAGGATCT 6591
1105 aCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCysHisPr 1125
6590 GTGTCCGCGCAAGTGTGCGCGGAAAGTACTCCGCGACCGGACTGTGCACCTCTGCTGCC 6531
1125 oCysProArgAspTyrTrpGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysProPh 1145
6530 GTGCCCACTGATCATTTACAGGAGCGCGGGTGGCGAGAGCTGCAACAGTGTCCGAG 6471
1145 eTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSerSerPheSerSe 1165
6470 TAAATGAGAACCGATTACCCCGCTCCAGGAGCGGACAGTGC----- 6425

1165 rThrPheSerAlaAlaGluGluSerValValProProAlaSerLeuGlyHisIleLysLy 1185
6424 -----AAGCCGTTGTA----- 6413
1185 sArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHisAsnSe 1205
6412 -----TGTGGTGAAGTGTCTTGCACGACG 6387
1205 rGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrThrGl 1225
6386 CGGACTGTGTGCTCCCATGGCCCATCAGATGCTTCTGTCGCGCGGATTTCTCTGG 6327
1225 yLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnGlyVa 1245
6326 AGTCTCTCGAACACAGACATGACAGTGGCTCTCCAGCCCTGCTACATGTGTGTCA 6267
1245 lCysLysAspLeuValGlyLysPheIleCysGluCysProSerGlyTyrThrGlyGlnAr 1265
6266 GTGCAAGGATCTGCCGCGAGGCTATCGCTGTGAGTGCCTGCTGATCTCGGGCATCAA 6207
1265 gCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLysGlyIleCysVa 1285
6206 TTGCCAGAGGAGGCGGAGTGTGCTGACGACACACCTGTCCGCGCGGCGCATGTGCAA 6147
1285 lAsp-----GlyValAlaGly----- 1290
6146 GAACGAGCGGGCTACAGAACGTGACCTGTCTGTGCGCGAGTGGCTACACCGCGGATCA 6087
1290 ----- 1290
6086 GTCCGAGCTGACCATCGATCGTCCGCGAGGCAATGGCAATCCGTGCGAAGACGCGCAG 6027
1291 -----TyrArgCysThrCysValLysGlyPheValGlyLe 1302
6026 CTGCCAGGCTTGGAGCAGGCTGCTACAAGTGCAGTGTGTGCCGCGATGGGGGCGCAT 5967
1302 uHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCy 1322
5966 CCACTGTGACGAGATATCAATGACTGTTCGAGATCCCTGCTCTGTGGCGCGCACTG 5907
1322 sGluAspGlnValGlyLysPheLeuCysLysCysProProGlyPheLeuGlyThrArgCy 1342
5906 CACAGATCTGTGTCATGACTTCCAGTGCCTGTGCCCGCAGGATTTACGGGCAAGCGATG 5847
1342 sGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAs 1362
5846 CGAGCAAAAGATCGATCTCTGCTTATCGGAACCATGCAAGCATGSC---ACCTCGTGGA 5790
1362 pGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLe 1382
5789 TCTCTGTTCGATCAAGTGTGTGTTCCTATCCGCGCTGACGCGGATCCGCTCGGACAT 5730
1382 uAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLe 1402
5729 CAACATCGAGCTCGAGAACCGACCTCGGCCAATGAGGGAACCTGGTGCACCTGGT 5670
1402 uAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGlu-ThrGluG 1422
5669 CGAGCGGTATAGCTGCAACTGTGAACCCGCTACACGCGCAAGAATTTGCCAGCACCAT 5610
1422 lnsrThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuA 1442
5609 CGAGCTGCG----- 5599
1442 spGlyMetLeuProSerLeuHisAlaLeuThrCys-----ThrPheTrpMetL 1458
5598 -----CCTCGAATCCCTGCCAGCACGCGCGCCACCTGTGTGGACCATGCTGGATGG 5550
1458 ySerSerAspAspMetAsnTyrGlyThrProIleSerTyrAlaValAsnGlySerA 1478
5549 CTTTCAGCTGCAATATCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5506

QY 1478 spAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluL 1498
 Db 5505 -----AGCCGA 5499
 QY 1498 ysIlleThrAsnCysProSerValAsnAspGlyArgTyrHisIleAlaIleThrTpt 1518
 Db 5498 GATCGACGAGTCTCGAGGACCCCTGCAATCCGTGGGCACGG----- 5455
 QY 1518 hrSerAlaAsnGlyIleTyrIleAspGlyLysLeuSerAspGlyGlyAlaG 1538
 Db 5454 --AGCGCTGCTCGATCGACACAAAT--TCGAGTGGTGTGGCG 5412
 QY 1538 lyLeuSer-ValGlyLeuProIleProGlyGly-----GlyAlaLeuVal 1552
 Db 5411 GCACGATTCAGGACCCCTGTGCGCCAGCAGATCGATGATCGGAGCGACCCGTG 5352
 QY 1553 -Leu-----GlyGlnGluGlnAspLysGlyGlu-----GlyPheSerProAl 1567
 Db 5351 TCTGAACACGCGATCTGCGGATCGGCTGGTGGCTTTGAGTGGCGCTCGAGCCAGG 5292
 QY 1567 aGluSerPheValGlySerIleSerGlnLeuAsnLeuTyrAspTyrValLeuSerProGl 1587
 Db 5291 A-----TCGAGTGGCATCGCTGGCGAGCA 5268
 QY 1587 nGlnValLysSerLeuAlaThrSerCysProGluLeuSerLysGlyAsnValLeuAl 1607
 Db 5267 GCAGGTGACCGATCGGAGCTCGAGCGCGTGCAGAACGATGCCAGTCGATCGACCT 5208
 QY 1607 aTyrProAspPheLeuSerGlyIleValGlyLysValLysIleAspSerLysSerIlePhe 1627
 Db 5207 GTTCAGGACTAC-----TT 5193
 QY 1627 eCysSerAspCysProArgLeuGlyGlySerValProHisLeuArgThrAlaSerGluAs 1647
 Db 5192 CTGCGTG--TGTCCAGC--GGCACCGATGGCAAGAACTCGAGACCGCTCCGCA-- 5141
 QY 1647 pleuLysProGlySerLysValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAs 1667
 Db 5140 -----CGCTGATCGGTGA 5127
 QY 1667 nProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGlu-- 1686
 Db 5126 TCCT-----TGCATCGACGTTGGCAAG-----TGCAGGA 5097
 QY 1687 -----ArgIleSerCysGlyValProProLeuGluAsnGlyPheHisSerAl 1703
 Db 5096 CTTTGGCTCTGCTTAACTGCAGTTGCCCT-----GC 5064
 QY 1703 aAspAspPheTyrAlaGlySerThrValThrTyrGln----- 1715
 Db 5063 GGAT-----TACTCGGGGCTTGGGTGTGAGTACGAGTACGAGTACGAGGACATGT 5010
 QY 1716 -CysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySe 1735
 Db 5009 CTGTCAAGATGCG-----GCCACTTGTGTGCAATGGTGC 4974
 QY 1735 rTrpAsnGlyValSerProSerCys-----LeuAs 1745
 Db 4973 T-----GGCTACAGCTGCGAGTGGCCACCTGGCTTACCGGTCCCAATTGCGAACAGGA 4920
 QY 1745 pValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAsnValAs 1765
 Db 4919 CATCGTGAGTCAAGGACAACTCT--TGCCACCGGGCGCCAGTGGTGGATCTTAC 4863
 QY 1765 pGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyLysAsnCysAlaGl 1785
 Db 4862 CAACGGCTTCTACTTCTAGTGC-----CCCTTCAATATGACCGGAGCAGATTGCGCAA 4809
 QY 1785 uProfileLys 1788
 Db 4808 GGCCATCCAA 4799

RESULT 19

AAH07752
 ID AAH07752 standard; cDNA; 801 BP.
 AC AAH07752;
 XX 26-JUN-2001 (first entry)
 DT
 DE Human cDNA clone (5'-primer) SEQ ID NO:4587.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 98JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 (HELL-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 1; SEQ ID NO 4587; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide comprising a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

Sequence 801 BP; 217 A; 198 C; 194 G; 184 T; 0 U; 8 Other;

Alignment Scores:
 Pred. No.: 3,77e-68 Length: 801
 Score: 1304.00 Matches: 247
 Percent Similarity: 91.18% Conservative: 1
 Best Local Similarity: 90.81% Mismatches: 16
 Query Match: 12.76% Indels: 8
 DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x AAH07752 (1-801)

PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 29-SEP-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246533P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 PR 29-SEP-2000; 2001-488777/53.
 PR P-PSDB; AAU18120.
 PR New nucleic acid molecules encoding 49 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives.
 PR Claim 4; SEQ ID NO 37; 524pp; English.
 PR The present invention relates to the isolation of novel human uterine
 CC motility-association polypeptides (AAU18094-AAU18152), and cDNA and
 CC genomic sequences encoding for these polypeptides. The sequences of the
 CC invention are useful in the diagnosis, treatment, prevention and/or
 CC prognosis of diseases associated with uterine motility such as pregnancy
 CC and labour, and menstrual disorders. The polynucleotide sequences of the
 CC invention are also useful in gene therapy. AAU28936-AAU28994 represent
 CC cDNA sequences encoding for novel human uterine motility-association
 CC polypeptides. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 PR SQ Sequence 680 BP; 190 A; 138 C; 168 G; 183 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 1,06e-66 Length: 680
 Score: 1278.00 Matches: 224
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 0
 Query Match: 12.51% Indels: 0
 DB: 4 Gaps: 0
 US-09-977-053-6 (1-1842) x AAU28962 (1-680)
 QY 1284 CysValAspGlyValAlaGlyThrArgCysThrCysValGlyGlyPheValGlyLeuHis 1303
 DB 3 TGTGTGATGGTGGTGGCTGCTATCGTGCATGTTGGAAGATTTGTAGCGCTGCAT 62
 QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGlu 1323
 DB 63 TGTGAAACAGAGTCAATGATGCCAGTCAACCCATGCTTAATAATGCACTGTGGAA 122
 QY 1324 AspGlnValGlyGlyPheLeuCysValGlyCysProGlyPheLeuGlyThrArgCysGly 1343
 DB 123 GACCAAGTTGGGGGATTCATGTGCAAAATGCCACCTGGATTTTGGGTACCCATGTGGA 182
 QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLeuAsnGlyAlaThrCysValGlyAspGly 1363
 DB 183 AAGAAGCTCGATGAGTGTCTCAGTCAGCATGCAAAATGGAGCTACCTGTAAAGACCGT 242
 QY 1364 AlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 DB 243 GCCAATAGCTTCAGATGCTGTGTGTCAGCTGGCTTCACAGGATCACACTGTGAATTGAA 302
 QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
 DB 303 ATCAATGAATGTCAGTCAATCATGTAGAATCAGGCCACCTGTGTGGATGAATTAAT 362
 QY 1404 SerThrSerCysValGlyCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer 1423
 DB 363 TCATACAGTTGTAATGTGAGCAGGATTTTCAGGCAAAAGGTGTGAACAGACAGTCT 422
 QY 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleThrGlyThrValMetLeuAspGly 1443
 DB 423 ACAGGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGATATGTCTATGCTAGATGGC 482
 QY 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSerAspAspMet 1463
 DB 483 ATGCTCCCATCTCTCCATGCTCTAACTGTACCTTCTGGATGAAATCTCTTCGACATG 542
 QY 1464 AsnThrGlyThrProIleSerThrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
 DB 543 AACTATGGAAACCAATCTCTCTATGCGTTGATACGGCAGGACCAATACCTTGTCTCTG 602

Qy 1484 ThrAspTyrRhenGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
 Db |||||
 603 ACTGATTATACCGCTGGGTTCTTATGTGATGCGAGGAAAGATAACAACTGTCCC 662
 Qy 1504 SerValAsnAspGlyArg 1509
 Db |||||
 663 TCGGTGAATGATGGCAGA 680

RESULT 21
 AAS26930
 ID AAS26930 standard; cDNA; 680 BP.
 AC AAS26930;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human cDNA encoding a novel secreted protein, SEQ ID 122.
 XX
 KW Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective;
 KW antibacterial; virucide; fungicide; opthalmological; vulnerary;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiogenesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;
 KW preservative; antiproliferative.
 XX
 OS Homo sapiens.
 XX
 PN WO200155441-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001320.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216980P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
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 PR 14-AUG-2000; 2000US-0224518P.
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 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
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 PR 14-AUG-2000; 2000US-0225477P.
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 PR 22-AUG-2000; 2000US-0226681P.
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 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
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 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 21-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234937P.
 PR 25-SEP-2000; 2000US-0234984P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
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 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
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 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
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 PR 17-NOV-2000; 2000US-0249207P.
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 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
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 PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249298P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476222/51.

P-PSDB; AAU17025.

Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

Claim 1; SEQ ID NO 122; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, CC minerals, cofactors and other nutritional components. The present CC sequence encodes a novel secreted protein of the invention. Note: The

Alignment Scores:
 Pred. No.: 1,06e-66 Length: 680
 Score: 1278.00 Matches: 224
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 12.51% Indels: 0
 DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x AAS26930 (1-680)

QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValIleGlyPheValGlyLeuHis 1303
 DB 3 TGTGTTGATGTTGGCTGCTATCTGTCACATGTTGAAAGGATTTGTAGCCTGCAT 62
 QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGlu 1323
 DB 63 TGTGAAACAGAGTCAATGAAATGCCAGTCAGTCAAAACCCATGCTTAATAATACAGTCTGTGAA 122
 QY 1324 AspGlnValGlyGlyPheLeuCysIleCysProGlyPheLeuGlyThrArgCysGly 1343
 DB 123 GACCAAGTTGGGGATTCATGTGCAATGCCACCTGGATTTTGGTACCCGATGTGA 182
 QY 1344 LysAsnValAspGluCysLeuSerGlnProCysIleAsnGlyAlaThrCysIleAspGly 1363
 DB 183 AAGAACGTGCGATGAGTCTCAGTCAGGCATGCCAATAATGGAGTACCTGTTAAAGCGGT 242
 QY 1364 AlaAsnSerPheArgCysLeuCysAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 DB 243 GCCAATAGCTTCAGATGCTGTGTCAGCTGCTTCACAGGATCACACTGTGAATGAAC 302
 QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
 DB 303 ATCAATGATGTCACTTAATCCATGTAGAAATCAGGCCACCTGTGTGATGAATTAAT 362
 QY 1404 SerTyrSerCysIleCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer 1423
 DB 363 TCATACAGTTGTAAATGTCCAGCCAGATTTTCAGGCGAAAGGTGTGAAACAGAACAGTCT 422
 QY 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
 DB 423 ACAGGCTTTAACTGATTTTGAAGTTCTGCAATCTATGGATATGTCATGTAGATGGC 482
 QY 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetIleSerSerAspMet 1463
 DB 483 ATGCTCCCATCTCTCCATGCTTAACCTGTACCTTCTGATGAATCTCTGACGACATG 542
 QY 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
 DB 543 AACTATGGAACACCAATCTCTATGCAAGTTGATAACGGCAGCGACAAATACCTTGTCTCTG 602
 QY 1484 ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyValGluValIleThrAsnCysPro 1503
 DB 603 ACTGATTAATACGGCTGGGTCTTTATGGAATGGCAGGAAAGATAACAACTGTCTCC 662
 QY 1504 SerValAsnAspGlyArg 1509
 DB 663 TCGGTGAATGATGGCAGA 680
 RESULT 22
 ABA06507
 ID ABA06507 standard; cDNA; 680 BP.
 AC ABA06507;
 XX
 DT 10-JAN-2002 (first entry)
 XX
 DE Human cDNA SEQ ID NO: 173.
 XX
 KW Human; gene therapy; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200154474-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001349.
 XX

PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
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 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226686P.
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 PR 05-DEC-2000; 2000US-0251988P.
 PR 06-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476161/51.

P-PSDB; ABB10285.

Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical

PT condition.

XX PS Claim 1; SEQ ID NO 173; 859pp + Sequence Listing; English.

XX CC The present invention provides human cDNAs, proteins and related genomic
 CC DNAs. These can be used in the treatment of neural, immune system,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal and proliferative disorders and inflammation. The present sequence
 CC is a cDNA of the invention

XX SQ Sequence 680 BP; 190 A; 138 C; 168 G; 183 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.06e-66 Length: 680
 Score: 1278.00 Matches: 224
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 12.51% Indels: 0
 DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x ABA06507 (1-680)

Qy 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
 Db 3 TGTGTTGATGGTGGCTGCTATCGTGCAATGTTGAAGGATTTGTAGCCCTGCAT 62
 Qy 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGlu 1323
 Db 63 TGTGAACAGAAAGTCAATGATGCCAGTCAACCCAGTCTTAATAATGACAGTCTGTGAA 122
 Qy 1324 AspGlnValGlyPheLeuGlyCysLysCysProGlyPheLeuGlyThrArgCysGly 1343
 Db 123 GACCAAGTGGGGGATTCATGTGCAATGCCACCTGGATTTTGGGTACCCGATGTGGA 182
 Qy 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyValAlaThrCysLysAspGly 1363
 Db 183 AAGAAGTCGATGATGTTCTAGTCAGCCATGCCAATAATGGAGCTACCTGTAAAGACGT 242
 Qy 1364 AlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 Db 243 GCCAATAGCTTCAGATGCTGTGTGCGAGTGGCTTCACAGGATCACACTGTGAATTGAAC 302
 Qy 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
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 Qy 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer 1423
 Db 363 TCATACAGTTGTAATGTCAGCAGGATTTTCAGGCAAGGTGTGAACAGACAGTCT 422
 Qy 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
 Db 423 ACAGGCTTTAACCCTGGATTTTGAAGTTTCTGGCATCTATGGATATGTCATGCTAGATGC 482
 Qy 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetLysSerSerAspMet 1463
 Db 483 ATGCTCCCATCTCTCCATGCTCTTAACCTGTACTTCTGATGAATTCCTCTGACGACATG 542
 Qy 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeu 1483
 Db 543 AACTATGNAACCAATCTCTATGCAATGATACGGCAGGACCAATACCTTGTCTCTG 602
 Qy 1484 ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
 Db 603 ACTGATTAACCGCTGGGTTCTTTATGTAATGGCAGGAAAGATAACAACAACTGTCCC 662
 Qy 1504 SerValAsnAspGlyArg 1509
 Db 663 TCGGTGAATGATGGCAGA 680

RESULT 23

AAS31580

ID AAS31580 standard; cDNA; 680 BP.

XX AC AAS31580;
 XX DT 04-DEC-2001 (first entry)
 XX DE cDNA encoding novel human calcium-binding protein #4.
 XX KW Human; calcium-binding protein; calcium flux; neurological disease;
 KW immune dysfunction; digestive disorder; neoplastic disease;
 KW blood disorder; infectious disease; gene therapy; immunosuppressive;
 KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
 KW virucide; ss.
 XX OS Homo sapiens.
 XX PN WO200155304-A2.
 XX PD 02-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US001302.
 XX PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
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 PR 02-MAR-2000; 2000US-0186350P.
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 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
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 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
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 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.

Db 243 GCCAATAGCTTCAGATGCTGTGTCAGCTGCTTCACAGATCACACTGTGAATTGAAC 302

Qy 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
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Db 303 ATCAATGAATGTCACTCTAATCCATGTAGAAATCAGGCACCTGTGTGATGAATTAAT 362

Qy 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlnSer 1423
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Db 363 TCATACAGTTGTAAATGTGACGACGANTTTTCAGGCMAAAGGTGTGAACAGAACAGTCT 422

Qy 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
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Db 663 TGGTGAATGATGGCAGA 680

RESULT 24

ABT07797

ID ABT07797 standard; DNA; 680 BP.

XX AC ABT07797;

XX DT 14-NOV-2002 (first entry)

DE Novel human nucleic acid SEQ ID NO 37.

XX KW Immunostimulant; antirheumatic; antiarthritic; neuroprotective;

XX KW antiallergic; antidiabetic; antiaesthetic; antiinflammatory; nootropic;

XX KW immunosuppressive; anticoagulant; thrombolytic; antiatherosclerotic;

XX KW cytosatic; nephrotropic; antiparkinsonian; gynecologic; virucide;

XX KW antibacterial; antiarrhythmic; fungicide; HCFAT05; HMAAE95; HTNBM01;

XX KW immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular;

XX KW inflammatory condition; graft-versus-host disease; reproductive system;

XX KW blood-related disorder; hyperproliferative; endocrine; neurological;

XX KW respiratory; renal; infectious disease; gastrointestinal; gene therapy;

XX KW neuronal growth; neuronal disorder; neuro-degenerative condition;

XX KW keratinocyte growth; human; ds.

OS Homo sapiens.

XX US2002086330-A1.

XX PD 04-JUL-2002.

XX PP 17-JAN-2001; 2001US-00764893.

XX PP 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

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PR 14-AUG-2000; 2000US-0225758P.

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PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 05-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229513P.

PR 08-SEP-2000; 2000US-0231413P.

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PR 27-SEP-2000; 2000US-0235834P.

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PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

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PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241809P.

PR 01-NOV-2000; 2000US-0244617P.

PR 17-NOV-2000; 2000US-0249299P.

PR 08-DEC-2000; 2000US-0251856P.

PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX Rosen CA, Ruben SM, Barash SC;

XX WPI; 2002-665432/71.

XX Novel polypeptide useful for diagnosis, prognosis, prevention, and

PT treatment of immune, hyperproliferative, renal, respiratory,

PT cardiovascular, reproductive, endocrine, gastrointestinal and

PT neurological disorders.

XX Disclosure; Page 226; 335pp; English.

XX The invention relates to an isolated polypeptide comprising a sequence at

CC least 90% identical to a full length protein sequence selected from 55

CC sequences given in the specification such as a sequence of 163, 74 or 140

CC amino acids fully defined in the specification, or the encoding sequence

CC contained in 49 cDNA clones given in specification e.g. HCFAT05, HMAAE95

CC or HTNBM01. The protein and its encoding nucleic acid are useful for

CC diagnosing a pathological condition or susceptibility to a pathological

CC condition in a subject and for preventing, treating or ameliorating a

CC medical condition. The protein, its encoding nucleic acid and an isolated

CC antibody that can bind to the protein are useful in treating, preventing,

CC diagnosing and/or prognosing immunodeficiencies, autoimmune disorders,

CC allergic reactions and conditions, inflammatory conditions, graft-versus-

CC host disease, blood-related disorders, hyperproliferative disorders,

CC renal disorders, cardiovascular disorders, respiratory disorders,

CC neurological disorders, endocrine disorders, reproductive system

CC disorders, infectious diseases, and gastrointestinal disorders. The

CC protein of the invention is useful to stimulate neuronal growth and to

CC treat, prevent, and/or diagnose neuronal damage which occurs in certain

CC neuronal disorders or neuro-degenerative conditions, for stimulating

CC keratinocyte growth, to prevent hair loss, to modulate mammalian

Qy	1424	ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly	1443
Db	423	ACAGCCTTAAACCTGGAGTTTGAAGTTCTGGCACTATAGATATATGTCATGCTAGATGGC	482
Qy	1444	MetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetIysSerSerAspAspMet	1453
Db	483	ATGCTCCCATCTCTCCCATGTGCTTAACCTGTACCTTCTGGATGAATACCTCTGACGACATG	542
Qy	1464	AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeu	1483
Db	543	AACTATGGACACCCAAATCTCTATGTCAGTTGTATAAOAGCAGCGACAATACCTTCTCTCTG	602
Qy	1484	ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro	1503

Search completed: May 9, 2004, 16:20:25
Job time : 1579.96 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 10, 2004, 15:48:01 ; Search time 265.768 Seconds

(without alignments)
3846.286 Million cell updates/sec

Title: US-09-977-053-6

Perfect score: 10219

Sequence: 1 MWPLAPCCGLALVSGWAT.....GVTKICLBSGEWHILPVC 1842

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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5: /cgn2_6/prodata/2/ina/PCUTS COMB seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	8652.5	84.7	11230	4	US-09-911-842A-3
3	914.5	8.9	9723	1	US-08-083-590A-21
4	914.5	8.2	763	3	US-08-532-384-21
5	838	8.2	763	4	US-09-484-970B-110
6	829	8.1	8091	4	US-09-230-652-1
7	829	8.1	8257	4	US-09-484-970B-65
8	764.5	7.5	6677	4	US-08-939-366-27
9	764.5	7.5	6677	4	US-09-467-597-6
10	749	7.3	4208	3	US-09-214-278-6
11	749	7.3	4208	4	US-09-855-722-6
12	745	7.3	5458	4	US-09-199-865-2

13	745	7.3	6464	2	US-08-400-159-5	Sequence 5, Appli
14	745	7.3	6464	3	US-08-611-729A-5	Sequence 5, Appli
15	744	7.3	4208	4	US-09-068-740A-10	Sequence 10, Appli
16	744	7.3	5590	2	US-08-882-046-1	Sequence 1, Appli
17	690	6.8	3582	3	US-08-400-159-9	Sequence 9, Appli
18	690	6.8	3582	3	US-08-611-729A-9	Sequence 9, Appli
19	674	6.6	3955	3	US-09-214-278-4	Sequence 4, Appli
20	674	6.6	3955	4	US-09-855-722-4	Sequence 4, Appli
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22	671	6.6	4464	2	US-08-611-729A-7	Sequence 7, Appli
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24	633	6.2	2508	3	US-08-981-392-1	Sequence 1, Appli
25	633	6.2	2508	3	US-08-981-392-3	Sequence 3, Appli
26	631.5	6.2	2663	4	US-09-068-740A-8	Sequence 8, Appli
27	631.5	6.2	2663	4	US-09-423-753-8	Sequence 8, Appli
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30	620.5	6.1	2892	1	US-08-083-590A-1	Sequence 1, Appli
31	620.5	6.1	2892	1	US-08-465-500-5	Sequence 5, Appli
32	620.5	6.1	2892	2	US-08-346-126-5	Sequence 5, Appli
33	620.5	6.1	2892	2	US-08-346-128-5	Sequence 5, Appli
34	620.5	6.1	2892	3	US-08-532-384-1	Sequence 1, Appli
35	620.5	6.1	2892	3	US-08-893-828-5	Sequence 5, Appli
36	606	5.9	5561	2	US-08-400-159-1	Sequence 1, Appli
37	606	5.9	5561	3	US-08-611-729A-1	Sequence 1, Appli
38	602	5.9	8378	5	PCT-US91-09055-1	Sequence 1, Appli
39	594	5.8	5176	4	US-09-182-024A-1	Sequence 1, Appli
40	592	5.8	2857	3	US-08-981-392-4	Sequence 4, Appli
41	587	5.7	3231	4	US-09-866-028-14	Sequence 14, Appli
42	585	5.7	2055	3	US-08-872-855-3	Sequence 3, Appli
43	585	5.7	2800	3	US-08-872-855-1	Sequence 1, Appli
44	585	5.7	3339	4	US-09-423-753-4	Sequence 4, Appli
45	583.5	5.7	5583	4	US-09-312-283C-372	Sequence 372, App
46	572	5.6	4758	3	US-09-191-647-1	Sequence 1, Appli
47	572	5.6	4758	3	US-09-540-245A-1	Sequence 1, Appli
48	572	5.6	4758	3	US-09-540-153-1	Sequence 1, Appli
49	549.5	5.4	2481	3	US-09-188-930-64	Sequence 64, Appli
50	549.5	5.4	2481	4	US-09-312-283C-64	Sequence 64, Appli
51	549.5	5.4	6951	4	US-09-023-655-1265	Sequence 1265, Ap
52	548.5	5.4	6951	6	5256642-1	Patent No. 5256642
53	548.5	5.4	6951	6	5472939-1	Patent No. 5472939
54	546.5	5.3	7313	6	5256642-3	Patent No. 5256642
55	525.5	5.1	5420	6	5472939-3	Patent No. 5472939
56	525.5	5.1	5420	6	5472939-3	Patent No. 5472939
57	502	4.9	5499	3	US-08-479-722B-1	Sequence 1, Appli
58	502	4.9	5502	5	PCT-US95-02251-17	Sequence 17, Appli
59	499.5	4.9	1981	3	US-08-981-392-26	Sequence 26, Appli
60	471.5	4.6	11272	4	US-09-341-461-1	Sequence 1, Appli
61	467	4.6	1434	4	US-09-833-381-926	Sequence 926, App
62	454	4.4	2899	3	US-08-981-392-24	Sequence 24, Appli
63	452.5	4.4	5089	6	517197-31	Patent No. 517197
64	429.5	4.2	1556	1	US-08-597-545-3	Sequence 3, Appli
65	429.5	4.2	1556	1	US-08-457-135-3	Sequence 3, Appli
66	427.5	4.2	1158	4	US-09-142-027A-11	Sequence 11, Appli
67	427.5	4.2	1158	4	US-09-142-027A-13	Sequence 13, Appli
68	427.5	4.2	1573	1	US-08-597-545-4	Sequence 4, Appli
69	427.5	4.2	1573	1	US-08-457-135-4	Sequence 4, Appli
70	406.5	4.0	1161	4	US-09-833-381-2046	Sequence 2046, Ap
71	395.5	3.9	3142	1	US-08-110-158-3	Sequence 3, Appli
72	395.5	3.9	3142	4	US-09-023-655-1090	Sequence 1090, Ap
73	395.5	3.9	3144	5	PCT-US91-05059-1	Sequence 1, Appli
74	390	3.8	1785	4	US-09-148-545-112	Sequence 112, App
75	389.5	3.8	3759	3	US-08-479-722B-3	Sequence 3, Appli
76	382.5	3.7	6942	2	US-08-460-309-3	Sequence 3, Appli
77	382.5	3.7	6942	2	US-08-125-077-3	Sequence 3, Appli
78	382.5	3.7	9534	4	US-09-562-702A-5	Sequence 5, Appli
79	382.5	3.7	9534	4	US-09-561-709B-8	Sequence 8, Appli
80	382.5	3.7	9535	4	US-09-562-702A-1	Sequence 1, Appli
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82	378.5	3.7	9420	4	US-09-562-702A-3	Sequence 3, Appli
83	377.5	3.7	3934	4	US-09-023-655-1066	Sequence 1066, Ap
84	372.5	3.6	1448	4	US-09-130-491-9	Sequence 9, Appli
85	368	3.6	5197	4	US-09-833-381-1910	Sequence 1910, Ap

86 362.5 3.5 1117 4 US-09-148-545-54 Sequence 54, Appl
 87 362.5 3.5 9391 4 US-09-562-702A-11 Sequence 11, Appl
 88 362.5 3.5 9511 4 US-09-562-702A-9 Sequence 9, Appl
 89 360 3.5 3753 5 PCT-US95-02251-2 Sequence 2, Appl
 90 360 3.5 4314 1 US-08-199-780-2 Sequence 2, Appl
 91 360 3.5 4314 2 US-08-316-650-2 Sequence 2, Appl
 92 359 3.5 3149 4 US-09-016-434-1453 Sequence 1453, Ap
 93 359 3.5 3149 4 US-09-023-655-1478 Sequence 1478, Ap
 94 358 3.5 1592 2 US-08-252-493C-1 Sequence 1, Appl
 95 358 3.5 1592 3 US-09-276-197-1 Sequence 1, Appl
 96 358 3.5 1833 1 US-08-365-470-2 Sequence 2, Appl
 97 358 3.5 1834 3 US-09-209-668-18 Sequence 18, Appl
 98 358 3.5 3854 1 US-08-365-470-1 Sequence 1, Appl
 99 358 3.5 3858 2 US-08-344-155C-98 Sequence 98, Appl
 100 358 3.5 3858 4 US-09-009-490A-88 Sequence 88, Appl

ALIGNMENTS

RESULT 1

US-09-911-842A-1
 ; Sequence 1, Application US/09911842A
 ; Patent No. 6656707
 ; GENERAL INFORMATION:
 ; APPLICANT: Amgen Inc.
 ; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
 ; FILE REFERENCE: 01017/37592
 ; CURRENT APPLICATION NUMBER: US/09/911,842A
 ; CURRENT FILING DATE: 2001-07-24
 ; PRIOR APPLICATION NUMBER: US 60/222,438
 ; PRIOR FILING DATE: 2000-08-01
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1

LENGTH: 10878

TYPE: DNA

ORGANISM: Homo sapiens

US-09-911-842A-1

Alignment Scores:

Pred. No.: 0 Length: 10878
 Score: 10208.00 Matches: 1838
 Percent Similarity: 99.95% Conservative: 3
 Best Local Similarity: 99.78% Mismatches: 1
 Query Match: 99.89% Indels: 0
 DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-911-842A-1 (1-10878)

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 Qy 21 PheGlnGlnMetSerProSerArgAsnPheserPheArgLeuPheProGluThrAlaPro 40
 Db 71 TTTTACGACAGATGTCCCGTCGCGCAATTTACGTTCCGCCCTCTTCCCGGAGACCGCGCC 130
 Qy 41 GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg 60
 Db 131 GGGGCCCCCGGGAGTATCCCGCGCGCGCGCTCTGGCGGACGAGCGCGGGGAGCAGA 190
 Qy 61 ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu 80
 Db 191 GTGAGCGGCTGGGCGAGCGTTCGGCGACGCGTGGCGGCTGCTCGCGGAGCTCAGCGAG 250
 Qy 81 ArgLeuGluLeuValPheLeuValAsnPheserSerValGlyGluValAsnPheArg 100
 Db 251 GCGCTGGAGCTGTCTTCTCGTGGATGATTCGTCAGCGTGGGGAAGTCAACTTCCGC 310
 Qy 101 SerGluLeuMetPheValArgLysLeuLeuSerAspPheProValProThrAlaThr 120
 Db 311 AGCGAGCTCATGTTCTGTCGCGCAAGTGTGTCTCGACTTCCCGGTGCTGCCCGGCGCAG 370

Qy 121 ArgValAlaIleValThrPheSerSerIysSerValValProArgValAspTyrIle 140
 Db 371 CGCGTGGCCATCGTGACCTTCTCGTCCAAGAACTACGTGGTGGCGCGTCAATATCATC 430
 Qy 141 SerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGlnIleProAlaIle 160
 Db 431 TCCACCCCGCGCGCGCGCGCCAGCAAGTGGCGCTGCTCTCCCAAGAGATCCCTGCCATC 490
 Qy 161 SerThrArgGlyGlyGlyThrThrThrLysGlyAlaPheGlnGlnAlaIleLeu 180
 Db 491 TCCTACCGAGGTGGCGGACCTTACCAAGGCGGCTTCCAGCAAGCGCGCAATTCCT 550
 Qy 181 LeuHisAlaArgGluAsnSerThrLysValValPheLeuLeuLeuThrAspGlyTyrSerAsn 200
 Db 551 CTTTCATGCTAGAGAAACTCAACAAAGTTGTATTTCTCATCACTGATGATATTCAT 610
 Qy 201 GlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThr 220
 Db 611 GGGGAGACCTTAGACCAATTCAGCGTCACTGCGAGATTCAGGAGTGAGATCTTCACT 670
 Qy 221 PheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu 240
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 Qy 241 GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeu 260
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 Db 1331 CTCGCCAGCGGAAACATGGCCACATCAGCTGTTCTACAAAGGGAATGTTATATAGACA 1390
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1931 AAGTTATTGATGCAGAACCACTGTCNTAGACTGTGTGCAGATCTCCACTCCCGTCCAG 1990
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3611 CTTGGCACAAATAGTGGAACTGCGCAACCTGGGGGTGGTATATGTTGTCTCTGTCCA 3670

Qy	1221	LeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCys	1240
Db	3671	CTTGGATATACAGGCTTAAAGTGTGAACACAGACATCGATGAGTGACGCCACTGCCTTGC	3730
Qy	1241	LeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGly	1260
Db	3731	CTCAACAATGAGATTGTAAAGACTAGTTGGGGAATTCATTTGTGAGTGGCCATCAGGT	3790
Qy	1261	TyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsn	1280
Db	3791	TACACAGGTGAGCGGTGTGAAGAAATATATAATCAGTGTAGCTCCAGTCTCTTGTTTAAAT	3850
Qy	1281	LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal	1300
Db	3851	AAAGGAATCTGTGTTCATGGTGTGGCTGGCTATCTGTTCGCACATGTGTGAAGGATTTGTA	3910
Qy	1301	GlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAla	1320
Db	3911	GGCTCTGATATTGTGAACACAGAAGTCATAGTAATGCCAGTCAACACCANTGCTTAAATAATGCA	3970
Qy	1321	ValCysGluAspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThr	1340
Db	3971	GTCTGTGAGACACAGGTGGGGGATCTTGTGCAAAATGCCACCTGATTTTGGGTACC	4030
Qy	1341	ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysLysAsnGlyAlaThrCys	1360
Db	4031	CGATGTGGAAGAAACGTGCATGAGTGTCTCAGTCAGCCATGCCAAAAATGGAGCTACCTGT	4090
Qy	1361	LysAspGlyAlaAsnSerPheArgCysLeuCyValaAlaGlyPheThrGlySerHisCys	1380
Db	4091	AAAGCGGTGCCAATAGCTTCAGATGGCTGTGTGCAGTGCCTTCAGAGATCACACTGT	4150
Qy	1381	GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp	1400
Db	4151	GAATTGAACATCAATGAATGTCTAGTCTAAATCCATGTAGAAATCAGGCCACCTGTGTGGAT	4210
Qy	1401	GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr	1420
Db	4211	GAATTAAATTCATACAGTTGTAAATGTTCAGCCAGGATTTTCAGGCAAAAGGTGTGAACA	4270
Qy	1421	GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet	1440
Db	4271	GAACAGTCTACAGGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGATATGTCATG	4330
Qy	1441	LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSer	1460
Db	4331	CTAGATGGCATGCTCCCATCTCTCCATGCTCTAACCTGTACCTTCTGGATGAATCCCTCT	4390
Qy	1461	AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr	1480
Db	4391	GACGACATGAACATATGGAACACCAATCTCTCATGACGTTGATATACGCGACGCAATACC	4450
Qy	1481	LeuLeuLeuThrAspTyrAsnGlyTyrPheValLeuTyrValAsnGlyArgGluLysIleThr	1500
Db	4451	TTGCTCTCTGACTGATTTAAACCGCTGGGTCTTTTATGTGAATGGCAGGGAAGAATAACA	4510
Qy	1501	AsnCysProSerValAsnAspGlyArgTrpHisIleAlaIleThrTrpThrSerAla	1520
Db	4511	AACTGTCCCTCGGTGAATGATGGCAGATGGCATCATATTGCCAATCACTTGGACAAGTGCC	4570
Qy	1521	AsnGlyIleTrpLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer	1540
Db	4571	AATGGCATCTGGAAGTCTATATCTGATGGGAATTTATCTCAGCGGTGTGTGCGCTCTCT	4630
Qy	1541	ValGlyLeuProIleProGlyGlyGlyAlaLeuValLeuGlyGlnGluGlnAspLysLys	1560
Db	4631	GTGCTTTGCCCATACTCTGGTGGTGGTCCGTAGTCTCTGGGCGAGAGCACAAAAA	4690
Qy	1561	GlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrp	1580
Db	4691	GGAGAGGATTCAGCCAGCTGAGTCTTTTGTGGGCTCCATAGCAGAGCTCAACCTCTGG	4750

Qy	1581	AspTyrValLeuSerProGlnGlnValValSerLeuAlaThrSerCysProGluGluLeu	1600
Db	4751	GACTATGTCCTGCTCCACACGACGAGTGAAGTCACTGGCTACCTCTGCTCCAGAGGAATC	4810
Qy	1601	SerIysGlyAsnValLeuAlaTTPProAspPheLeuSerGlyVleValGlyValLys	1620
Db	4811	AGTAAGAAGAACGTGTAGCATGCGCTGATTTCTTGTTCAGAAATTTGGGGAAGTGAAG	4870
Qy	1621	IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis	1640
Db	4871	ATCGATTCTAAGAGCATATTTTGTTCTGATTGTCGCCACGCTTAGGAGGGTCAGTGCCTCAT	4930
Qy	1641	LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro	1660
Db	4931	CTCAGAACTGCATCTCAAGATTAAAGCCACAGGTTCCAAAGTCAATCTGTTCTGTGATCCA	4990
Qy	1661	GlyPheGlnValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTTPThrGln	1680
Db	4991	GGCTTTCAGCTGGTCGGGAACCCCTGTGCAGTACTGTCTGAAATCAGGAACAGTGGACACAA	5050
Qy	1681	ProLeuProHisCysGluAlaGlyIleSerCysGlyValProProProLeuGluAsnGlyPhe	1700
Db	5051	CCACTTCTCACTGTGAAACCATAGCTGTGGGGTGGCCACTCTCTTTGGAGATGGCTTC	5110
Qy	1701	HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr	1720
Db	5111	CATTCAAGCCGATGACTTCTATGCTGGCAGCACAGTAACCTTACCAGTGCACCAATGGCTAC	5170
Qy	1721	TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSer	1740
Db	5171	TATCTATTGGGTGACTCAAGGATGTTCTGTACAGATAATGGGAGCTGGAAACGGCGTTCA	5230
Qy	1741	ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer	1760
Db	5231	CCATCTGCTCTGATGTCGATGATGTGCAATGGATGCAATTTGTAGTGAGCATGCTTCT	5290
Qy	1761	CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGly	1780
Db	5291	TGCTGAACGTAGATGGATCCTACATATGTTCAATGTTGTCCTCCACCGTACACAGGAGATGGG	5350
Qy	1781	LysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer	1800
Db	5351	AAAACATGTGCGAACCTATATAAATGTAAAGGCTCCAGGAATCCGGAATAATGGCCACTCC	5410
Qy	1801	SerGlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGln	1820
Db	5411	TCAGTGAGATTTATACATGATAGTGGCGAAGTCAATTTTCGTGTACAGAGATACCAG	5470
Qy	1821	LeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluTrpAsnHisLeuIlePro	1840
Db	5471	TTGATGGAGGTAAACCAAAATCACATGTTTGGAGTCTGGAGATGGGAATCATCTTAATACCA	5530
Qy	1841	TyrCys	1842
Db	5531	TATTGT	5536

RESULT 2
 US-09-911-842A-3
 ; Sequence 3, Application US/09911842A
 ; Patent No. 6656707
 ; GENERAL INFORMATION:
 ; APPLICANT: Amgen Inc.
 ; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
 ; FILE REFERENCE: 01017/37592
 ; CURRENT APPLICATION NUMBER: US/09/911,842A
 ; CURRENT FILING DATE: 2001-07-24
 ; PRIOR APPLICATION NUMBER: US 60/222,438
 ; PRIOR FILING DATE: 2000-08-01
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 11230
 ; TYPE: DNA

i ORGANISM: Mus musculus

US-09-911-842A-3

Alignment Scores:

Pred. No.: 0 Length: 11230
 Score: 8652.50 Matches: 1532
 Percent Similarity: 90.56% Conservatives: 137
 Best Local Similarity: 83.13% Mismatches: 171
 Query Match: 84.67% Indels: 3
 DB: 4 Gaps: 3

US-09-977-053-6 (1-1842) x US-09-911-842A-3 (1-11230)

QY 1 MetTrpProArgLeuAlaPheCysCysTrpGlyLeuAlaLeuValSerGlyTrpAlaThr 20
 DB 176 ATGTGTGTCGCGCTGTCCTTTTGTGCTGGCTCTGGCACTGTGTGCTGGGCTGGACCAAC 235
 QY 21 PheGlnGlnMetSerProSerArgAgnPheSerPheArgLeuPheProGluThrAlaPro 40
 DB 236 TTCACGCGGTGGCCCTTGGCTCACTTCAGCTTCGGCTGTTCGGAGGCTCTCCG 295
 QY 41 GlyAlaProGlySerIleProAlaProProAlaProGly---AspGluAlaAlaGlySer 59
 DB 296 GGGGCTCTGGGCAGACTGGCGGTACCTTCCCGCTCCAGTGAGGAGGAGGAGGAGGAGC 355
 QY 60 ArgValGluArgLeuGlnAlaPheArgArgValArgValArgLeuLeuLeuSer 79
 DB 356 AAGTGTGAGCGCTGGCGCGCGCTTCCGAGCGCGGTGGCGGACTTGGCGGAGCTCAGC 415
 QY 80 GluArgLeuGluLeuValPheLeuValAspSerSerValGlyGluValAlaSerPhe 99
 DB 416 GCGNGCTTGGAGCTCTCTCTGCTGGTGGAGAGTGGTGGAGCTGGCGCAACCACTTC 475
 QY 100 ArgSerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAla 119
 DB 476 CTCACGAGCTCAAGTTCGTGGCAAGCTCTCTGTCGAGCTTCCCGGTGTGCCAGGCC 535
 QY 120 ThrArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyr 139
 DB 536 AGCGGTGTGGCATCGTCACCTTCTCATCAAGAACACACAGTGGTGGCGGTGGATTC 595
 QY 140 IleSerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluIleProAla 159
 DB 596 ATCTCCACGAGCGCGGCGACCAACACAGTGGCGCTGTCTCAGCGCGGAGATCCCGGC 655
 QY 160 IleSerThrArgGlyGlyThrThrThrLysGlyAlaPheGlnGlnAlaGlnIle 179
 DB 656 ATCACCCTACCGCGTGTGGCACTATACCAAGGGCGCTTCCAGCAAGCGCGCAATC 715
 QY 180 LeuLeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSer 199
 DB 716 CTTCGTCACTCTAGAGAAACTCCACAAAGTCATATTTCTCATCCGCGCTATTTCC 775
 QY 200 AsnGlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePhe 219
 DB 776 AATGGCGGAGACCCAGACCTATTGCGCATCGCTTCGGGATTCGGAGTGGAGATCTTC 835
 QY 220 ThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLys 239
 DB 836 ACGTTCGGGATTTGGCAGGGAATATCCGGGAATCGAATGACATGGCTTCCACCCCGAAG 895
 QY 240 GluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAla 259
 DB 896 GAAGAACATTGTACTCTGCTCCACAGTTTGAAGAAATTTGAGGCTTTAGCTCGAGGGCG 955
 QY 260 LeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyr 279
 DB 956 TTGCATGAAGATCTACTCTCTGGAGTTTATCCAGAGATATGGCCCACTCTCTAT 1015
 QY 280 LeuCysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHis 299
 DB 1016 CTCTGTGAGGCTGGGAAGACTCTGTGTGACAGAAATGGCCAGCTGCAATGTGGGACACAC 1075

QY 300 ThrGlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGlu 319
 DB 1076 ACGGCTCAATTTGATTCATCTGTGAGAGGGCTATTACGGGAAGGCTCTGAGCATGAG 1135
 QY 320 CysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSer 339
 DB 1136 TGCACAGCTTGGCCCATCAGGCACATATAAGCCGAGCTTCTCCAGGAGGAATCAGCACC 1195
 QY 340 CysIleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluLeu 359
 DB 1196 TGCATCCCATGTCTGACGTAAAGCCACACTCCCACTCGAAGCACTTCCCTCGAAGAC 1255
 QY 360 CysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysPro 379
 DB 1256 TGTGTGCGAGAGGATACAGAGATCTGGCCAGACTGTGAGTGTGTCCACTGTCTCT 1315
 QY 380 AlaLeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsn 399
 DB 1316 GCCTGAAGCTCTCTGAATAATGGTTTTTTTATACAAACACTTGCATAAACTACTTCAAT 1375
 QY 400 AlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeu 419
 DB 1376 GCGGCTGTGGGTCGATGTGCGCCGCGCTTTGACCTTGTGGGAAGCAGCATTCATTG 1435
 QY 420 CysLeuProAsnGlyLeuTrpSerGlySerGlySerTyrCysArgValArgThrCysPro 439
 DB 1436 TGTCAACCCAAATGGTTTGTGTGTGGAGCAGAAAGCTTCTGCAGAGTGAAGACGTGCC 1495
 QY 440 HisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLys 459
 DB 1496 CACTCGACAGCCCAACACAGCCACATCAGCTGCTCCACTGCGGAATGTCTTACAAC 1555
 QY 460 ThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThr 479
 DB 1556 ACCCTGTGTTTGTGTACCTGCAATGAAGSATACAGATTAGAAGCAGCAGCTAGGCTTACC 1615
 QY 480 CysGlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSer 499
 DB 1616 TGTCAAGGAATGCCCAGTGGATGGCCAGAGGCCCGGTGTGTAGAACGCCATTGTGCC 1675
 QY 500 ThrPheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAla 519
 DB 1676 ACCTTCAGGAAGCCCAAGAGCGTCATCATTTCTCACCCAGCTGCGGAGCAGCGCCGCC 1735
 QY 520 LysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLys 539
 DB 1736 AGCCCTGGGATGACCTGTGAGTAAAGCTGCGCGCAGGAGTACATTTTATCCGGGTGAGA 1795
 QY 540 GluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCys 559
 DB 1796 GAA---GTGAGATGTGCCACATCTGGGAGTGGAGTGCCTCAAGTTCAGACAGCTGTGTC 1852
 QY 560 LysAspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGlu 579
 DB 1853 AAGATGTGGAGGCTCCACAAATCAGCTGTCCAAATGACATTTGAGGCAAGACTGGGAG 1912
 QY 580 GlnGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGlu 599
 DB 1913 CAGCAGGACTCTGTATATGTCACCTGGCAAGTCCCAACAGCTCAAGACAACTCTGGTGA 1972
 QY 600 LysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp 619
 DB 1973 AAGGTGTCAGTCCACGCTCCACCCAGCCTTATCCCACTTACCTCTTCCCAATTTGGAG 2032
 QY 620 ValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHis 639
 DB 2033 GTGGCCATCACTACAGCGCAACCCACTCATCGGTAAACCAAGCCAGCTGCACTTCTTAC 2092
 QY 640 IleLysValIleAspAlaGluProProValIleAspTrpCysArgSerProProVal 659
 DB 2093 ATTAAGGTCAATGATGTGGAACCGCTGTATAGATTGGTGCCGATCTTCCACCTCCAATC 2152
 QY 660 GlnValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSer 679

Db 2153 CAGGTGGTAGAAGAGAGACCCCTCAAGCTGGAGTGGCTCAGTTCTCAGCAACTCC 2212
Qy GlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGlu 699
Db 2213 GGGGCTGAATTTGGTCAATTACAGCAGTACACACAGGGGACATGTTCTCATGGGAA 2272
Qy ThrIleValGlnIleThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHis 719
Db 2273 ACGGTGGTGTGTGTACACAGCCACTGACCCCTCAGGCAACACAGGACCTGTGCATCCAC 2332
Qy IleValIleLeuGlySerProCysGluIleProPheThrProValAsnGlyAspPheIle 739
Db 2333 ATTGTCAATAAAGGTTCTCCCTGTGAGTCCCTTCACCCCTGTAAACGGGACATTATC 2392
Qy CysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPhe 759
Db 2393 TGTGCCAGGATAGTGTGGAGTTAACTGTACCTGTGAGCTGCAGGAGGGCTATGATTTC 2452
Qy ThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValIlePheProThr 779
Db 2453 ACAGAGGGTCACTGAGAGTACTACTGTGCTTTTGAAGATGGTATCTCGAGAGCCACCA 2512
Qy TyrThrThrGluTyrProAspCysAlaLysIleArgPheAlaAsnHisGlyPheLysSer 799
Db 2513 TACTCTACAGAAATGGCCAGACTGTGCTATAAACCGTTTTCGAACCATGGTTTCAGTCC 2572
Qy PheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSer 819
Db 2573 TTTGAAATGCTATACAAACCACTCGCTGTGATGACATGATCTGTTTAAAGATTTCCT 2632
Qy GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
Db 2633 GCAGCAATTGAGACTACCTCGGGAAACATGGTCCCGTCTCTTTTGTAAACGATCTGATGAC 2692
Qy IleAspCysArgLeuGluLeuAsnLeuThrLysTyrCysLeuGluTyrAsnTyrAsp 859
Db 2693 ATTGATCGAGACTGGAGAC---CTGACCAAAATACTGCTATGAGTATTAATTACAC 2749
Qy TyrGluAsnGlyPheAlaIleGlyProGlyTyrGlyValAlaAlaAsnArgLeuAspTyr 879
Db 2750 TATGAATAATGGCTTTGCAATTGACAGGAGCTGGGGTGCAGGCAACAGGCTGGATTAT 2809
Qy SerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLys 899
Db 2810 TCTACGACTCACTTCTGATGTTGTACAGGAAACACCCACCGGATGTGGGCAAGCCAGA 2869
Qy SerSerArgIleIleArgSerAlaProLeuSerAspTyrLysIleLeuIlePheAsn 919
Db 2870 TGTTCACGGANTTAAAGAACTGTCCCAATGTCTGACCCCAAAATTCAGCTAATTTTAAAC 2929
Qy IleThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGln 939
Db 2930 ATCAGAGTGTGGTGCATCTCCAGAGGAAAGAAACGATACCTTGAATGTGAGAAATCAG 2989
Qy GlnArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLys 959
Db 2990 CAGCGACTCATTAAGACATTGGAAACAATCACCATCGCTGAAAAGCACCTTGAATAAA 3049
Qy AspProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeu 979
Db 3050 GAGCCCATATGATTTCTTTCAGCTCGCTCGGAAACAGTGGTGGCTGACAGCAATTCCTTC 3109
Qy GluThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCys 999
Db 3110 GAACAGAAAGGCTTTCTCTCTGACAGCCAGGCTCTGTGCTGAGGGGCGCATGTGT 3169
Qy ValAsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArg 1019
Db 3170 GTCAACTGCCCCCTGGGAACCTTCTACTCTCTGGAGCAATCCACCTGTGAAAGCTGCCCTC 3229
Qy 1020 IleGlySerTyrGlnAspGluGlnGluLeuGluCysLysLeuCysProSerGlyMet 1039
:::

Db 3230 ATGGGATCTCAACAGATGAAGAGGGCAGCTGGAATGCAAGCTCTGTCTCCCCAAGACT 3289
Qy TyrThrGluTyrIleHisSerArgIleSerAspCysIleValGlnCysLysGlnGly 1059
Db 3290 CACGGGGAATACCTCCATTTCAAGAACGCTCTCTGAATGCAAGCTCAGTGTGAAGCAAGGC 3349
Qy 1060 ThrTyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnPro 1079
Db 3350 ACTTACTCTTCAGTGGGCTGGAGACCTCGGAATCGTGTCCGCTGGGTACTTATCAACCG 3409
Qy LysPheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGly 1099
Db 3410 GAATTTGGATCCGGAGCTGCTCTATGCCAGAAACACCAACACGGTGAAGAGGA 3469
Qy AlaValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGly 1119
Db 3470 GCGGTGGACATCTCTGCTTTGTGGAGTGCCTGCCAGTAGGAGAAATCTCCCGTCTCGGG 3529
Qy LeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPhe 1139
Db 3530 CTAAACCTCTGCTACCTTGGCTCGAGCTATTACCAACCCANTGCGGAGTCTCTTC 3589
Qy CysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGlu 1159
Db 3590 TGCCTGCTTGTCTTTTATGNACTACCAACCATCACTGGCGCCACGTCATCACAGAC 3649
Qy CysSerSerPheSerSerThrPheSerAlaAlaGluGluSerValValProProAlaSer 1179
Db 3650 TGCCTCAAGTTTGTAGCTCTACTTTCTCAGCAGCAGAAAGCAATGTGCCCTCGTGGCC 3709
Qy LeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePhe 1199
Db 3710 CCTGGACATCCAGAACAGTACGAGTACGAGCTCAGGTCTTTCAAGATGCTCTTA 3769
Qy AsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCys 1219
Db 3770 AACCCCTGCCACCAACAGTGGAACTGCCAACAGCTTGGGCGTGGTATGTCTGTCTGC 3829
Qy ProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuPro 1239
Db 3830 CCACCTGGATACACAGGCTTAAAGTGTGAACAGATATTGAATGATGACGCTCTCTGCT 3889
Qy GlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeu 1279
Db 3950 GGCCTATTCAAGTCAATAATGTGAAGAAATATATAATGAGTGTATCTCCAGCCCTTGTCTTA 4009
Qy AsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPhe 1299
Db 4010 AATAAAGGAACCTGCACCTGACGCTGGCAAGCTACCGCTGTACCTGTGTGAAGAGGATAC 4069
Qy ValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsn 1319
Db 4070 ATGGGTGTGCTGTGAAACAGACGTCATGATGCGAGTCAAGCCCTCTCTTAAACAC 4129
Qy AlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGly 1339
Db 4130 GCAGTTTGAAGAACCAAGTTGGGGGGTCTCTCGTGCAAAATGCCCAACCCCGATTTTGGGT 4189
Qy ThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyValThr 1359
Db 4190 ACTCGGTGTGAAGAAATGTGGATGTGTCTCAGTCAGCTACCGCTGTGTGAAGAGGACACT 4249
Qy CysLysAspGlyValAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHis 1379
Db 4250 TGTAAAGATGTGCGAACAGCTTCAGGTGTCAATGTCCAGCAGGCTTTCACAGGACACAC 4309
Qy CysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysVal 1399
Db 4310 TGTGAATGAACATCAACGAGTGTCTCAGTCCACCCGTGTAGGAACCAAGGCCACCTGTGTG 4369

QY 1400 AspGluLeuAsnSerTyrSerCysValProGlyPheSerGlyGlnArgCysGlu 1419
DB 4370 GATGAACCTAACTCATACAGTGTAAATGTCAGCGAGGATTTTCAGGCCACAGSTGTGAG 4429
QY 1420 ThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyLeuTyrVal 1439
DB 4430 ACAGAACAGCGCTTCGCGTATTAACCTGGATTTTGAAGTTTCTGCGATCTACGGGTACGTC 4489
QY 1440 MetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetLeuSer 1459
DB 4490 CTGCTAGATGAGTGTGCGCAACCTCCATGCGGTAACTGCGCATTTCTCGATGAATCC 4549
QY 1460 SerAspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsn 1479
DB 4550 TCTGATGTCATCACTAAGGAGCGCCCATCTCTATGCACTTGAGGATGACAAAGACAAC 4609
QY 1480 ThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLeu 1499
DB 4610 ACCTTCCTCTGACTGATTAACAACGGCTGGGTCTTTATGTGAATGAAAGAAAGATC 4669
QY 1500 ThrAsnCysProSerValAsnAspGlyArgTyrHisIleAlaLeuThrTyrThrSer 1519
DB 4670 ACCAACTGCCCCCTCCGTAATATGATGCGCATTTGGCATCATATTCATATGCAATGACACAAAGT 4729
QY 1520 AlaAsnGlyLeuTyrLeuValTyrLeuAspGlyLysLeuSerAspGlyGlyAlaGlyLeu 1539
DB 4730 ATTTGGTGGAGCCCTGGAGGCTTATATAGATGGGAATATCTACGGTGTACTGGGCTC 4789
QY 1540 SerValGlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGluInAspLys 1559
DB 4790 TCCATTGGCAAGCCATACCTGCTGGCGGTGCATTAGTTCTTGGGCAAGAGCAAGACAA 4849
QY 1560 LysGlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeu 1579
DB 4850 AAGGAGAGAGGGTTCACCCGCGCTGATCTTTTGTGGGCTCCATTAAGCCAGCTCAACCTC 4909
QY 1580 TrpAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGlu 1599
DB 4910 TGGGACTATGCTCTGTCTCAGAGAGGTGAGATGCTGCGCAGCTCTCTCCACAGGAA 4969
QY 1600 LeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGlyLeuValGlyLysVal 1619
DB 4970 CTGAGTGGGGAACGTTTAGCATGCGCGATTTCTGTCGGGAATCAGCGGAGGTG 5029
QY 1620 LysIleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValPro 1639
DB 5030 AAGGTTGATTCACGACGACATGTTCTGCTGTGATTTGTCGGCTTTAGAAAGGATCCGTGCT 5089
QY 1640 HisLeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAsp 1659
DB 5090 CACTGAGACCTGCATCAGGAATTCGAAAGCCAGGCTCCAAAGTCAGTCTGTTCTGTGAT 5149
QY 1660 ProGlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyInTyrThr 1679
DB 5150 CCGGGCTTCAGATGTTGGGAATCTCTGATGATTTGTCGAACCAAGGCGCAGTGGACA 5209
QY 1680 GlnProLeuProHisCysGluArgIleSerCysGlyValProProPheLeuGluAsnGly 1699
DB 5210 CAACCACTCCCCACCTGTGAACGCATTCGCTGGGCTGCTCCCGCTTTGGAGATGGC 5269
QY 1700 PheHisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGly 1719
DB 5270 TTCTACTCAGCGGAGCTTCATATGCGGCGAGCAGCGGTGACCTATCAGTGCCACAGTGGC 5329
QY 1720 TyrTyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTyrAsnGlyVal 1739
DB 5330 TACTACTGCTGGTGTATTCCTCGAATGTTCTGCRGACAGCAACCGGAGCTGGAAAGCGCAT 5389
QY 1740 SerProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAla 1759
DB 5390 TCACCATCTCTCGATGTCGATGATGTGCGACTGCGCTCGGACTGTATGTAGCAGCGCC 5449

QY 1760 SerCysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAsp 1779
DB 5450 TCTGCTGTAACACCAACGAGATCTAGCTATGCTCTGTAACCCACCATACACGGGAGAT 5509
QY 1780 GlyLysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHis 1799
DB 5510 GGGAAACATGTGCAGAACCTGTAAATGTAAAGCTCCAGAAATCCAGAAATGCGCGC 5569
QY 1800 SerSerGlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGlyTyr 1819
DB 5570 TCTTCTGGCAGATTACACCGTGGTACTGCACTGCATCTTCTGTGACGAGGCGAC 5629
QY 1820 GlnLeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluTyrAsnHisLeuLeu 1839
DB 5630 GAGCTGGTGGAGTAGCAGCATCATCGTGTGGAGACTGGCGAGTGGGATCGCCTCAGG 5689
QY 1840 ProTyrCys 1842
DB 5690 CCGTCTGT 5698
RESULT 3
US-08-083-590A-21
; Sequence 21, Application US/08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..7419
; US-08-083-590A-21
Alignment Scores:
Pred. No.: 3,08e-72 Length: 9723
Score: 914.50 Matches: 395
Percent Similarity: 34.59% Conservative: 174
Best Local Similarity: 24.01% Mismatches: 529
Query Match: 8.95% Indels: 550
DB: 1 Gaps: 86

	: : :	3376	GST-...GTCTGCATCAATGCTGGCAAACAGCATTA	CTGTCAGTGGCCCC---CTGGGCTATT	3429
D _b					
	: : : : : : :	1637	SerValProHisLeu---	ArgThrAlaSerGluAspLeuIysProGly	1651
Q _y					
	: : : : : : :	3430	ACTGGGAGCTACTGTCGAGGAGCAACTCGATGAGTG	TGGCGTCCAAACCCCTGCCAGCAGCGG	3489
D _b					
	: : : : : : :	1652	SerLysValAsnLeuPhe-----	CysAspProGlyPheGlnLeu	1664
Q _y					
	: : : : : : :	3490	GCAACATGCACTGACTTCATTGTTGGATACAGATGCG	AGTGTCTCCAGCATTAAGGGT	3549
D _b					
	: : : : : : :	1665	ValGlyAsnProVal-----	GlnTyrCysLeuAsnGlnGlyGln	1677
Q _y					
	: : : : : : :	3550	GTCAACTGTCAGTATGAAGTGGATGATGCCAATCAG	CCCTGCCAGAATGGAGGCACC	3609
D _b					
	: : : : : : :	1678	TrpThrGlnProLeuProHisCysGluArgIleSerCys	GlyValProProProLeuGlu	1697
Q _y					
	: : : : : : :	3610	TGTAATTGACCTTGTAACCAT-----	TTCAAGTGCTCTTGCCCAACA	3651
D _b					
	: : : : : : :	1698	AsnGlyPheHisSerAlaAspPheTyrAlaGlySerThr	ValThrValThrTyrGlnCysAsn	1717
Q _y					
	: : : : : : :	3651	-----	-----	3651
D _b					
	: : : : : : :	1718	AsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCys	ThrThrAspAsnGlySerTrpAsn	1737
Q _y					
	: : : : : : :	3652	-----GGCACTCGGGGCTACTCTGTGAAGAAC	-----	3681
D _b					
	: : : : : : :	1738	GlyValserProSerCysLeuAspValAspGluCysAla	ValGlySerAspCysSerGlu	1757
Q _y					
	: : : : : : :	3682	-----ATTGATGACTGTGCCC GGCGGTCCCCATTG	CGCTTAAT	3717
D _b					
	: : : : : : :	1758	HisAlaSerCysLeuAsnValAspGlySerTyrIleCys	SerCysValProProTyrThr	1777
Q _y					
	: : : : : : :	3718	GGTGGTCAGTCATGCATAGATTGGAGGCTACAGTGT	CGCTGCTTGCTGCGCTTGCT	3777
D _b					
	: : : : : : :	1778	GlyAspGlyLysAsnCysAlaGluProIleLys-----	CysLysAla	1791
Q _y					
	: : : : : : :	3778	GGGGAG-----CGTTGTGAGGGAGACATCAACG	ATGAGTGCCTCTTCCAACCCCTGCAGCTCT	3831
D _b					
	: : : : : : :	1792	ProGlyAsn	1794	
Q _y					
	: : : : : : :	3832	GAGGGCAGC	3840	
D _b					

RESULT 4

US-08-532-384-21
Sequence 21, Application US/08532384
Patent No. 6083904
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennite & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:

GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 110
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 009051.5CB1
US-09-484-970B-110

Alignment Scores:
Pred. No.: 3,32e-67 Length: 763
Score: 838.00 Matches: 148
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.20% Indels: 0
DB: 4 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-484-970B-110 (1-763)

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Qy 720 IleValIleLysGlySerProCysGluLeuProPheThrProValAsnGlyAspPheIle 739
Db 763 ATTGTCTATAAAGGTTCTCCCTGTGAAATCCATTTCACACCTGTAATGGGATTTTATA 704
Qy 740 CysThrProAspThrGlyValAsnCysThrIleuThrCysLeuGluGlyTyrAspPhe 759
Db 703 TGCACCTCCAGATAATACTGGAGTCAACTGTACATTAACTTCTTGGAGGCGTATGATTTC 644
Qy 760 ThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThr 779
Db 643 ACAGAGGGTCTACTGACAGTATTATTGTCTTATGAGATGGCTCTGGAAACCAACA 584
Qy 780 TyrThrThrGluTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSer 799
Db 583 TATACCACCTGAATGGCCAGAGCTGTGCCAAAAACGTTTTCACAAACACCGGTTCAATCC 524
Qy 800 PheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSer 819
Db 523 TTTGAGATGTTCTACAAAGCAGCTCGTTGTGTGATGACACAGATCTGATGAAAGATTTTCT 464
Qy 820 GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
Db 463 GAGCATTTGAGACGACCTCGGGAANAATGTCCTCATCATTTTGTAGTATGACAGAGAC 404
Qy 840 IleAspCysArgLeuGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAsp 859
Db 403 ATTGACTGCAGACTGGAGGAGAACCTGACCAAAAAATATTGCTAGATATATAATTATGAC 344
Qy 860 TyrGluAsnGlyPheAlaIleGly 867
Db 343 TATGAAATGGCTTTGCAATTTGGT 320
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RESULT 6

US-09-230-652-1
; Sequence 1, Application US/09230652A
; Patent No. 653775
; GENERAL INFORMATION:
; APPLICANT: Tournier-Lasserre, Elisabeth
; APPLICANT: Joutel, Anne
; APPLICANT: Bousser, Marie-Germaine
; APPLICANT: Bach, Jean-Francois
; TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
; TITLE OF INVENTION: THERAPEUTIC APPLICATION
; FILE REFERENCE: 03715.0048-00000

CURRENT APPLICATION NUMBER: US/09/230,652A
; CURRENT FILING DATE: 1999-05-17
; EARLIER APPLICATION NUMBER: FR 96 09733
; EARLIER FILING DATE: 1996-08-01
; EARLIER APPLICATION NUMBER: FR 97 04680
; EARLIER FILING DATE: 1997-04-16
; EARLIER APPLICATION NUMBER: PCT/FR97/01433
; EARLIER FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8091
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(7041)
; OTHER INFORMATION: human ADNC No. 6537775sch 3
US-09-230-652-1

Alignment Scores:
Pred. No.: 1.55e-64 Length: 8091
Score: 829.00 Matches: 259
Percent Similarity: 37.07% Conservative: 85
Best Local Similarity: 27.91% Mismatches: 287
Query Match: 8.11% Indels: 298
DB: 4 Gaps: 46

US-09-977-053-6 (1-1842) x US-09-230-652-1 (1-8091)

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Qy 988 CysArgProGlySerValLeuArg---GlyArgMetCysValAsn----- 1001
Db 562 TGCGGGTGGTGGAGCCCTGCGCGCATGTGGCCACCTGCTCAACACACCTGGCTCTTC 621
Qy 1002 -----CysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSer--- 1017
Db 622 CGCTGCCAGTGTCCAGCTGGCTACACAGGGCCACTA-----TGAGAGAACCCC 669
Qy 1018 -----CysArgIleGlySerTyrGlnAspGluGluGln 1029
Db 670 GCGGTGCCCTGTGGCCCTCACCATGCGTAACGGGGGCACCTGCAGGAGAGTGGCGAC 729
Qy 1030 Leu-----GluCysLysLeuCysPro-----SerGlyMetTyrThrGluTyrIleHis 1045
Db 730 CTCACCTACGACTGTGCTGCTCTCTCTGAGGGTTGAGGGTCAGAAATTGTGAAGTG--- 783
Qy 1046 SerArgAsnIleSerAspCysLysAlaGln-----CysLysGln 1058
Db 784 -----AACGTGGACGACTGTGCCAGSACCCGATGTCTCAATGGGGGACATGCGTGGAT 837
Qy 1059 GlyThrTyrSerTyrSer-----GlyLeuGlu 1067
Db 838 GGCTCAACACCTATACTGCCAGTGCCTCTGAGTGGACAGGCCAGTCTTGACAGGAG 897
Qy 1068 ThrCysGluSerCysProLeu-----GlyThrTyrGlnPro 1079
Db 898 GAGCTGATGATGTGCTGAGCTGCAGCCCAACGCTGCCACATGGGGGTACCTGCTTCAAC 957
Qy 1080 LysPheGlySerArgSerCysLeu-----SerCysProGlu 1091
Db 958 ACGCTGGTGGCCACAGCTGCTGTGTGTCAATGGCTGGACAGGTGAGAGCTGCAGTCAG 1017
Qy 1092 Asn-----ThrSerThrValLysArgGlyAlaVal-----AsnIle 1103
Db 1018 AATATCATGACTGTGCCACAGCGTGTCTTCCATGGGGCCACTGCGCATCAGCGGTG 1077
Qy 1104 SerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCys 1123
Db 1078 GCTTCTTTTACTGTGCTGCTGCCCATGGCAAG-----ACTGGCTCTCTG---TGT 1125
Qy 1124 His-----ProCysProArgAspTyrTyr-----Gln 1132
Db 1126 CACCTGGATGACCGCTGTGTGTGTCAGCAACCCCTGCCACGAGGATGCTATCTGTGACACAAAT 1185
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Qy	1133	ProAsnAlaGlyLysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAla	1152
Db	1186	CCGCTGAACGCGCGGCCCAITTTGC---ACCTGTCTCT---CCCGCTTCACGGGTGGGGCA	1239
Qy	1153	GlySerArgSerIleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluGlu	1172
Db	1240	TGTGACCAAGATGTGGACGAGTGTCTATTCGGCGCCAAACCCCTCGCAGCAGCTTGGGGAAG	1299
Qy	1173	SerValValProAlaSerLeu-----GlyHisIleLysAsp	1186
Db	1300	TGCTGTAACACGACGGGCTCTTCTCTGTGCCAGTGCCTGTGTGCTACACTGGACCTGCG	1359
Qy	1187	HisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHisAsnSerGly	1206
Db	1360	TGTGAGACCGAT-----GTCAACGAGTGTCTGTGGCGGCGCTCGCCGAAACCAAGGCC	1410
Qy	1207	ThrCys---GlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrThrGly	1225
Db	1411	ACGTGCTTCGACCGCATAGCCAG---TTCACTGTATCTGTATGGCAGGCTTCCACAGGA	1467
Qy	1226	LeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsnGlyVal	1245
Db	1468	ACCTATTGCGAGGTGGACATTGACAGTGTTCAGATAGCCCTGTGTCTACGGTGGGTC	1527
Qy	1246	CysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGlyGlnArg	1265
Db	1528	TGCAAGCACCGAGTCAATGGCTTCAGCTGCACCTGCCCTCGGCTTCAGCGGCTCCACG	1587
Qy	1266	CysGluGlnAsnIleAsnGluCysSerSerSerProCysLeuAsnLysGlyIleCysVal	1285
Db	1588	TGTGAGCTGGGACGTGGACGAATGGCCAGACGCCCTTCAGAGGAATGGCCCAATGGGTG	1647
Qy	1286	AspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHisCysGlu	1305
Db	1648	GACAGCCCGATGGCTACGAGTGGCTGTGCCGAGGGCTTTGAGGCGCACGCTGTGTGAT	1707
Qy	1306	ThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGluAspGln	1325
Db	1708	CGCAACGTGGACGACTGCTCCCTTGACCCATATGC---CACCATGTGTGCTCGCTGGATGGC	1764
Qy	1326	ValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCysGlyLysAsn	1345
Db	1765	ATGCCAGCTTCTCATGTGCTGTGCTCTCGGCTACACGGGCACACGCTCGCAGAGCCAG	1824
Qy	1346	ValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsn	1365
Db	1825	GTGGACGAATGCCGACGACCGCCCTGCGCGCATGGCGGCAATGCTTAGACCTGTGTGGAC	1884
Qy	1366	SerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsn	1385
Db	1885	AAGTACCTCTGCCCTGCCCTTCGGGACACACAGGTGTGAACCTGCGAAGTGAACATTGAC	1944
Qy	1386	GluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyr	1405
Db	1945	GACTGTGCCAGCAACCCCTGC---ACCTTTGGAGTCTGCCGTGATGGCATCAACCGCTAC	2001
Qy	1406	SerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSerThrGly	1425
Db	2002	GACTGTGCTGCCAACCTGGCTTCACAGGGGCCCTTTGTAACTGGAG-----	2049
Qy	1426	PheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAsp-GlyMetLe	1445
Db	2050	-----ATCAATGATGTTGTCT-----	2064
Qy	1445	uProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSerAspAspMetAsnTy	1465
Db	2065	TCCAGCCCATCGCGCGGAGGTTCTCTGTGTGATG-----	2101
Qy	1465	rgLysThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeuThrAs	1485
Db	2102	GGGAAATGGCTTCGCTGCC-----	2122

RESULT 7


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QY 1615 IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArgLeu 1634
DB 2726 TTCCAGGGGCTGCACCTGTGAGGAGAAGACTAACCCAGCTGTGTGCACAGCCCTGCAGG 2785
QY 1635 GlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerIleVal 1654
DB 2786 AAC-----AAGGCACTGCGCAGAGACACACTCGAGGGGCGCCG----- 2824
QY 1655 AsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProValGlnIleCysLeuAsn 1674
DB 2825 ---TGCCCTCTGAGCCCTGGCTAT-----ACAGGAAGCAGCTGCAGACTCTGTATGAC 2875
QY 1675 GlnGlyGlnIleThrGlnProLeuProHisCysGluArgIleSerCysGlyValProPro 1694
DB 2876 TTG-----TGTCGCCGGAAGCCCTGTCCA----- 2899
QY 1695 ProLeuGluAsnGlyPheHisSerAlaAspPheTyrAlaGlySerThrValThrTyr 1714
DB 2900 -----CACACTGCTCGATGCTCCAGAGTGGGCCCTCGTTCCAGTGC 2941
QY 1715 GlnCysAsnAsnGlyTyrTyr---LeuLeuGlyAspSerArgMetPheCysThrAspAsn 1733
DB 2942 CTGTGCTCCAGGATGAGGAGGGCTCTGTGTGACTTCCACTGTCTCCAGAGGCC 3001
QY 1734 GlySerTyrAsnGlyValSerProSerCysLeuAspValAspGluCysAlaValGlySer 1753
DB 3002 CGCATGAGCCAGGATAGATGCTCTGCGCTG----- 3034
QY 1754 AspCysSerGluHisAlaSerCysLeuAsnValAspGlySerTyrIleCysSerCysVal 1773
DB 3035 ---TGCCAGATGAGGAGCTCTGTATGTACACGGGCTCTCTCTATTTCTGCGCTGCCCT 3091
QY 1774 ProProTyrThrGlyAspGlyLysAsnCysAlaGluProIleLysCysLysAlaProGly 1793
DB 3092 CTGGAATTC-----CAAGCAAGTTATGCCAGGATAATGTGAAC-----CCCTGC 3136
QY 1794 AsnProGluAsnGlyHisSerSerGlyGluIleTyrThrValGlyAlaAlaValThrPhe 1813
DB 3137 GAGCCCAATCCCTGCCATCAGGGCTCTACCTGTGTGCTCCAGCCAGTGTGCTGTGC 3196
QY 1814 SerCysGlnGluGlyTyrGlnLeuMetGlyValThrLysIle-----ThrCysLeuGlu 1831
DB 3197 CAGTGTGCCCGCCAGGCTATGAGGAGACAGAACTGTCTCAAAAGTACTTTCAGCTTGT 3256
QY 1832 SerGlyGluTyrAsnHis 1837
DB 3257 CAGCCCTGCCACACACCAC 3274

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RESULT 9
US-09-467-997-6
; Sequence 6, Application US/09467997
; Patent No. 6379925
; GENERAL INFORMATION:
; APPLICANT: Kitajewski, Jan
; APPLICANT: Uytendaele, Hendrik
; TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
; FILE REFERENCE: 53863-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/467,997
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6677
; TYPE: DNA
; ORGANISM: mouse
US-09-467-997-6

Align. No.: 9,08e-59 Length: 6677
Score: 764.50 Matches: 273
Percent Similarity: 36.35% Conservative: 108
Best Local Similarity: 26.05% Mismatches: 399

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Query Match: 7.48% Indels: 268
DB: 4 Gaps: 47
US-09-977-053-6 (1-1842) x US-09-467-997-6 (1-6677)
QY 927 ProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnGlnArgLeuLeuGlnThrLeu 946
DB 530 CTGACCCCTGAGGAGTACCCCACTCTCCAGAGATGGTGGCAGCTGCCAAGCCCTGCTC 589
QY 947 GluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyrSerPheGln 966
DB 590 CCCACACCCCAAGCTCCGCTAGTCTCTTCCACTGACCCCTCACTTCTCTCTGACC 649
QY 967 LeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSerPro 986
DB 650 TGCCCTCTGCGC---TTCAACCGGTGATGATGCAAAACCATCTGCAAGAGCTCTGTCCA 706
QY 987 -----PheCysArgProGlySer-----ValLeuArgGlyArgMetCysVal 1000
DB 707 CTTCTTTCTGTCCACCGGGGTCACTGTATGTTGAGGCTCAGGCCGCCACAGTGC 766
QY 1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
DB 767 TCTGTGCGAGCTGGG-----TGCACAGGTGACCAATGCCAGCTC 805
QY 1021 GlySerTyrGluAspGluGlu-----Gly 1028
DB 806 CGAGACTTCTGTGCTAGCCCAACCCCTGTGCCAACGGAGGGGTGTGCTGGCCACATACCCC 865
QY 1029 GlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAsn 1048
DB 866 CAGATCCAGTGGCGC---TGTCCACTGGG---TTCAGGGTCAACCTGTGTGAAGCGAC 919
QY 1049 IleSerAspCys-----LysAlaGlnCysLysGlnGlyThrTyrSerTyrSerGly 1065
DB 920 ATCAACAGAGTGTCTTCTGAGCGCGGACCTGTGCTCAGGGCACCTCTCTGCCATAACACC 979
QY 1066 LeuGluThrCysGluSer---CysProLeuGlyThrTyrGlnProLysPheGlySerArg 1084
DB 980 TTGGGTCTCTACCACTGTCTCTGCTGCGGCGGAGAGGTCCCGAGTCAAGCTCAGG 1039
QY 1085 -----SerCysLeuSer-----CysProGlu 1091
DB 1040 AAGGAGCTGTGCTCTCTGAGAGCTGTCTCAATGGGGGACCTGCCAGCTGTGCCAGAG 1099
QY 1092 AsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGlyValPro----- 1109
DB 1100 GGACACTCCACC-----TTTCATCTCTGCTCTCTGCTGCCAGGT 1138
QY 1110 -----CysProGlu 1112
DB 1139 TTCAACGGGCTGGACTGTGAGATGAACCCAGATGATGTGTGTCAGGCACCACTGTCAAGAC 1198
QY 1113 GlyLysPheSerArgSerGlyLeu-----MetProCysHisProCysProArgAspTyr 1130
DB 1199 GGGGCCACCTGTCTGATGGCTGGATACCTACACTGC---CCCTGCCCCCAAGACATGG 1255
QY 1130 ----- 1130
DB 1256 AAGGGCTGGAGCTGTCTGAAGATATAGATGAATGTGAAGCCCGGGTCCCTCTGCTGC 1315
QY 1131 -----TyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysProPhe 1145
DB 1316 AGGAACGGTGGACCTGCCAGAACACAGCTGGCAGCTTTCACCTGTGTGCTGGTGGTGGC 1375
QY 1146 TyrGly-----ThrThrProPheAla 1152
DB 1376 TGGGAGGTGTCAGGCTGTGAGGAGAACCTGTGATGATGTGTCAGCTGCCACCTGTGCCCG 1435
QY 1153 GlySerArgSerIleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluGlu 1172
DB 1436 GGATCCACCTGCATCGACCGTGTGGGCTCTTTCTCC----- 1471

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; Sequence 6, Application US/09214278

; Patent No. 6251210

; GENERAL INFORMATION:

; APPLICANT: Sakano, Seiji

; APPLICANT: Itoh, Akira

; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

; FILE REFERENCE: KP-8576

; CURRENT APPLICATION NUMBER: US/09/214, 278

; CURRENT FILING DATE: 1999-01-26

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 4208

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (409)..(4062)

; NAME/KEY: sig_peptide

; LOCATION: (409)..(501)

; NAME/KEY: mat_peptide

; LOCATION: (502)..(4062)

; US-09-214-278-6

Alignment Scores:

Pred. No.:	1.05e-57	Length:	4208
Score:	749.00	Matches:	257
Percent Similarity:	35.13%	Conservative:	127
Best Local Similarity:	23.51%	Mismatches:	347
Query Match:	7.33%	Indels:	362
DB:	3	Gaps:	48

US-09-977-053-6 (1-1842) x US-09-214-278-6 (1-4208)

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QY 834 CysSerAspAlaGlu-----AspIleAspCysArgLeuGluGluAsnLeuThrIys 850
DB 571 TCGCGCGCGCCGGACCCGGAGACCCAGTGCACCGGACGAGTCTGCACATAC 630
QY 851 ---LysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe---AlaIleGlyPro 868
DB 631 TTCAAAGTGTGCTCAAG-----GAGTATCAGTCCCGGTCAACGCGCGCGCGGCC 681
QY 869 GlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyrAspPheLeuAspThrVal 888
DB 682 TCGAGCTTCGGCTCAGGG----- 699
QY 889 GlnGluThrAlaThr-SerIleGlyAenAlaLysSerSerArgIleLysArgSerAlaPro 908
DB 700 -----TCCAGCGCTGTATCGGGGCAACACCTTCAACCTCAAGCCAGCCCGCGC 750
QY 909 LeuSerAspTyrLysIleLysLeuIlePheAsnIle-----ThrAla 922
DB 751 AACGACCGCAACCGCATCGTGTCTTTCAGTTTCGCTTGGCCGCGAGTCTATAGCTTG 810
QY 923 SerValProLeuProAspGluArgAsnAspThrLeuGluThrIleThr 950
DB 811 CTGTGGAGCGTGGGATTCAGTAGTATGACACCGTTCAACCTGACAGTATTATTGAAAG 870
QY 938 -----AsnGlnGlnArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 950
DB 871 GCTTCTACTCGGCGATGATACCCCGCGCGAGTGGCAGACGCTGAAGCAGACACG 930
QY 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTyrSerPhe 965
DB 931 GCGGTGCGCACTTTGAGTATCAGATCCGCGTGACCTGTGATGACTACTACTATGCTTT 990
QY 966 GlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrIysLysAlaSer 985
DB 991 -----GGCTGCAAT 999
QY 996 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
DB 1000 AAGTTCTCGCGCGCCAGAGATGACTTCTTTGA----- 1032

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QY 1006 ThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAsp 1025
DB 1033 -----CACTATGCTGTGAC-----CAGATGGCAACAAACTTGC 1068
QY 1026 GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr 1041
DB 1069 ATGGAAGGCTGGATGGCCCGGATGTAACAGAGACTATTTCGCGACAGAGCTGCAGTCT 1128
QY 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
DB 1129 AAGCATGGGTCTTGCAAACTCCAGGTGACTGCGAGTGCAG-----TAC 1173
QY 1062 SerTyrSerGlyLeuGluThrCysGluSerCys-----ProLeuGlyThrTyr--- 1077
DB 1174 GCGTGGCAAGGCGCTG---TACTGTGATAAGTGCATCCACACCCGGATCGTCCACGGC 1230
QY 1078 -----GlnProLysPheGlySerArgSerCysLeu 1087
DB 1231 ATCTGTATGAGCCCTGGCAGTGCCTCTGTGAGACCAACTGGGGCGCGCAGCTCTGT--- 1287
QY 1088 SerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGly 1107
DB 1288 -----GACAAAGATCTCAATTACTGTGG 1311
QY 1108 Val-----ProCysProGluGly-----LysPheSer 1116
DB 1312 ACTCATCAGCCGTGTCTCAACGGGGAACTTTGAGCAACACAGGCCCTGCAATAATACAG 1371
QY 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
DB 1372 TGTTC-----TGCCTGAGGGGTATTCAGAGCCCACTCT--- 1407
QY 1137 LysAlaPheCysLeuAlaCysPropheTyrGlyThrThrProPheAlaGlySerArgSer 1156
DB 1407 ----- 1407
QY 1157 IleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluSerValPro 1176
DB 1407 ----- 1407
QY 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
DB 1408 -----GAATTGCTGAG-----CACGCC 1425
QY 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
DB 1426 TGCCTCTCTGATCCCTGTCAACAGAGCGAGCTGTAAAGGAGACCTCCCTGGGCTTTGAG 1485
QY 1217 CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236
DB 1486 TGTGAGTGTTCCTCCAGGCTGGACCGGCCCCACATGCTCTTACAACATTTGATGACTGTCT 1545
QY 1237 ProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGlu 1256
DB 1546 CTAATAACTGTGTCCACCGGGGCACTCCAGGACTTGGTTAACGATTTAAGTGTGTG 1605
QY 1257 CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSer 1276
DB 1606 TGCCTCCACAGTGCAGTGGGAAACGTCGAGTTAGATGCAATGAATGTGAGGCCAAA 1665
QY 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
DB 1666 CTTGTGTAAACGCCAAATCCCTGTAGAATCTCATTCGCGAGCTACTACTCGGACTGTCTT 1725
QY 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
DB 1726 CCGCGCTGATGGCTCAGATTTGTACATAATAATTAATGACTGCTTGGCCAG---TGT 1782
QY 1317 LeuAsnAlaValCysGluAspGlnValGlyPheLeuGlyCysLysCysProGly 1336
DB 1783 CAGAATGACGCTCTCTGCGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGGC 1842

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1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
1843 TATCCAGCGCATCACTGTGAGAGAGACATCGATGAATGTCACCAACCCCTGTTGAAT 1902
1357 GlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaIaGlyPheThr 1376
1903 GGGGGTCACTGTCCAGATGAATCAACAGATTCCAGTGTCTGTCTCCACTGGTTCCTCT 1962
1377 GlySerHisGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGluAla 1396
1963 GGAACCTCTGTAGCTGGAGCTGATTTATGAGCTTAATCTTCCAGACAGCGTGCC 2022
1397 ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGln 1416
2023 CAGTGTACAAACCGTCAGTCACTATTCTTCAAGTGCCTGAGGAGCTATGAGGCAAG 2082
1417 ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr 1436
2083 AACTGCTCACACCTGAAGAGCACTGCGCGCACGACCCCTGTGAAGTG----- 2130
1437 GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyr 1456
2131 -----ATGAC-----AGCTGCACAGTGGCC 2151
1457 MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp 1474
2152 ATGCTTCCAACGAC-----ACACTGAAGGGGTGGGTATATTTCCTCC 2196
1475 AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn 1494
2197 AAC-----GTCTGTGTCTCTCAC 2214
1495 GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTyrHisIleAla 1514
2215 GGGGAG-----TGCAAGAGTCAGTCGGAGGCAATTC----- 2247
1515 IleThrTyrThrSerAlaAsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAsp 1534
2248 ---ACCTGTGACTGTAAACAAGGCTTCACGGGAACATACTGCCATGAAATATTAAATGAC 2304
1535 GlyGlyAlaGlyLeuSerValGlyLeuProGlyGlyGlyAlaLeuValLeuGly 1554
2305 TGTGAGAGCAAC-----CCTGTAGAAACGGTGGCCTTGCATCGATGGT 2349
1555 GlnGluGlnAspLysGlyGluGlyPheSerProAlaGlnSerPheValGlySerIle 1574
2350 GTCAACTCTCTACAG-----TGCAATCTGTAGTACGGCTGGAGGGGGCTTAC 2397
1575 SerGlnLeuAsnLeuTyrAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr 1594
2398 TGTGAACCAATATTAAATGACTGACGAGCAGCAACCC----- 2433
1595 SerCysProGluGluLeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGly 1614
2434 ---TGCCACCAAT----- 2442
1615 IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg--- 1633
2443 -----GGGGCAGCTGTGGCAGCTGTGTAATGACTTCTACTGTACTGTAAAAATGGG 2496
1634 LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653
2497 TGGAAAGGAAGACCTGCCACTCAGTGCAGCTCAGTGTGATGAGGCGCAGCTGCAACAC 2556
1654 ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr 1671
2557 GGTGGCACCTGTCTATGATGAGGGGGTCTTTTAAG----- 2592
1672 CysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGluArgIleSerCysGly 1691
2593 TGCATGTCTCTGGCGGTGGGAAGGAGCAACCTGTGTACATAGCCCGGAACAGTAGTGTGC 2652
1692 ValProProLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAlaGlySerThr 1711

2653 CTGCCCAACCCCTGCCATAATGGG----- 2676
1712 ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThr 1731
2677 -----GGCACATGTGTGTACACGGGAGTCTCTTACGTGGCTC 2715
1732 AspAsnGlySerTyrAsnGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
2716 TGCAAGGAAGGCTGGAGGG-----CCCATCTGTGTCTCAGATACC----- 2757
1752 GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
2758 ---AATGACTGACGCTCATCTCTTACACAGCGGACCTGTGTGGATGAGATCAAC 2814
1767 SerTyrIleCysSerCysValProTyrThrGlyAsp----- 1779
2815 TGGTACCGTCCGATGTGCCCCGGGTTTGTGGCCGACTGCGAGATAAATCAATCAAT 2874
1780 -----GlyLysAsnCysAlaGluProIle----- 1787
2875 GAATGCCAGTCTTCACTTGTGCTTTGGAGCGACCTGTGTGGATGAGATCAATGGCTAC 2934
1788 LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTyrThrVal 1807
2935 CGGTGTGTCTGCTCT-----CCAGGGCAGCTGGTGCCCAAG----- 2970
1808 GlyAlaAlaValPheSerCysGlnGluGlyTyrGlnLeuMetGlyValThrLysIle 1827
2971 -----TGCCAGGA-----GTTTCAGGGAGA 2991
1828 ThrCysLeuGluSerGlyTyrAsnHisLeuIlePro 1840
2992 CTTTGCATCACATGGGAGT-----GTGATACCA 3021

RESULT 11

US-09-855-722-6
; Sequence 6, Application US/09855722
; Patent No. 6638741
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (409)..(4062)
; NAME/KEY: sig_peptide
; LOCATION: (409)..(501)
; NAME/KEY: mat_peptide
; LOCATION: (502)..(4062)
US-09-855-722-6

Alignment Scores:

Pred. No.:	1,05e-57	Length:	4208
Score:	749.00	Matches:	257
Percent Similarity:	35.13%	Conservative:	127
Best Local Similarity:	23.51%	Mismatches:	347
Query Match:	7.33%	Indels:	362
DB:	4	Gaps:	48

US-09-977-053-6 (1-1842) x US-09-855-722-6 (1-4208)

QY 834 CysSerAspAlaGlu-----AspIleAspCysArgLeuGluGluAsnLeuThrLys 850
DB 571 TCGCGCGCGCCCGACACCGACAGTGCACCGGACAGTCTGACACATAC 630
QY 851 ---LysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe---AlaIleGlyPro 868
DB 631 TTCAAAGTGTGCTCAAG-----GAGTATCAGTCCCGGTCAACGCGCGCGCGCC 681
QY 869 GlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrVal 888
DB 682 TGCAGCTTCGGCTCAGG----- 699
QY 889 GlnGluThrAlaThrSerIleGlyAsnAlaLysSerArgIleLysArgSerAlaPro 908
DB 700 -----TCCAGCGCTGATCGCGGCGCAACACCTTCAACCTCAAGCGCGCGCGC 750
QY 909 LeuSerAspTyrLysIleLysLeuIlePheAsnIle-----ThrAla 922
DB 751 AACGACCGCAACCGCATCGTGTCTTTCAGTTTCGCTGCGCGAGGTCTTATACGTTG 810
QY 923 SerValProLeuProAspGluArgAsnAspThrLeuGluThrIleThr 950
DB 811 CTTGTGGAGCGTGGGATTCAGATATGACACCGGTTCAACCTGACACGATATTATGAAAG 870
QY 938 -----AsnGlnGlnArgLeuLeuGlnThrLeuGluThrIleThr 950
DB 871 GCTTCTCACTCGCGCATGATCAACCCAGCGGAGTGGCAGCGCTGAAGCGAAGACG 930
QY 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTyrSerPhe 965
DB 931 GCGGTGGCCACTTTGAGTATCAGATCCCGGTGACCTGTGATGACTACTACTATGCTTT 990
QY 966 GlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSer 985
DB 991 -----GGCTGCAAT 999
QY 986 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
DB 1000 AAGTTCTCGCGCGCCAGAGATGACTCTTTTGA----- 1032
QY 1006 ThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAsp 1025
DB 1033 -----CACTATGCTGTGAC-----CAGATGGCAACAAACTGTC 1068
QY 1026 GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr 1041
DB 1069 ATGGAAGCTGGATGGCGCCGCAATGTAACAGAGACTATTTCGCGACAGGCTGCAGTCT 1128
QY 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
DB 1129 AAGCATGGGTCTTGCAAACTCCAGAGTGAAGTGTGCGTGCAG-----TAC 1173
QY 1062 SerTyrSerGlyLeuGluThrCysGluSerCys-----ProLeuGlyThrTyr--- 1077
DB 1174 GGTGGCAAGGCTG---TACTGTGATAAGTGTATCCACACCGGATGCGTCCACGCG 1230
QY 1078 -----GlnProLysPheGlySerArgSerCysLeu 1087
DB 1231 ATCTGTAATGAGCCCTGCGAGTGCCTCTGTGAGACCAACTGGGCGCGCGCTCTGT--- 1287
QY 1088 SerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGly 1107
DB 1288 -----GACAAAGATCTCAATCTACTGTGG 1311
QY 1108 Val-----ProCysProGluGly-----LysPheSer 1116
DB 1312 ACTCATCAGCGGTGTCTCAACGGGGGAACTTTAGCAACACAGCGCCCTGACAAATATCAG 1371
QY 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
DB 1372 TGTTC-----TGCCTGAGGGGTATTCAGGACCCCACTCT--- 1407
QY 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrProPheAlaGlySerArgSer 1156

1407 ----- 1407
QY 1157 IleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluGluSerValValPro 1176
DB 1407 ----- 1407
QY 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
DB 1408 -----GAATTTGCTCAG-----CAGGCC 1425
QY 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
DB 1426 TGCCTCTCTGATCCCTGTTCACACAGCAGCAGCTGTAAGGAGACCTCCCTGGGCTTGGAG 1485
QY 1217 CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236
DB 1486 TGTGAGTGTTCCTCCAGGCTGGACCGGCCCCACATGCTCTACAAACATTGATGACTGTCT 1545
QY 1237 ProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGlu 1256
DB 1546 CTTAATACTGTTCACCGGGGACCTGCCAGACCTGGTTAACGGATTTAAGTGTGTG 1605
QY 1257 CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSer 1276
DB 1606 TGCCTCCACAGTGGACTGGAAACGTGCCAGTTAGATGCAATGAATGTGAGGCCAAA 1665
QY 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
DB 1666 CTTGTGTAAACGCCAAATCCTGTAGAATCTCATTTGCCAGCTACTCTCGACTGTCTT 1725
QY 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
DB 1726 CCGGCTGGATGGTGCAGATTGTGCATAAATATTAAAGTACTGCTTGGCCAG---TGT 1782
QY 1317 LeuAsnAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGly 1336
DB 1783 CAGATGACGCTCTCTGCTGGATTGTTGTTAATGTTATCGCTGTATCTGTCCACCTGGC 1842
QY 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
DB 1843 TATGCAAGCGATCCTCTGTGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTGAT 1902
QY 1357 GlyValaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThr 1376
DB 1903 GGGGTCACTGTGAGATGAATCAACAGATTCAGTGTCTGTGCCACTGCTTCTCT 1962
QY 1377 GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
DB 1963 GGAACCTCTGTGAGTGCATCGATATTGTGAGCTTAATCCCTGCCAGAACGGTGC 2022
QY 1397 ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGln 1416
DB 2023 CAGTGTACACCGTCCAGTGAATTTCTGCAAGTGCCTCCAGGAGCTATGAGGGCAG 2082
QY 1417 ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr 1436
DB 2083 AACTGCTCACCTGAAAGACCACTCCCGCAGCACGCCCTGTCAGAGTG----- 2130
QY 1437 GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyr 1456
DB 2131 -----ATTGAC-----AGCTGCACAGTGGCC 2151
QY 1457 MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp 1474
DB 2152 ATGGCTTCCAAACGAC-----ACACCTGAAGGGGTGGGTATATTTCTCTCC 2196
QY 1475 AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn 1494
DB 2197 AAC-----GTCTGTGGTCTCTCAC 2214
QY 1495 GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTyrHisIleAla 1514

[illegible]

RESULT 13

Qy	889	GlnGluThrAlaThrSerIleGlyAsnAlaIysSerSerArgIleIysValGlySerAlaPro	908
Db	662	-----TCCACGCGCTGTATCGGGGGCAACACCTTCAACCTCAGGCCGCCCGCGGC	712
Qy	909	LeuSerAspTyrIzylsIleLysLeuIlePheAsnIle-----ThrAla	922
Db	713	AAAGACCCGACCGCATCGTGTGCTTTTCAGTTTCGCTGGCGAGGCTCTATACGTTG	772
Qy	923	SerValProLeuProAspGluArgAsnAspThrLeuGluTyrGlu-----	937
Db	773	CTTGTGGAGCGGTGGGATTCCTCAGTAATGACACCGTTTCAACCTGCACAGTATTATTGAA	832
Qy	938	-----AsnGlnGlnArgLeuGlnThrLeuGlnThrLeuGluThrIleThr	950
Db	833	GCTTCTCACTCGGGCATGATCAACCCAGCGCGAGTGGCAGACGCTGAAGCAGACACG	892
Qy	951	AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTyrSerPhe	965
Db	893	GGCGTTGCCCGACCTTTTGAGTATCAGATCCGCGTGTGATGACTACTACTATGCTTT	952
Qy	966	GlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrIzylsAlaSer	985
Db	953	-----GGCTGTATAT	961
Qy	986	ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly	1005
Db	962	AAAGTTCTGCGGCCAGAGATGACTTCTTTTGA-----	994
Qy	1006	ThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAsp	1025
Db	995	-----CACTATGCTGTGAC-----CAGATGGCACAACAACTTGC	1030
Qy	1026	GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr	1041

US-08-400-159-5
 ; Sequence 5, Application US/08400159
 ; Patent No. 5869282
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowitz, David
 ; APPLICANT: Henrique, Domingos M.P.
 ; APPLICANT: Lewis, Julian H.
 ; APPLICANT: Myat, Anna M.
 ; APPLICANT: Fleming, Robert J.
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; APPLICANT: Mann, Robert S.
 ; APPLICANT: Gray, Grace E.
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
 ; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM: disk
 ; MEDIUM TYPE: Floppy
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/400,159
 ; FILING DATE: 07-MAR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mierock, S. Leslie


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QY 1732 AspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
DB 2678 TGCAGGAGGCTGGAGGGG-----CCCATCTGTGTCAGATACC----- 2719
QY 1752 GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
DB 2720 ---AATGACTGCAGCCCTCATCCCTGTTACACAGCGCCACCTGTGTGGATGGAGACAAC 2776
QY 1767 SerTrpCysSerCysValProProTrpTrpGlyAsp----- 1779
DB 2777 TGTACCGGTGCGATGTGCCCCGGTTTCTGGGCGGCGACTGCAGATAAACATCAAT 2836
QY 1780 -----GlyAsnAsnCysAlaGluProIle----- 1787
DB 2837 GAATGCCAGCTTCCACCTGTGCTTGGAGCGACCTGTGTGGATGAGATCAATGGCTAC 2896
QY 1788 LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTrpVal 1807
DB 2897 CGGTGTCTGCTCCCT-----CCAGGGCACAGTGTGTGCCAAG----- 2932
QY 1808 GlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeuMetGlyValThrLysIle 1827
DB 2933 -----TGCAGGAA-----GTTTCAGGGAGA 2953
QY 1828 ThrCysLeuGluSerGlyGluTrpAsnHisLeuIlePro 1840
DB 2954 CCTGTGCATCACCATTGGGGAGT-----GTGATACCA 2983
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RESULT 14

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US-08-611-729A-5
; Sequence 5, Application US/08611729A
; Patent No. 6004924
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace E.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,729A
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-037
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6464 base pairs
; TYPE: nucleic acid
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STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 371..4024
US-08-611-729A-5
Alignment Scores:
Pred. No.: 5,27e-57 Length: 6464
Score: 745.00 Matches: 257
Percent Similarity: 34.95% Conservative: 125
Best local Similarity: 23.51% Mismatches: 349
Query Match: 7.29% Indels: 362
DB: 3 Gaps: 48
US-09-977-053-6 (11-1842) x US-08-611-729A-5 (1-6464)
QY 834 CysSerAspAlaGlu-----AspIleAspCysArgLeuGluGluAsnLeuThrLys 850
DB 533 TGCAGCGCGCGCCGGAACCCCGGAGACCGCAAGTGCACCCCGCAGCAGTGTGCACATAC 592
QY 851 ---LysTrpCysLeuGluTrpAsnTrpAspTrpGluAsnGlyPhe---AlaIleGlyPro 868
DB 593 TTCAAGGTGTCCCTCAAG-----GAGTATCAGTCCCGGTGCAGCCCGGGGGCCCC 643
QY 869 GlyGlyTrpGlyAlaAlaAsnArgLeuAspTrpSerTrpAspPheLeuAspThrVal 888
DB 644 TGCAGCTTCGGCTCAGGG----- 661
QY 889 GlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaPro 908
DB 662 -----TCCAGCGCTGTCTATCGGGGGCAACACCTTCAACCTCAAGGCCAGCGCGGC 712
QY 909 LeuSerAspTrpLysIleLysLeuIlePheAsnIle-----ThrAla 922
DB 713 AACGACCGCAACCGCATCTGCTGCTTTCAGTTTCGCTGCCGAGGTCCTATACGTTG 772
QY 923 SerValProLeuProAspGluArgAsnAspThrLeuGluTrpGlu----- 937
DB 773 CTGTGGAGGGGTGGGATTCAGTAATGACACCGTTCAACCTGACAGTATTATTGAAAG 832
QY 938 -----AsnGlnArgLeuLeuGlnThrLeuGluThrIleThr 950
DB 833 GCTTCTCACTCGGCGCATCATCAACCCAGCGGAGTGCAGACGCTGAAGCAGACACG 892
QY 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTrpSerPhe 965
DB 893 GCGGTGCCCCACTTTGAGTATCAGATCCGCTGACCTGTGATGACTACTACTATGGCTTT 952
QY 966 GlnLeuAlaSerGluIleLeuAlaAspSerAsnSerLeuGluThrLysLysAlaSer 985
DB 953 -----GCTGTAAAT 961
QY 986 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
DB 962 AAGTTCTGCGCGCCCGCAGAGATGACTTCTTTGGA----- 994
QY 1006 ThrTrpTrpAsnLeuGluHisPheThrCysGluSerCysAspGlyIleGlySerTrpGlnAsp 1025
DB 995 -----CATTATCCCTGTGAC-----CAGATGGCCACAAACTTGC 1030
QY 1026 GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTrpThr 1041
DB 1031 ATGGAAGGCTGGATGGGCCCCCGAATGTAACAGAGCTATTTCGCGACAGAGTCTCAGTCT 1090
QY 1042 GluTrpIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTrp 1061
DB 1091 AAGCATGGGCTCTTGCAAACTCCCGAGTGAAGTGCAGGTGCAG-----TAC 1135
QY 1062 SerTrpSerGlyLeuGluThrCysGluSerCys-----ProLeuGlyThrTrp--- 1077
DB 1136 GGCTGGCAAGGCGCTG---TACTGTGATAGTGCATCCACACCCGGGATGCGTCCACGGC 1192
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QY 1078 -----GlnProLysPheGlySerArgSerCysLeu 1087
DB 1193 ATCTGTAATGAGCCCTGGCAGTGCCTCTGTGAGACCAACTGGGGCGGCAGCTCTGT--- 1249
QY 1088 SerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGly 1107
DB 1250 -----GACAAAGATCTCAATTAAGTCTGGG 1273
QY 1108 Val-----ProCysProGluGly-----LysPheSer 1116
DB 1274 ACTCATCAGCCGTGCTCAACGGGGGAACTGTAGCAACACAGCCGCTGACAAATATCAG 1333
QY 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
DB 1334 TGTTCC-----TGCCCTGAGGGGTATTACAGGCCCAACTGT--- 1369
QY 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrProPheAlaGlySerArgSer 1156
DB 1369 ----- 1369
QY 1157 IleThrGluCysSerSerPheSerThrPheSerAlaAlaGluSerValValPro 1176
DB 1369 ----- 1369
QY 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
DB 1370 -----GAAATGTCTGAG-----CACGCC 1387
QY 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
DB 1388 TGCTCTCTGATCCCTGTGACACAGAGCAGCTGTAGAGAGACCTCCCTGGGCTTTGAG 1447
QY 1217 CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236
DB 1448 TGTGAGTGTTCACAGGCTGGACCGGCCCATGCTCTTACAAACATTGATGACTGTCT 1507
QY 1237 ProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGlu 1256
DB 1508 CCTAATAACTGTCTCCACGGGGGCACCTGCCAGGACCTGGTTTAACGGATTTAAGTGTGTG 1567
QY 1257 CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSer 1276
DB 1568 TGCCCCCAGCAGTGGGAAACCTGCCAGTTAGTAGCAATGAATGTGAGGCCAA 1627
QY 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
DB 1628 CTTGTGTAAACGCCAAATCCTGTGAAGAATCTCAATTGCCAGCTACTACTGCCAGCTGTCT 1687
QY 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
DB 1688 CCGGCTGGATGGGTGAGAAATGTGACATAAATATTAATGACTGCTTGGCCAG---TGT 1744
QY 1317 LeuAsnAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGly 1336
DB 1745 CAGAAATGACGCTCTCTGCGGATTTGGTTAATGTTATGCTGTATCTGTCTCACTGCG 1804
QY 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
DB 1805 TATGACGGCGATCACTGTGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAAT 1864
QY 1357 GlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThr 1376
DB 1865 GGGGGTCACTGTGAGAAATCAACAGATTCAGTGTCTGTGTGCCACTGGTTTCTCT 1924
QY 1377 GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
DB 1925 GGAACCTCTGTCACTGACATGATGATTTATGAGCCTTATCTCTGCCAGAACCGTGCC 1984
QY 1397 ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGln 1416
DB 1985 CAGTCTACACCGTGGCAGTGACTATTCTTGTCAAGTGGCCCGGAGGACTATGAGGGCAAG 2044

QY 1417 ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr 1436
DB 2045 AACTGCTCACCTGAAAGACACACTGCCGCGACGACCCCTGTGAAGTG----- 2092
QY 1437 GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyr 1456
DB 2093 -----ATTGAC-----AGCTGCACAGTGGCC 2113
QY 1457 MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp 1474
DB 2114 ATGGCTTCCAACGAC-----ACACCTGAAGGGTGGGTATATTTCTCTCC 2158
QY 1475 AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn 1494
DB 2159 AAC-----GTCTGTGGTCTCTCAC 2176
QY 1495 GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTyrHisIleAla 1514
DB 2177 GGGAG-----TGCAAGAGTCACTGGGAGGCAATTC----- 2209
QY 1515 IleThrTyrThrSerAlaAsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAsp 1534
DB 2210 ---ACCTGTGACTGTAAACAAGGCTTCACGGGAACATACTGCCATGAAATATTAAATGAC 2266
QY 1535 GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyAlaLeuValLeuGly 1554
DB 2267 TGTGAGAGCAAC-----CCTGTAGAAACGGTGGCACTTGCATCGATGCT 2311
QY 1555 GlnGluGlnAspLysGlyGluGlyPheSerProAlaGluSerPheValGlySerIle 1574
DB 2312 GTCAACTCTACAAAG-----TGCACTGTAGTGACGGCTGGGAGGGGCTTAC 2359
QY 1575 SerGlnLeuAsnLeuTyrAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr 1594
DB 2360 TGTGAACCAATATTATTAATGACTGCCGCCAGAACCC----- 2395
QY 1595 SerCysProGluGluLeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGly 1614
DB 2396 ---TGCCACAT----- 2404
QY 1615 IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg--- 1633
DB 2405 -----GGGGGCACCTGTCGCGACCTGGTCAATGACTTCTACTGTGACTGTAAATAATGGG 2458
QY 1634 LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653
DB 2459 TGAAGAAGAAAGACCTGCCACTCACGTGACAGTGTGTGTGAGGCCACGTCGCAACAC 2518
QY 1654 ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr 1671
DB 2519 GGTGGCACCTGTATGATGAGGGGGATGCTTTTAAG----- 2554
QY 1672 CysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGluArgIleSerCysGly 1691
DB 2555 TGCATGTGTCTGGCGGCTGGGAAGCAACACTGTAAACATAGCCCGAACAACAGTAGCTGC 2614
QY 1692 ValProProProLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAlaGlySerThr 1711
DB 2615 CTGCCCAACCCCTGCCATAATGG----- 2638
QY 1712 ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThr 1731
DB 2639 -----GGCAGATGTGTGGTTCACGGCGAGTCTTCTTACGTGGTC 2677
QY 1732 AspAsnGlySerTyrAsnGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
DB 2678 TGCAAGGAAGGCTGGGAGGG-----CCCATCTGTGCTCAGAAATACC----- 2719
QY 1752 GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
DB 2720 ---AATGACTGAGCCCTCATCCCTGTTACAAACAGCGGCACCTGTGTGTGATGAGACAC 2776
QY 1767 SerTyrIleCysSerCysValProProTyrThrGlyAsp----- 1779


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Db 2777 TGTACCGTGCAGATGTGCCCGGTTTCTGTCGGCCGACTGCAGAAATAACATCAAT 2836
Qy 1780 -----GlyLysAsnCysAlaGluProIle----- 1787
Db 2837 GAATGCCAGCTTCCACCTGTGCTTGGACGACCTGTGTGGATGAGATCAATGGCTAC 2896
Qy 1788 LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTyrThrVal 1807
Db 2897 CGGTGTGTCTCCCT-----CCAGGGACAGTGGTGCCAG----- 2932
Qy 1808 GlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeuMetGlyValThrLysIle 1827
Db 2933 -----TGCCAGGAA-----GTTTCAGGGAGA 2953
Qy 1828 ThrCysLeuGluSerGlyGluTrpAsnHisLeuIlePro 1840
Db 2954 CCTTGCATCACCATGGGAGT-----GTGATACCA 2983

RESULT 15
US-09-068-740A-10
; Sequence 10, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 4208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (409)..(4062)
; US-09-068-740A-10

Alignment Scores:
Pred. No.: 3,01e-57 Length: 4208
Score: 744.00 Matches: 257
Percent Similarity: 34.95% Conservative: 125
Best Local Similarity: 23.51% Mismatches: 349
Query Match: 7.28% Indels: 362
DB: 4 Gaps: 48

US-09-977-053-6 (1-1842) x US-09-068-740A-10 (1-4208)
Qy 834 CysSerAspAlaGlu-----AspIleAspCysArgLeuGluAsnLeuThrLys 850
Db 571 TGCAGCGCGCGCGGAGACCCCGGAGACCGCAAGTGCACCCCGCAGAGTGACACATAC 630
Qy 851 ---LysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe---AlaIleGlyPro 868
Db 531 TTCAAGTGTGCTCAAG-----GAGTATCAGTCCCGGTCCAGCGCGCGGGGCC 681
Qy 869 GlyGlyTrpGlyAlaAlaAsnArgLeuAspTyrSerTyrAspPheLeuAspThrVal 888
Db 682 TGCAGCTTCGCTCAGG----- 699
Qy 889 GlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaPro 908
Db 700 -----TCCAGCGCTGTATCGGGGCAACACCTTCAACCTCAAGCGCGCGCGG 750

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Qy 909 LeuSerAspTyrLysIleLysLeuIlePheAsnIle-----ThrAla 922
Db 751 AACGACCGCAACCGCATGTGCTGCTTTTCAGTTTTCGCTGCGCGAGGTCCTATACGTTG 810
Qy 923 SerValProLeuProAspGluArgAsnAspThrLeuGluTrpGlu----- 937
Db 811 CTGTGGAGGGGTGGGATTCAGTAAATGACACCGTTCAACCTGACAGATATTATTGAAAG 870
Qy 938 -----AsnGlnGlnArgLeuLeuGlnThrLeuGluThrIleThr 950
Db 871 GCTTCTCCTCGGGCATCATCAACCCGCGCGAGTGGCAGCGCTGAAGCAGAACACG 930
Qy 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTyrSerPhe 965
Db 931 GCGGTGGCCCATTTGAGTATCAGATCCGCGTGACCTGTGATGACTACTACTATGCTTT 990
Qy 966 GlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSer 985
Db 991 -----GGTGTCAAT 999
Qy 986 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
Db 1000 AAGTTCTGCGCGCCGAGAGATGACTTCTTTGGA----- 1032
Qy 1006 ThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAsp 1025
Db 1033 -----CACTATGCTGTGAC-----CAGAAATGGCAACAAACTTGC 1068
Qy 1026 GluGluGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr 1041
Db 1069 ATGGAAGGCTGGATGGGCCCGCAATGTAAACAGAGCTATTTCGCGACAGGTCGACGCTCT 1128
Qy 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
Db 1129 AAGCATGGTCTTGCAAATCCAGGTGCTGACAGTGCAG-----TAC 1173
Qy 1062 SerTyrSerGlyLeuGluThrCysGluSerCys-----ProLeuGlyThrTyr--- 1077
Db 1174 GGCTGGCAAGGCGCTG---TACTGTGATAAGTGCATCCACACCCGCGGATGCGTCCAGCG 1230
Qy 1078 -----GlnProLysPheGlySerArgSerCysLeu 1087
Db 1231 ATCTGTAAATGAGCCCTGGCAGTGCCTCTGTGAGACCAACTGGGGCGCGCAGCTCTGT--- 1287
Qy 1088 SerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGly 1107
Db 1288 -----GACAAAGATCTCAATTACTGTGG 1311
Qy 1108 Val-----ProCysProGluGly-----LysPheSer 1116
Db 1312 ACTCATCAGCGCTGTCTCAACGGGGGAACCTGTAGCAACACAGCGCCCTGACAAATATCAG 1371
Qy 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
Db 1372 TGTTC-----TSCCCTGAGGGGTATTTCAGGACCCCACTGT--- 1407
Qy 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
Db 1407 ----- 1407
Qy 1157 IleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluSerValPro 1176
Db 1407 ----- 1407
Qy 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
Db 1408 -----GAAATGCTGAG-----CACGCC 1425
Qy 1197 CysPheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
Db 1426 TGCCTCTCTGATCTCTCAACACAGAGCGAGCTGTAGGAGACCTCCCTCGGCTTGTAG 1485
Qy 1217 CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236

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Db 1486 TGTGAGTGTTCCTCCAGGCTGGACCGGCCCAATGCTCTACAAACATTGATGACTGTCT 1545
Qy 1237 ProLeuProCysLeuAsnAsnGlyValCysAspLeuValGlyGluPheLeuCysGlu 1256
Db 1546 CCTAATACTGTTCCACGGGGGACCTGCCAGGACCTGTTAAGCGATTAAGTGTGTG 1605
Qy 1257 CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnLeuAsnGluCysSerSer 1276
Db 1606 TGGCCCCACACAGTGGGAAACGTCGAGTTAGATGCAATGAATGTGAGGCGCAA 1665
Qy 1277 ProCysLeuAsnLysGlyLeuCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
Db 1666 CTTGTGTAAACGCGCAATCTCTGTAAGAAATCTATTGCCAGCTACTCTGCGACTGTCTT 1725
Qy 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
Db 1726 CCGGCTGGATGGGTGAGATTTGTCACATAATATTAAATGACTGCTTGGCCAG--TGT 1782
Qy 1317 LeuAsnAsnAlaValCysGluAspGlnValGlyPheLeuCysGlyCysProProGly 1336
Db 1783 CAGAACTGAGCTCTGCTGGGATTTGGTTAATGTTATGCTGCTATCTGTCTCCACTGCT 1842
Qy 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
Db 1843 TATGACGGCGATCACTGTGAGAGAGACATGCGATGAATGTCAGCAACCCCTGTTTGAAT 1902
Qy 1357 GlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThr 1376
Db 1903 GGGGTCACTGTGAGATGAATCAACAGATTCAGTGTCTGTGTCCACTGTTCTCT 1962
Qy 1377 GlySerHisCysGluLeuAsnLysGlnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
Db 1963 GGAACCTCTGTGAGTGGACATGATTAATGAGCCCTAATCCCTGCCAGAACGGTGC 2022
Qy 1397 ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGln 1416
Db 2023 CAGTCTCAACCGTGGCAGTCACTATTCTGCAAGTGCCTGAGGACTATGAGGCGAAG 2082
Qy 1417 ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr 1436
Db 2083 AACTGCTCACCTGAAGACCACTGCCCGCAGCCCTCTGTGAGTG----- 2130
Qy 1437 GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPhePro 1456
Db 2131 -----ATTGAC-----AGCTGCACAGTGGCC 2151
Qy 1457 MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp 1474
Db 2152 ATGGCTTCCACGAC-----ACACCTGAAGGGGTGGGTATATTTCCTCC 2196
Qy 1475 AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn 1494
Db 2197 AAC-----GTCTGTGCTCTCTAC 2214
Qy 1495 GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTyrHisIleAla 1514
Db 2215 GCGAAG-----TGCAAGAGTCACTGGGAGGCAAAATTC----- 2247
Qy 1515 IleThrThrThrSerAlaAsnGlyIleThrLysValTyrIleAspGlyLysLeuSerAsp 1534
Db 2248 ---ACCTGTGACTGTAACAAGGCTTCACGGGAACATATGCGCATGAAATAATTATGAC 2304
Qy 1535 GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyAlaLeuValLeuGly 1554
Db 2305 TGTGAGAGCAAC-----CCTTGTAGAAACGGTGGCACTTGCATCATGTGT 2349
Qy 1555 GlnGluGlnAspLysGlyGlyPheSerProAlaGluSerPheValGlySerIle 1574
Db 2350 GTCAACTCTACAG-----TGCAATCTGTAGTGCAGCGCTGGAGGGGGCTAC 2397
Qy 1575 SerGlnLeuAsnThrAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr 1594
Db -----

Db 2398 TGTGAACCAATATTATTGACTGACCGCCAGAACCC----- 2433
Qy 1595 SerCysProGluGluLeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGly 1614
Db 2434 ---TGCCACAAAT----- 2442
Qy 1615 IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg--- 1633
Db 2443 -----GGGGGACCTGTCGGGACCTGGTCAATGACTTCTACTGTGACTGTAAAAATGGG 2496
Qy 1634 LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653
Db 2497 TGAAGAAGGAAGACCTGCCACTCAGTGCACCTGAGTGTGTGAGCCACGTCGCAACAC 2556
Qy 1654 ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr 1671
Db 2557 GGTGGCACCTGTATGATGAGGGGCGATGCTTTTAAG----- 2592
Qy 1672 CysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGluArgIleSerCysGly 1691
Db 2593 TGCATGTGTCTGCGCGCTGGGAAGAAACACTGTAAACATAGCCCGAAACAGTAGCTGC 2652
Qy 1692 ValProProProLeuGluAsnGlyPheHisSerAlaAspPheTyrAlaGlySerThr 1711
Db 2653 CTGCCCAACCTCGCCATAATGG----- 2676
Qy 1712 ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThr 1731
Db 2677 -----GGCACATGTGTGTGTCACGGCGAGTCTTTTACGTGCGTC 2715
Qy 1732 AspAsnGlySerTyrAsnGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
Db 2716 TGCAAGGAAGGCTGGGAGGG-----CCCATCTGTGTGTCAGAAATACC----- 2757
Qy 1752 GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
Db 2758 ---ATGACTGACGCTCATCTCTTACACAGCGGACCTGTGTGATGGAGACAC 2814
Qy 1767 SerTyrIleCysSerCysValProTyrThrGlyAsp----- 1779
Db 2815 TGGTACCGTGGCAATGTCCCGCGGTTTGTGCGCGGCTGCGAGATTAACATCAAT 2874
Qy 1780 -----GlyLysAsnCysAlaGluProIle----- 1787
Db 2875 GAATCCAGTCTTACCTTGTGCTTGGAGCGACCTGTGTGATGAGATCAATGGCTAC 2934
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Qy 1808 GlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeuMetGlyValThrLysIle 1827
Db 2971 -----TGCCAGGAA-----GTTTCAGGAGAGA 2991
Qy 1828 ThrCysLeuGluSerGlyGluTyrAsnHisLeuLeuPro 1840
Db 2992 CCTTGATCATTGCGGAGT-----GTGATACCA 3021

RESULT 16

US-08-882-046-1
; Sequence 1, Application US/08882046
; Patent No. 6136952
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Kwantz, Ian D.
; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 25-JUN-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UW 2637
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5590 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 414..4068
 US-08-882-046-1

Alignment Scores: 5,01e-57 Length: 5590
 Pred. No.: 744.00 Matches: 257
 Score: 34.95% Conservative: 125
 Best Local Similarity: 23.51% Mismatches: 349
 Query Match: 7.28% Indels: 362
 DB: 3 Gaps: 48

US-09-977-053-6 (1-1842) x US-08-882-046-1 (1-5590)

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 QY 851 ---LysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe---AlaIleGlyPro 868
 DB 636 TTCAAAGTGTGCTCAAG-----GAGTATCAGTCCCGCGTCAACGCGCGGGGCGCC 686
 QY 869 GlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrVal 888
 DB 687 TGCAGCTTCGGCTCAGGG----- 704
 QY 889 GlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaPro 908
 DB 705 -----TCCAGCGCTGTGCATCGGGGGCAACACCTTCACTCAAGCGCGCGCGG 755
 QY 909 LeuSerAspTyrIleLysLeuIlePheAsnIle-----ThrAla 922
 DB 756 AACGACCGCAACCGCATCGTGTGCTTTCAGTTTCGCTTCGCGCGAGGTCTATACGTTG 815
 QY 923 SerValProLeuProAspGluArgAsnAspThrLeuGluThrGlu----- 937
 DB 816 CTTGTGGAGCGGTGGATTCCAGTAATGACACCGTTCACTCACTGACAGTATTATGAAAG 875
 QY 938 -----AsnGlnGluArgLeuLeuGlnThrLeuGluThrIleThr 950
 DB 876 GCTTCTCACTCGGCGATGATCAACCCGCGGAGTGGCAGCGCTGAGCAGCAACACG 935
 QY 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTyrSerPhe 965
 DB 936 GGGGTTGCCACCTTTGAGTATCAGATCCGCGTGACCTGTGATGACTACTACTATGCGCTTT 995

QY 966 GlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSer 985
 DB 996 -----GGCTGCAAT 1004
 QY 986 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
 DB 1005 AAGTTCTGCGCGCCAGAGATGACTTCTTTGGA----- 1037
 QY 1006 ThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAsp 1025
 DB 1038 -----CACTATGCTGTGAC-----CAGATGGCAACAAACTTGC 1073
 QY 1026 GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr 1041
 DB 1074 ATGGAGGCTGGATGGGCGCCGATGTAACAGAGCTATTTCGCGAGGCTGCAGTCT 1133
 QY 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
 DB 1134 AAGCATGGGTCTTGCAAACTCCAGGTGACTGCAGGTGCCAG-----TAT 1178
 QY 1062 SerTyrSerGlyLeuGluThrCysGluSerCys-----ProLeuGlyThrTyr--- 1077
 DB 1179 GGCTGGCAAGGCGCTG---TACTGTGATAAGTGCATCCACACCGCGGATGCGTCCACGGC 1235
 QY 1078 -----GlnProLysPheGlySerArgSerCysLeu 1087
 DB 1236 ATCTGTAATGAGCCCTGGCAGTGCCTCTGTGAGACCACTGGGGCGGCGAGTCTGT--- 1292
 QY 1088 SerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGly 1107
 DB 1293 -----GACAAAGATCTCAATTACTGTGGG 1316
 QY 1108 Val-----ProCysProGluGly-----LysPheSer 1116
 DB 1317 ACTCATCAGCGGTGTCTCAACGGGGGAACTTGTAGCAACACAGGCGCTGACAAATATCAG 1376
 QY 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
 DB 1377 TGTTC-----TGCTCTGAGGGGTATTTCAGGACCCCACTGT--- 1412
 QY 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
 DB 1412 ----- 1412
 QY 1157 IleThrCysSerSerPheSerSerThrPheSerAlaAlaGluGluSerValPro 1176
 DB 1412 ----- 1412
 QY 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
 DB 1413 -----GAAATTGCTGAG-----CACGCC 1430
 QY 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
 DB 1431 TGCCTCTGTCTCTGCTCAACAGGCGAGCTGTAAAGAGAGACCTCCCTGGGCTTTGAG 1490
 QY 1217 CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236
 DB 1491 TGTGAGTGTTCCTCCAGGCTGGACCGCGCCCACTGCTCTACAAATGATGAGTGTCT 1550
 QY 1237 ProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGlu 1256
 DB 1551 CCTAATAACTGTTCCACAGGGGGCACCTGCCAGGACCTGGTTAAGGATTTAAGTGTGTG 1610
 QY 1257 CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSer 1276
 DB 1611 TGGCCCCCAGTGGAGTGGGAAAACGTCGCCAGTTAGATGCAAAATGATGTGAGGCCAAA 1670
 QY 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
 DB 1671 CCTGTGTAAACGCCCAAACTCTGTGAAGAACTCTATTGCCAGCTACTACTGCGACTGTCTT 1730

1297	Qy	LySGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys	1311
1731	Db	CCCGCTGGATGCTGAGATTTCTGCACATAAAATTAATGACTGACCTTGCCACAG---TGT	1787
1317	Qy	LeuAsnAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysGlyCysProGly	1336
1788	Db	CAGAAATGACGCCCTCTGTGCGGATTGTGTTAATGGTTATCGCTGTATCTGTCACCTGGC	1847
1337	Qy	PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn	1356
1848	Db	TATCCAGCGCATCTCTGAGAGAGACATCGATGATGTGCCAGCAACCCCTGTGTGAAT	1907
1357	Qy	GlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThr	1376
1908	Db	GGGGTCACTGTGAGATGAAATCAAAGATTCAGGTGTCTGTGTGCCACTGTGTCTCT	1967
1377	Qy	GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla	1396
1968	Db	GGAAACCTCTGTGAGCTGGACATCGATTATTGTGAGCCTAATCCCTGCCAGAACGGTGCC	2027
1397	Qy	ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGln	1416
2028	Db	CAGTGTCTAACCGTGCAGCTGACTATTCTGCAAGTGCCCGGAGACTATGAGGCGAAG	2087
1417	Qy	ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr	1436
2088	Db	AACCTGCTCACACCTGAAAGACCACTGCGCCACAGCCCTGTGAAGTG-----	2135
1437	Qy	GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyr	1456
2136	Db	---ATTGAC-----ATTTGAC-----ATTTGAC-----ATTTGAC-----	2156
1457	Qy	MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp	1474
2157	Db	ATGCTTCCACGCAC-----ACACCTGAAGGGTGGGTATATTCTCTCC	2201
1475	Qy	AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn	1494
2202	Db	AAC-----GTTCTGTGGTCTCTAC	2219
1495	Qy	GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTyrHisIleAla	1514
2220	Db	GGGAAG-----TGCAAGATCAGTCGGGAGGCAATTC-----	2252
1515	Qy	IleThrTyrThrSerAlaAsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAsp	1534
2253	Db	---ACCTGTGACTACTAACAAAGCGCTTCCGGACATACCTGCCATGAAATATTATGAC	2309
1535	Qy	GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyAlaLeuValLeuGly	1554
2310	Db	TGTGAGAGCAAC-----CCTTGTAGAAACGCTGGCACTTCATCGATGGT	2354
1555	Qy	GlnGluGlnAspLysGlyGlyPheSerProAlaGluSerPheValGlySerIle	1574
2355	Db	GTCAACTCCTTACAG-----TGCACTGTGTAGTACCGCTGGGAGGGGGCTAC	2402
1575	Qy	SerGlnLeuAsnLeuTyrAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr	1594
2403	Db	TGTGAACCAATATTATATGACTCGCGCCAGACCCC-----	2438
1595	Qy	SerCysProGluGluLeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGly	1614
2439	Db	---TGCCACAAT-----	2447
1615	Qy	IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg---	1633
2448	Db	-----GGGGGCACGTGCGCGACCTGGTCAAATGACTTCTACTGTGACTGTAAATAATGGG	2501
1634	Qy	LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys	1653
2502	Db	TGGAAAGGAAGACCTGCCACTCACGTGACAGCTGATGATGAGGCGCAGTGCACACAC	2561
1654	Qy	ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr	1671

Db	2562	GGTGGCACCTGCTATGATGAGGGGGATGCTTTTAAG-----	2597	----
Qy	1672	CysLeuAsnGlnGlyInThrGlnProLeuProHisCysGluArgIleSerCysGly	1691	----
Db	2598	TGCATGTGCTCGCGCTGGGAGGAACAACCTGTAACAATAGCCCGAACAAGTAGCTGC	2657	----
Qy	1692	ValProProLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAlaGlySerThr	1711	----
Db	2658	CTGCCAACCCCTGCCATAATGG-----	2681	----
Qy	1712	ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAaspSerArgMetPheCysThr	1731	----
Db	2682	-----GGCACATGTGTGGTCAACCGCGAGTCTTTAAGTCGCTC	2720	----
Qy	1732	AspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspValaaspGluCysAlaVal	1751	----
Db	2721	TGCAGGAAGGCTGGGAGGG-----CCATCTGTGCTCAGATACC-----	2762	----
Qy	1752	GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValaaspGly	1766	----
Db	2763	--AATGACTGCAGCCCTCATCCTGTTACAACAGCGGCACCTGTGTGGATGGAGACAAC	2819	----
Qy	1767	SerTyrIleCysSerCysValProProTyrThrGlyAsp-----	1779	----
Db	2820	TGGTACCGGTGCGAATGTGCCCCCGGGTTTGTCTGGGCCCGAGCTGCAGATAAACATCAAT	2879	----
Qy	1780	-----GlyLysAsnCysAlaGluProfile-----	1787	----
Db	2880	GAATGCCAGTCTTCACTTGTGCTTGGAGCGACCTGTGTGGATGAGATCAATGGCTAC	2939	----
Qy	1788	LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTyrThrVal	1807	----
Db	2940	CGGTGTGTCTGCCCT-----CCAGGCGACAGTGGTGCACAG-----	2975	----
Qy	1808	GlyAlaAlaValThrPheSerCysGlnGlnGlyTyrGlnLeuMetGlyValThrLysIle	1827	----
Db	2976	-----TGCCAGGA-----GTTTCAGGGAGA	2996	----
Qy	1828	ThrCysLeuGluSerGlyGluTrpAsnHisLeuIlePro	1840	----
Db	2997	CCCTGCATCACCATTGGGAGT-----GTGATACCA	3026	----

RESULT 17

US-08-400-159-9
: Sequence 9, Application US/08400159
: Patent No. 5869282
: GENERAL INFORMATION:
: APPLICANT: Ish-Horowicz, David
: APPLICANT: Henrique, Domingos M.P.
: APPLICANT: Lewis, Julian H.
: APPLICANT: Myat, Anna M.
: APPLICANT: Fleming, Robert J.
: APPLICANT: Artavanis-Tsakonas, Spyridon
: APPLICANT: Mann, Robert S.
: APPLICANT: Gray, Grace E.
: TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
: TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/400,159

FILING DATE: 07-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Miarock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7326-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3582 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3582
 US-08-400-159-9

Alignment Scores:
 Pred. No.: 2,03e-52 Length: 3582
 Score: 690.00 Matches: 238
 Percent Similarity: 36.34% Conservative: 113
 Best Local Similarity: 24.64% Mismatches: 301
 Query Match: 6.75% Indels: 315
 DB: 2 Gaps: 48

US-09-977-053-6 (1-1842) x US-08-400-159-9 (1-3582)

QY 987 PheCysArgProGlySerValLeuArgGlyMetCysValAenCysProLeuGlyThr 1006
 DB 517 TTTTGTGCGCCGAGAT----- 534
 QY 1007 TyrTyAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyGlnAspGlu 1026
 DB 535 -----GACTTCTTCACTCACCATACCTGT-----GACCAG 564
 QY 1027 GluGlyGlnLeuGluCys-----LysLeuCys 1035
 DB 565 AATGGCAACAAACCTGCTTGGAGGCTGGACGGACCAAGATGCACAAAGCTATTGT 624
 QY 1036 ProSerGlyMetTyThrGluTyIleHisSerArgAsnIleSerAspCysLysAlaGln 1055
 DB 625 CGTCAGGATGTAGCCCAAGCATGGTCTTGCACAGTTCAGGAGAGTGCAGTGTCTAG 684
 QY 1056 CysLysGlnGlyThrTySerTySerGlyLeuGluThrCysGluSerCys----- 1072
 DB 685 -----TATGGATGCAAGGC---CAGTACTGTGATAGTGCATTCCACAC 726
 QY 1073 ProLeuGlyThrTyGlnProLysPheGlySerArgSerCysLeuSerCysProGluAsn 1092
 DB 727 CCGGGATGTGTCATGTCACCTTGCAITGGAACCATGCGCAGTGCCTC---TGTGAACCAAC 783
 QY 1093 ThrSerThrValLysArgGlyAlaVal-----AsnIleSerAlaCysGlyVal--- 1108
 DB 784 TGGGGT-----GGTCAGCTCTGTGACAAAGACCTGAACTACTGTGGAAACCCAC 831
 QY 1109 ---ProCysProGluGly-----LysPheSerArgSer 1118
 DB 832 CCACCTGTTTGAATGTTGGTGTACCTGCGCAACACAGTGCCTCCGATATAATACCACTGTTCC 891
 QY 1119 GlyLeuMetProCysHisProCysProArgAspTyThrGlnProAsnAla-----Gly 1136
 DB 892 -----TGCCTCTGAGGGTTACTCAGGACAGAACTGTGAAATAGCG 930
 QY 1137 LysAlaPheCysLeuAlaCysProPheTyThrProPheAlaGlySerArgSer 1156
 DB 931 GAGCATCGGCTCTCTGATCTCGCCACAC-----GAGGAGAC----- 972
 QY 1157 IleThrGluCysSerPheSerSerThrPheSerAlaAlaGluSerValPro 1176

DB 973 -----TGCCTAGAAAAGCTCTACAGATTT-----GAATGTGTGTGTCGA 1011
 QY 1177 ProAlaSerLeuGlyHisIleLysArgHisGluIleSerSerGlnValPheHisGlu 1196
 DB 1012 CTTGGCTGGGCTGGA-----CCAATTCGCACTGATAATATTGATGAT 1053
 QY 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyVal 1216
 DB 1054 TGTTCCTCAAAATCCCTGTGTGTCATGGAGAACTTGCACAGATCTAGTTGATGATTTAAG 1113
 QY 1217 CysLeuCysProLeuGlyTyThrGlyLeuLysCysGluThrAspIleAspGlyCysSer 1236
 DB 1114 TGTATTGTCCTCCTCAGTGGACTGGCAAAACATGCCAGCTAGATGCGAATGATGTGAG 1173
 QY 1237 ProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGlu 1256
 DB 1174 GGCAAACCTCTGTGTCAATGCCAATCTCTGAGGAACCTTGTATGGAGCTACTATTGTGAC 1233
 QY 1257 CysProSerGlyTyThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSer 1276
 DB 1234 TGCATTACTGCTGCTGGCCCAACTGTGTGATATAATAATATTGATTGTCGTGGACAA 1293
 QY 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyArgCysThrCysVal 1296
 DB 1294 ---TGTGAGATGGAGGATCCTGTCGGGACTTGGTTAATGGTTATCGTGTGATCTGTTCA 1350
 QY 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
 DB 1351 CTTGGCTATGCGAGGATCACTGTGAGAAAGACATCAATGAATGTGCAAGTAACCTTGC 1410
 QY 1317 LeuAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProGly 1336
 DB 1411 ATGAATGGGGTCACTGCCAGATGAATCAATGCAATGCTGCTGCTGCTGCTGCT 1470
 QY 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
 DB 1471 TTCTCAGGAACCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
 QY 1357 GlyAlaThrCys-----LysAsp----- 1360
 DB 1531 GGTGCCAGCTGCTTCAATCTTGTGCTATGCACTATTCTGTAACTGCCCTGAAGATTACGAA 1590
 QY 1361 -----LysAsp----- 1362
 DB 1591 GGCAAGAAAGTCTCCACCTCGAAAGATCACTGCGCACCACTCTTGTGAAAGTAATCGAC 1650
 QY 1363 -----GlyAlaAsnSer----- 1366
 DB 1651 AGCTGTACAGTGGCAGTGGCTTCTTACACGACACACAGAGGAGTTCGTTCATTCTTCA 1710
 QY 1367 -----PheArgCysLeu 1370
 DB 1711 AATGCTGTGCTCTCATGGAAATGCAAGAGCCAGCGGTGGAAATTCACCTGTGNA 1770
 QY 1371 CysAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsn 1390
 DB 1771 TGCAACAAAGGATTCCTGCGCACCTACTGTGATGAGATATCAATGATGCTGTGAGAGCAAC 1830
 QY 1391 ProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTySerCysLysCysGln 1410
 DB 1831 CCCTGTAAATAATGTTGGCAGCTTGTATTGACCGTGTAAACTCTTCAAAATGATTATTGTAGT 1890
 QY 1411 ProGlyPheSerGlyGlnArgCysGluThrGluGlnSer---ThrGlyPheAsnLeuAspPh 1430
 DB 1891 GATGATGGGAGGACATATTGTGAACAATAATATTATGACTGCGAGTAAACCCCT--- 1948
 QY 1430 eGluValSerGlyIleTyThrGlyTyValMetLeuAspGlyMetLeuProSerLeuHisAl 1450
 DB 1949 -----GCCACAATGAGGGA 1962
 QY 1450 aLeuThrCysThrPheTrpMetLysSerSerAspMetAsnTyThrProIleSe 1470

Db 1963 ACTGCCAGACTTGGTCAATGACTTCTCTCTGATGTAAATGGGT----- 2011
Qy 1470 rTyralaValAspAsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrpVa 1490
Db 2011 ----- 2011
Qy 1490 lLeuTyrValAsnGlyValGluValThrAsnGlySerProSerValAsnAspGlyValGTr 1510
Db 2012 -----GGAAAGGAAATCTTCCCTCTCTGACGCCAGCTGTGATGATGAGGA 2058
Qy 1510 phis-----HisleAlaalleThrTrpThrSerAlaAsnGlyIleTyrpLy 1525
Db 2059 ACATGCAATATGGAGGACATGTTATGATGAGGGGACACTTTCAGTGCATGT----- 2113
Qy 1525 sValTyrleAspGlyLys-----LeuSerAspGlyGlyAlaGlyLeuSerValGl 1542
Db 2114 -GTCTGCAGGATGGAAAGGACCACTTGTATATAGCAAGGAACAGCAGCTGCTGCCA 2172
Qy 1542 yLeuProfileProGlyGlyValAlaLeuValLeuGlyGlnGluGlnAspLysLysGlyGl 1562
Db 2173 AACCCCTGTAC-AATGGTGTGACTGTGTAGTT-----AGTGGGA 2213
Qy 1562 uGlyPheSerProAla-----GluSerPheValGlySerlleSerGlnLeuAsnLeuTr 1580
Db 2214 TTCTTTGACTGTGTCGACGAGGGCTGGGAGGACCGACATGACTCTACAGACAA 2273
Qy 1580 pAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGlu----- 1598
Db 2274 TGAC-----TGCAGTCTCATCTTGTATACACAGTGTACT---TGTGTGGATGAGA 2324
Qy 1599 -----GluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSe 1613
Db 2325 CAACTGTACCGCTGTGAGTGGCTCCCGC-----TTCGAGGTCCCGACTGT----- 2373
Qy 1613 rGlylleValGlyLysValLysValLysSerLysSerllePheCysSerAspCysProAr 1633
Db 2374 -----AGCATCAATCAATGAA-----TGTGAGTCTCACCTG 2408
Qy 1633 gLeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerly 1653
Db 2409 TGCCTTTGGGCT-----ACTTGTGTGATGAAAT-----AATGG 2444
Qy 1653 sValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProValGlnTyrCysle 1673
Db 2445 GTACCGTTCATTTGTCACCGGGT----- 2469
Qy 1673 uAsnGlnGlyGlnTrpThrGlnProLeuProHisCysGluArgIleSerCysGlyValPr 1693
Db 2470 -----CGCAGTGTCCAGGATCCAGGAAGTTTACA---GGCAGGCC 2507
Qy 1693 o-----ProProLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAl 1708
Db 2508 TTGCTTTACAGTATTCAGTAAATCCAGACGGTCTAAGTGGGATGATGAC----- 2559
Qy 1708 aGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMe 1728
Db 2560 -----TGTAATACTTGTCACTGTTTGAATGA-----AAGT 2591
Qy 1728 tPheCysThrAspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspVal----- 1746
Db 2592 CACCTGTTCTAAG-----GTTTGTGTGTCTCTGACCTTGTATATAATACATGCCAAGG 2645
Qy 1747 -----AspGluCysAlaValGlySerAspCys-----SerGluHisAlaSerCys 1761
Db 2646 TCATAATGAATCCAGCTGGACAGCTGTGTCTGTGTTAAAGAGACCAT-----TG 2699
Qy 1761 sLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyLy 1781
Db 2700 TTTCATCATCTCTGTGCTGCAGTGGGTGAATGTGGCCT----- 2739
Qy 1781 sAsnCysAlaGlaProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSerSe 1801
Db 2740 -TCTAATCAGCAGCTGTGAGACCAATGC-----AATTC 2774

Qy 1801 rGlyGluIleTyrThrValGlyAlaAla---ValThrPheSerCysGlnGluGlyTyrGl 1820
Db 2775 TGATTTCTTATACCAAGATAATGTGCCCAATCACCCTTCACTTTAATAGGAATGAT 2834
Qy 1820 nLeuMetGlyValThr 1825
Db 2835 GGCACCAAGCCTTACC 2850

RESULT 18

US-08-611-729A-9
; Sequence 9, Application US/08611729A
; Patent No. 6004924
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Taikonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace S.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,729A
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3579
US-08-611-729A-9

Alignment Scores:
Pred. No.: 2,038-52 Length: 3582
Score: 630.00 Matches: 238
Percent Similarity: 36.34% Conservative: 113
Best Local Similarity: 24.64% Mismatches: 301
Query Match: 6.75% Indels: 315
DB: 3 Gaps: 48

US-09-977-053-6 (1-1842) x US-08-611-729A-9 (1-3582)

Qy 987 PheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThr 1006
|||||

Db 517 TTTTGTGCGACGAGAGAT----- 534
Qy 1007 TyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAspGlu 1026
Db 535 -----GACTTCTTCACTCACTACCTGCT-----GACCAG 564
Qy 1027 GluGlyGlnLeuGluCys-----LysLeuCys 1035
Db 565 AATGGCAACAAACCTGCTTGGAGGCTGGACGGGACAGAAATGCAACAAGCTATTTGT 624
Qy 1036 ProSerGlyMetTyrThrGluTyrIleHisSerArgAsnIleSerAspCysAlaGln 1055
Db 625 CGTCAGGATGTAGCCCAAGCATGGTCTCTTGACAGTTCACAGAGAGTGCAGGTGCAG 684
Qy 1056 CysLysGlnGlyThrTyrSerTyrSerGlyLeuGluThrCysGluSerCys----- 1072
Db 685 -----TATGGATGGCAAGGC-----CAGTACTGTGATAGTGCATTCACAC 726
Qy 1073 ProLeuGlyThrTyrGlnProLysPheGlySerArgSerCysLeuSerCysProGluAsn 1092
Db 727 CCGGGATGTCTCGGCACTTCGATTCGAACCATGCGAGTGCCTC-----TGTGAACCAAC 783
Qy 1093 ThrSerThrValLysArgGlyAlaVal-----AsnIleSerAlaCysGlyVal--- 1108
Db 784 TGGGGT-----GCTCAGCTCTGTGCAACAGACCTGAACCTACTCTGTGAACCCAC 831
Qy 1109 ----ProCysProGluGly-----LysPheSerArgSer 1118
Db 832 CCACCTGTGTTGAATGGTGTGCTCTGACCAACACTGGCCCGCATAAATACCAGTGTTC 891
Qy 1119 GlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAla-----Gly 1136
Db 892 -----TGCCTGAGGGTACTCAGACAGAACTGTGAAATAGCG 930
Qy 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
Db 931 GAGCATGCGTGCCTCTCTGATCGTGCACAAC-----GGAGGAAGC----- 972
Qy 1157 IleThrGluCysSerSerPheSerThrPheSerAlaAlaGluGluSerValPro 1176
Db 973 -----TGCTAGAAACGCTACAGGATTT-----GAATGTGTGTGCA 1011
Qy 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
Db 1012 CTGGCTGGGCTGGA-----CCAACTGCACTGATATATATGATGAT 1053
Qy 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
Db 1054 TGTCTCCAAATCCCTGTGTGTCTATGAGGAACTTGCCAGATCTAGTTGATGATTAAG 1113
Qy 1217 CysLeuCysProLeuGlyThrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236
Db 1114 TGATATTGCCCACTCAGTGGAGTGGCAAAACATGCCAGCTAGATGCAATGAATGTGAG 1173
Qy 1237 ProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGlu 1256
Db 1174 GGCAAACTGTGTCAATGCAACTCTGAGGAACTTGATGGCAGCTACTATTGTGAC 1233
Qy 1257 CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSer 1276
Db 1234 TGCAATTACTGGCTGGTCTGGCCCAACTGTGATATAATAATAATAATGATGTCGTGACAA 1293
Qy 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
Db 1294 ---TGTCAAAATGGAGGATCTCTGGGACCTGGTTAATGGTTATCGGTGCATCTGTCA 1350
Qy 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
Db 1351 CTGGGTATGCGAGGATCACTGTGAGAAGACATCAATGAATGTCCAGTAACCTTGC 1410
Qy 1317 LeuAsnAsnAlaValCysGluAspGlnValGlyPheLeuCysLysCysProGly 1336
Db 1411 ATGAATGGGGGTCACTGCGCAGGATGAATCAATGGATTCGAATGTCTGTCTGTCTGTGT 1470

Qy 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
Db 1471 TTTCTGAGAAACCTCTGTCTGCTGATATAGACTACTGTGAGCCCAACCCCTTGCAGAAC 1530
Qy 1357 GlyAlaThrCys----- 1360
Db 1531 GGTGCCCAGTGCTCAATCTTCTATGGACTATTCTGTAACTGCCCTGGAAGATTACGAA 1590
Qy 1361 -----LysAsp----- 1362
Db 1591 GGCAAGAACTGCTCCCACTGAAAGATCACTGCCGCACTCTCTGTGAAAGTAATCGAC 1650
Qy 1363 -----GlyAlaAsnSer----- 1366
Db 1651 AGCTGTACAGTGGCAGTGGCTTCTAACAGCACACCAGAGGAGTTCGTACATTCTTCA 1710
Qy 1367 -----PheArgCysLeu 1370
Db 1711 AATGCTCTGTCTCTCATGGAATAATGCAAGACCAAGCGGTGGAATAATCACCTGTGAA 1770
Qy 1371 CysAlaIaIaGlyPheThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsn 1390
Db 1771 TGCAACAAAGAGATTCACCTGGCACCTACTGTCATGAGAATATCAATGACTGTGAGAGCAAC 1830
Qy 1391 ProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGln 1410
Db 1831 CCTGTAAATGTGGCACTTGTATGACGGTGAACCTCTACAAATGTATTGTAGT 1890
Qy 1411 ProGlyPheSerGlyGlnArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPh 1430
Db 1891 GATGGATGGGAAGCAACATATTGTGAACAAATATTAACTGCTGAGTCAAAAAACCCCT-- 1948
Qy 1430 eGluValSerGlyIleTyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAl 1450
Db 1949 -----GCCACATGGAGGA 1962
Qy 1450 aLeuThrCysThrPheTyrMetLysSerSerAspMetAsnTyrGlyThrProIleSe 1470
Db 1963 ACTTGGCGACACTGTGTCATGACTTCTTCTGCAATGTAATAAATGSGT----- 2011
Qy 1470 rTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrVa 1490
Db 2011 ----- 2011
Qy 1490 lLeuTyrValAsnGlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTr 1510
Db 2012 -----GGAAGGAAGAACTTGCCACTCTGTCACACCCAGTGTGATGAGGCA 2058
Qy 1510 pHis-----HisIleAlaIleThrTyrThrSerAlaAsnGlyIleTyrLy 1525
Db 2059 ACATGCATTAATGGAGGAACATGTTATGATGAGGGGACACTTTCAGTGCATGT----- 2113
Qy 1525 sValTyrIleAspGlyLys-----LeuSerAspGlyGlyAlaGlyLeuSerValGl 1542
Db 2114 -GTCTGCGAGATGGGAAGGAGCCACTTGTAAATATAGCAAGAACAGCAGCTGCTGCCA 2172
Qy 1542 yLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGluAspLysLysGlyGl 1562
Db 2173 AACCCCTGTGAC--AATGGTGGTACTCTGTGTAGT-----AGTGGGA 2213
Qy 1562 uGlyPheSerProAla-----GluSerPheValGlySerIleSerGlnLeuAsnLeuTr 1580
Db 2214 TTTCTTCACTGTGCTGCAAGGAGGCTGGGAAGGACCGACATGTACTCAGAACACAA 2273
Qy 1580 pAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGlu----- 1598
Db 2274 TGAC-----TGCACTCTCATCTTGTACACACAGTGGTACT---TGTGTGATGAGGA 2324
Qy 1599 -----GluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSe 1613
Db 2325 CAACCTGTAACCTGTGAGTGCCTCCGCGC-----TTGCGAGGTCCCGACTGT----- 2373

Qy	1613	rgIleValglYylsValIleAspSerIlePheCysSerAspCysProAr	1533
Db	2374	-----AGGATCAACATCAATGAA-----TGTCAAGTCTTCAACCTG	2408
Qy	1633	gLeuGlYclYSerValProHisIleuArGThrAlaSerGluAspLeuIysProGlySerLy	1653
Db	2409	TGCTTTGGGGCT-----ACTGTGTGGATGAAATT-----AATGG	2444
Qy	1653	sValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProValGlnTyrCysLe	1673
Db	2445	GTACCGTGTGATTTGTCTCACCGGGT-----	2469
Qy	1673	uAsnGlnGlyGlnTrpThrGlnProLeuProHisCysGluArgIleSerCysGlyValPr	1693
Db	2470	-----GCGAGTGGTCCAGGATGCCAGAAATTTACA---GGGAGGCC	2507
Qy	1693	o-----ProProLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAl	1708
Db	2508	TTGCTTTACCAGTATTCAGGTAATGCCAGACGGTGCTAAGTGGGATGATGAC-----	2559
Qy	1708	aGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMe	1728
Db	2560	-----TGTAATACTTGTCTAGTGTTCGAATGGA-----AAAGT	2591
Qy	1728	tPheCysThrAspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspVal-----	1746
Db	2592	CACCTGTCTAAG-----GTTTGGTGTGGTCTCGACCTTGTATAATACATGCCAAAGG	2645
Qy	1747	----AspGluCysAlaValGlySerAspCys-----SerGluHisAlaSerCy	1761
Db	2646	TCATAATGAATGCCAGCTGCACACGCTTGTGTCTCTGTGTTAAAGAACACCAT-----TG	2699
Qy	1761	sLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyLy	1781
Db	2700	TTTCACATCATCTTGTCTGCAGTGGGTGAATGCTGCGCT-----	2739
Qy	1781	sAsnCysAlaGluProIleIysCysLysAlaProGlyAsnProGluAsnGlyHisSerSe	1801
Db	2740	-TCTAATCAGCAGCCTGTGAAGACCAATGCG-----AATTC	2774
Qy	1801	rgIyGluIleTyrThrValGlyAlaAla----ValThrPheSerCysGlnGluGlyTyrGl	1820
Db	2775	TGATTCTTATTACCAAGATTAATTGTGCCAATCATCACCTTCACCTTTTAATAAGGAATGAT	2834
Qy	1820	nLeuMetGlyValThr	1825
Db	2835	GGCACCAGGCGCTTACC	2850

RESULT 19

Accession	DB	Seq ID	Length	Type	Organism	Feature	Name/Key	Location	Name/Key	Location	Name/Key	Location	Name/Key	Location
US-09-214-278-4	Db	924	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
Sequence 4, Application US/09214278	Qy	1161	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
Patent No. 6291210	Db	945	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
GENERAL INFORMATION:	Qy	1181	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
APPLICANT: Sakano, Seiji	Db	951	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
APPLICANT: Itoh, Akira	Qy	1201	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE	Db	957	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
FILE REFERENCE: KP-8576	Qy	1220	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
CURRENT APPLICATION NUMBER: US/09/214,278	Db	1017	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
CURRENT FILING DATE: 1999-01-26	Qy	1240	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
NUMBER OF SEQ ID NOS: 32	Db	1077	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
SOFTWARE: PatentIn Ver. 2.1	Qy	1260	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
SEQ ID NO 4	Db	924	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
LENGTH: 3955	Qy	1161	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
TYPE: DNA	Db	945	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
ORGANISM: Homo sapiens	Qy	1181	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
FEATURE:	Db	951	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
NAME/KEY: CDS	Qy	1201	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
LOCATION: (12)..(3725)	Db	957	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
NAME/KEY: signature peptide	Qy	1220	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
LOCATION: (12)..(689)	Db	1017	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
NAME/KEY: mat_peptide	Qy	1240	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
LOCATION: (90)..(3725)	Db	1077	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide
US-09-214-278-4	Qy	1260	3955	DNA	Homo sapiens	CDS	(12)..(3725)	signature peptide	(12)..(689)	signature peptide	(90)..(3725)	signature peptide	(90)..(3725)	signature peptide

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1280 AsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPhe 1299
1197 GCGGTGGCACCTGTGTGGACCAAGTGGACGGCTTTGAGTGATCTGCCCGGAGAGTGG 1256
1300 ValGlyLeuHisCysGluThrGluValAsnGluCysLysSerAsnProCysLeuAsnAsn 1319
1257 GTGGGGGCCACCTGCCAGCTGGAGCGCCATGATGTGAGGAGGAGCATTGCTTAAAGCT 1316
1320 AlaValCysGluAspGlnValGlyPheLeuCysLysCysProGlyPheLeuGly 1339
1317 TTTTCTTGC AAAAACCCTGATTTGGCGCTATTACTGTGATTGATCCCGGGCTGGAGGGC 1376
1340 ThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyValThr 1359
1377 ATCAACTGCCCATATCAACGTCACAGACTGTCGGGGCAG---TGTCAGCATGGGGCACC 1433
1360 CysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHis 1379
1434 TGCAGGACCTGTGTAAACGGGTACAGTGTGTGCCACCGGGCTTCGGAGCGCGCAT 1493
1380 CysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysVal 1399
1494 TGGAGCTGGACAGACAGCAAGTGTGCCAGCAGCCCTGCCACAGCGCGCGCTCTGCCAG 1553
1400 AspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlnArgCysGlu 1419
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1614 GTGGAT-----GTC 1622
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1455 PheTyrMetLysSerSerAspMet-----AsnTyrGlyThrProLysTyr 1471
1683 TATTACTGGCGCTGCCCTGTGATGATTTGGTGGCAAGAACTGCTCCGTCGCC----- 1733
1472 AlaValAspAsnGlySerAspAsnThrLeuLeuThrLeuLeuThrAspTyrAsnGlyTyrValLeu 1491
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1512 HisIleAlaIleThrTyrThrSerAlaAsnGlyIleTyrLysValTyrIleAspGlyLys 1531
1749 -----GGCGGGCGCTGCGAGTG---ATCGATGGCTGC 1778
1532 LeuSerAspGlyValAlaGlyLeuSerValGlyLeuProIleProGlyGlyGlyAlaLeu 1551
1779 GGGTCAGACCGGGCGCTGGAGT-----CCTGGCAGCAGCGCTCC 1820
1552 ValLeu-----GlyGlnGluAsnLysLysGlyGluGlyPheSerProAla 1567
1821 GCGGTGTGTGGCCCCCATGGACGCTGGCTCAGCCAGCGCGGGCAACTTTTCTGTCATC 1880
1568 -----GluSerPheValGlySerIleSerGlnLeuAsnLeuTyrAspTyrValLeuSer 1585
1881 TGTGACAGTGGCTTTACTGTCACCTATGCTGATGAGAACATTCAGCACTGCCCTGGGCCAG 1940
1586 Pro-----GlnGlnValLysSerLeuAlaThrSerCysPro 1597
1941 CCTGCCGCATGGGGGCATCATCATGATGAGGTGAGCGCTTCCGCTCTCTGCCCC 2000
1598 GluGluLeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGlyIleValGly 1617
2001 -----AGCGCTGGAGGGC 2015

1618 LysValLysIleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySer 1637
2016 GAGCTC---TGCACACCAATCCACAGACTGCTTCCGATCCC----- 2057
1638 ValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPhe 1657
2058 ---TGCCACAGCGCGCGCTGCTACGACCTG-----GTCAATGACTTC 2099
1658 CysAspProGlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGln 1677
2100 -----TACTGTGCTGGCAGCAGCGC 2120
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2121 TGAAGGGCAGACCTGCCACTCCAGTTCAGTGGAGTTCAGTGGATGCTACACCTGC----- 2174
1693 ProProLeuGluAsnGly-----PheHisSerAlaAspPhe----- 1706
2175 -----AGCAAGGTGGCACCTGCTACGACAGCGCGCACACCTTCGGCTGGCGCC 2222
1707 -----TyrAlaGlySerThr-----ValThr 1713
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1714 TyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPhe----- 1729
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1730 -----CysThrAspAsnGlySer----- 1735
2343 CGGAGCGCTGGAGGGTGTGCTTGTGCACTCACAATACCAACGACTGCAACCTCTGCT 2402
1736 ---TrpAsnGly----- 1738
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1739 -----ValSerProSerCys---LeuAspValAspGluCysAlaValGlySerAspCys 1755
2463 GCGTTCGGGGGCTGACTGCGCATCAATCAGCAGTGCCAG---TCCTGGCCCTGT 2519
1756 SerGluHisAlaSerCysLeuAsnValAspGlySerTyrIleCysSerCysValPro 1775
2520 GCCTACGGGGCCAGCTGTGTGGATGAGATCAACGGGTATGCTGTAGCTGCCACCGCC 2579
1776 TyrThrGlyAspGlyLysAsnCysAlaGluProIle-----LysCysLysAla 1791
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RESULT 20

US-09-855-722-4
; Sequence 4, Application US/09855722
; Patent No. 6638741
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 3955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:


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1586 Pro-----GlnGlnValLysSerLeuAlaThrSerCysPro 1597
1941 CCCTGCCCAATGGGGGCACATGATGAGTGGAGCGCTTCGGCTGCTTGGCCC 2000
1598 GluGluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGly 1617
2001 -----AGCGGCTGGGAGGCG 2015
1618 LysValLysIleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySer 1637
2016 GAGCTC---TGGCACCACATCCCAACGACTGCCTTCCGATCC--- 2057
1638 ValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPhe 1657
2058 ---TGCACAGCGCGCGCTGCTACGACTG-----GTCAATGACTTC 2099
1658 CysAspProGlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGln 1677
2100 -----TACTGTGGCTGGCAGCAGCGC 2120
1678 TrpThrGlnProLeuProHis-----CysGluArgIleSerCysGlyVal 1692
2121 TGGAGGGCAGACCTGCCTCAGCGAGTTCAGTGGGAGCTCCTACACCTGC----- 2174
1693 ProProLeuGluAsnGly-----PheHisSerAlaAspAspPhe----- 1706
2175 -----AGCAAGGTGGCAGCTGCTACGACAGCGGCGACCTTCGGCTGGCGCC 2222
1707 -----TyrAlaGlySerThr-----ValThr 1713
2223 TGGCCCCCGCTGGAGGGCAGCAGCTGCGCGCTGCGCAAGAACAGCAGCTGGCTGCC 2282
1714 TyrGlnCysAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPhe----- 1729
2283 AACCCCTGTGTGAATGGTGGCAGCTGCTGGGCGCGCGGCGCTCTCTCTGCAATGCG 2342
1730 -----CysThrAspAsnGlySer----- 1735
2343 CGGAGCGCTGGAGGGTGTGCTGCTGCACTCAACAGCTGCAACCTCTGGCT 2402
1736 ---TrpAsnGly----- 1738
2403 TGCTACAATGCTGGCATCTGTGTGACGGCTCACTGTTCCGCTGCGAGTGTGCACCT 2462
1739 -----ValSerProSerCys---LeuAspValAspGluCysAlaValGlySerAspCys 1755
2463 GCGTTCGGCGGCGCTGACTGCGGATCAACATCGACGAGTGGCCAG---TCTCGCCCTGT 2519
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2520 GCCTACGGGGCAGCTGTGTGTGATGAGATCAACGGGTATCGCTGTAGCTGCCACCGCGC 2579
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2580 CGAGCC-----GGCCCCGGTGGCAGGAGTATCGGGTTCGGGAGATCTCTGTGGTCC 2633
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RESULT 21
US-08-400-159-7
; Sequence 7, Application US/08400159
; Patent No. 5869282
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace E.

```

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; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,159
; FILING DATE: 07-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-400-159-7

Alignment Scores:
Pred. No.: 1,67e-50 Length: 4464
Score: 671.00 Matches: 233
Percent Similarity: 34.38% Conservative: 86
Best Local Similarity: 25.11% Mismatches: 271
Query Match: 6.57% Indels: 338
DB: 2 Gaps: 46

US-09-977-053-6 (1-1842) x US-08-400-159-7 (1-4464)
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Qy 987 PheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThr 1006
Db 449 TTCGCCGCGCCCGCATGACTTTTCGCGC----- 478
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Qy 1047 ArgAsnIleSerAspCysLys---AlaGlnCysLysGlnGlyThrTyrSerTyrSerGly 1065
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Db 584 -----GGATGCACCGCTGCTGGGAGTGCAGGTGCAGCTACGCTGGCAA 628
Qy 1083 SerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsn 1102
Db 629 GGGAGGTTCTGGATGAGTGT----- 649

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QY 1103 IleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetPro 1122
DB 650 -----GTCCCTTACCCC-----GGCTCGGTGCATGCGAGTGTGTGGAGCCC 691
QY 1123 -----CysHisProCysProArgAspTyrGlnProAsnAlaGlyLysAlaPheCys 1140
DB 692 TGGCAGTGCAC-----TGT-----GAGACCACTGGCGCGGCTGCTGTGT 733
QY 1141 LeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCys 1160
DB 734 -----GACAAAGACCTGAATCTACTGT 754
QY 1161 SerSerPheSerThrPheSerAlaAlaGluGluSerValProProHlaSerLeu 1180
DB 755 GGCAGC----- 760
QY 1181 GlyHisIleLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn 1200
DB 761 -----CACAC 766
QY 1201 ProCysHisAsnSerGlyThrCys-----GlnGlnLeuGlyArgGlyTyr 1215
DB 767 CCTCTGCACCAACGGAGGACGGTGCATCAACGCCGAGCCTGACAC-----TAC 814
QY 1216 ValCysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCys 1235
DB 815 CGCTGCACCTGCCCTACTCGGCGCAAGNACTGTGAGAAGCCTGAGCACGCCCTGC 874
QY 1236 SerProLeuProCysLeuAsnAsnGlyValCysLysAspValGlyGluPheIleCys 1255
DB 875 ACCTCAACCCGTGTGCCAACGGGGGCTCTTCCATGAGGTGCCCTGCCGTTCGAAATGC 934
QY 1256 GluCysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSer 1275
DB 935 CACTGCCCATCGGCTGGAGCGGGCCACCTGTGCCCTTGACATCGATGAGTGTGCTCG 994
QY 1276 SerProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCys 1295
DB 995 AACCGGTGTGCCCGCGGTGGACCTGTGTGGACCAAGTGGCGGCTTTGAGTGCATCTGC 1054
QY 1296 ValLysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnPro 1315
DB 1055 CCGAGAGTGGTGGGGCCACCTGCCAGCTGGAGCCCAATGATGTGAAGGAGCCA 1114
QY 1316 CysLeuAsnAsnAlaValCysGluAspGlnValGlyPheLeuCysLysCysProPro 1335
DB 1115 TGCCCTTAACGCTTTTCTTGCAAAAACCTGATGGCGGCTATTACTGTGATTCATCCCG 1174
QY 1336 GlyPheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLys 1355
DB 1175 GGCTGGAAGGGCATCAACTGCCATATCAACGTCACGACTGTGCGGGCAG-----TGTGAG 1231
QY 1356 AsnGlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPhe 1375
DB 1232 CATGGGGGACCTGACAGACCTGTGTGACGGGTACCACTGTGTGCCCCAGGGGCTTC 1291
QY 1376 ThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGln 1395
DB 1292 GGAGGCGCGCATTCGAGCTGGAACGAGACAAAGTGTGCCAGCAGCCCTGCCACAGCGGC 1351
QY 1396 AlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGly 1415
DB 1352 GGCCTCTCGAGGACCTGGCGCAGCGCTTCCACTGCCACTGCCCCCAGGGCTTCTCCGGG 1411
QY 1416 GlnArgCysGluThrGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIle 1435
DB 1412 CCTCTCTGTGAGGTGAT----- 1429
QY 1436 TyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCys----- 1453
DB 1430 -----GTGACCTTTGTGAGCCACGACCTGCCGGAACGGCGCTCGCTGTATAAC 1480

QY 1454 -----ThrPheTyrMetLysSerSerAspAspMet-----AsnTyrGlyThr 1467
DB 1481 CTGGAGGGTGAATATCTATCTGCGCCTGCCCTGATGACTTTGGTGGCAAGAACTGCTCCGTG 1540
QY 1468 ProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsn 1487
DB 1541 CCC----- 1543
QY 1488 GlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsnCysProSerValAsnAsp 1507
DB 1544 -----CGCGAGCCG-----TGCCCT----- 1558
QY 1508 GlyArgTyrHisHisIleAlaIleThrTyrThrSerAlaAsnGlyIleTyrLysValTyr 1527
DB 1559 -----GGCGGGCGCTCCAGAGTG----- 1576
QY 1528 IleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeuProIleProGly 1547
DB 1577 ATCGATGGCTGGGGTTCAGACGGGGCTCGGATG-----CCTGGC 1618
QY 1548 GlyGlyAlaLeuValLeu-----GlyGlnGluGlnAspLysGlyGluGly 1563
DB 1619 ACAGCAGCCTCGGGGTGTGGCCCCCATGAGCGCTGCGTACGCCAGCCAGGGGCAAC 1678
QY 1564 PheSerProAla-----GluSerPheValGlySerIleSerGlnLeuAsnLeuTyrAsp 1581
DB 1679 TTTTCTGCTGATCTGTGACAGTGGCTTTACTGGCACCTACTGCCATGAGAACTTGGACGAC 1738
QY 1582 TyrValLeuSerPro-----GlnGlnValLysSerLeuAla 1593
DB 1739 TGCCTGGGCGACCCCTGCCCAATGGGGGCACATGATCGATGAGTGGACGCTTCCGC 1798
QY 1594 ThrSerCysProGluGluLeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSer 1613
DB 1799 TGCCTTCTGCCCC-----AGC 1813
QY 1614 GlyIleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg 1633
DB 1814 GFTTGGAGGGCGAGCTC-----TGGACACCAATCCCAACGACTGCTTCCCGATCCC--- 1867
QY 1634 LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653
DB 1868 -----TGCCACAGCGCGCGCGCTGTCTACGACCTG----- 1897
QY 1654 ValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProValGlnTyrCysLeu 1673
DB 1898 GTCAATGACTTC-----TACTGTGCG 1918
QY 1674 AsnGlnGlyGlnTyrThrGlnProLeuProHis-----CysGluArgIle 1688
DB 1919 TGGCAGCAGCGCTGGAGGGCAAGACCTGCCACTCAGCGGAGTTCCAGTGCAGTCCCTAC 1978
QY 1689 SerCysGlyValProProProLeuGluAsnGly-----PheHisSerAlaAspAsp 1705
DB 1979 ACCTGC-----AGCAACGGTGGCACCTGTCTACGACAGCGCGCACC 2020
QY 1706 Phe-----TyrAlaGlySerThr----- 1711
DB 2021 TTCCGCTGGCGCTGGCCCCCGCTGGAAGGGGAGCAGCACTTGCCTGCGCCGTGCGCAAGACAGC 2080
QY 1712 -----ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPhe 1729
DB 2081 AGCTGCTGCCCAACCCCTGTGTGATGTGGCACCTGTGGTGGCGAGCGGGCTCCTCTTC 2140
QY 1730 -----CysThrAspAsnGlySer----- 1735
DB 2141 TCTGCTGCTGCGCGGACCGCTGGAGGGTGTGTTGCACTTGTGCACTCAATACCAAGACTGC 2200
QY 1736 -----TrpAsnGly----- 1738
DB 2201 AACCTCTGCTGCTGTGCTACAAATGTTGTCATCTGTGTGACGGCGTCAACTGCTTCCGTGCG 2260
QY 1739 -----ValSerProSerCys---LeuAspValAspGluCysAlaVal 1751

Db 2261 GAGTGTGACCTGGCTTCGGGGCCCTGACTGGCGCATCAACATCGAGTGCAG--- 2317
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 Db 2318 TCCTGCGCCCTGTGCTACCGGGCCAGCTGTGTGATGAGATCAACGGGTATCGCTGTAGC 2377
 Qy 1772 CysValProProThrGlyAspGlyLysAsnCysAlaGluProIle 1787
 Db 2378 TGCCACCCGGCGGAGCC-----GGCCCCGGTGCCAGGAGTGTGCGGTTCGGGAGA 2431
 Qy 1788 LysCysLysAlaProGlyAsnPro 1795
 Db 2432 TCCTGTGTGCTCCGGGGCACTCG 2455

RESULT 22

US-08-611-729A-7
 ; Sequence 7, Application US/08611729A
 ; Patent No. 6004924
 ; GENERAL INFORMATION:
 ; APPLICANT: Ish-Horowicz, David
 ; APPLICANT: Henrique, Domingos M.P.
 ; APPLICANT: Lewis, Julian H.
 ; APPLICANT: Myat, Anna M.
 ; APPLICANT: Fleming, Robert J.
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; APPLICANT: Mann, Robert S.
 ; APPLICANT: Gray, Grace B.
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
 ; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/611,729A
 ; FILING DATE: 06-MAR-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Miarock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7326-037
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4483 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 332..4102
 US-08-611-729A-7

Alignment Scores:
 Pred. No.: 1.68e-50
 Score: 671.00
 Percent Similarity: 34.38%
 Best Local Similarity: 25.11%
 Query Match: 6.57%
 Length: 4483
 Matches: 233
 Conservative: 86
 Mismatches: 271
 Indels: 338

DB: 3 Gaps: 46
 US-09-977-053-6 (1-1842) x US-08-611-729A-7 (1-4483)
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 Qy 987 PheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThr 1006
 Db 449 TTCTGCGCGCCCGCAATGACTTTTTCGCC----- 478
 Qy 1007 TyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAspGlu 1026
 Db 479 -----CACTACACTTGC-----GACCAG 496
 Qy 1027 GluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSer 1046
 Db 497 TACGGCAAC-----AAGGCTGCATGCGCGCTGGATGGCAAG----- 535
 Qy 1047 ArgAsnIleSerAspCysLys---AlaGlnCysLysGlnGlyThrTyrSerTyrSerGly 1065
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 Db 584 -----GGATGCACGGTGCCTGGGGAGTGGAGTGCAGCTACGGCTGGCA 628
 Qy 1083 SerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsn 1102
 Db 629 GCGAGGTTCTCGCATGAGTGT----- 649
 Qy 1103 IleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetPro 1122
 Db 650 -----GTCCCTTACCCC-----GGCTGCTGCATGCGAGTGTGTGGAGCCC 691
 Qy 1123 -----CysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
 Db 692 TGGCAGTGCAC--TGT-----GAGACCACTGGGGGGGGCTGCTCTGT 733
 Qy 1141 LeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCys 1160
 Db 734 -----GACAAAGACCTGAATCTACTGT 754
 Qy 1161 SerSerPheSerSerThrPheSerAlaAlaGluSerValValProProAlaSerLeu 1180
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 Qy 1201 ProCysHisAsnSerGlyThrCys-----GlnGlnLeuGlyArgGlyTyr 1215
 Db 767 CCTTGCACCAACCGAGGACGTGCATCAACCGCCGAGCTGACCAG-----TAC 814
 Qy 1216 ValCysLeuCysProLeuGlyThrGlyLeuLysCysGluThrAspIleAspGluCys 1235
 Db 815 CGCTGCACCTGCGCTGACCGCTACTCGGGCAGGAACCTGTGAGAGGCTGAGCAGCGCTGC 874
 Qy 1236 SerProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCys 1255
 Db 875 ACCTCCACCGTGTGCCAAACGGGGGCTCTTGCATGAGGTGCGCTCGGGTTCGATGC 934
 Qy 1256 GluCysProSerGlyThrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSer 1275
 Db 935 CACTGCCCCATCGGGCTGGAGCGGCCCCACCTGTGCTCCCTTGACATCGATGAGTGTCTCG 994
 Qy 1276 SerProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCys 1295
 Db 995 AACCCGTGTGCGCGCGCTGGACCTGTGTGGACAGGTGACCGCTTTAGTGTATCTGC 1054
 Qy 1296 ValLysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnPro 1315

Db 1055 CCCGAGCAGTGGGTGGGGCCACCTGCCAGCTGGACGCCAATGAGTGTGAAGGGAGGCCA 1114
Qy 1316 CysLeuAsnAlaValCysGluAspGlnValGlyGlyLeuCysLysCysPro 1335
Db 1115 TGCCTTAACGCTTTCTTTCGAAACCTGATGGGGCTATTACTGTGATGTCATCCG 1174
Qy 1336 GlyPheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLys 1355
Db 1175 GCCTGGAAGGGCATCAACTGTCATCAACGCTCAACGACTGTGGGGGCGAG---TGTGAG 1231
Qy 1356 AsnGlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaGlyPhe 1375
Db 1232 CATGGGGGACCTGCAAGAGACCTGTGTGAACGGGTATCCAGTGTGTGGCCACGGGGCTTC 1291
Qy 1376 ThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGln 1395
Db 1292 GGAGGCGGCGATTCGAGCTGGAACAGACAGCAAGTGTGCCAGCAGCCCTGTCACAGCGCG 1351
Qy 1396 AlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGly 1415
Db 1352 GGCCTCTCGAGGACCTGGCGGACGGCTTCCACTGCCACTGCCCGCCAGGGCTTCTCCGGG 1411
Qy 1416 GlnArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIle 1435
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Qy 1436 TyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCys 1453
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Qy 1454 -----ThrPheTrpMetLysSerSerAspAspMet-----AsnTyrGlyThr 1467
Db 1481 CTGAGAGGTGACTATTACTGCGCCTGCTGATGACTTTGGTGGCAAGAACTGCTCCGTG 1540
Qy 1468 ProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsn 1487
Db 1541 CCC----- 1543
Qy 1488 GlyTrpValLeuTyrValAsnGlyArgGluLysIleThrAsnCysProSerValAsnAsp 1507
Db 1544 -----CGCAGCGG-----TGCCCT----- 1558
Qy 1508 GlyArgTrpHisIleAlaIleThrTrpThrSerAlaAsnGlyIleTrpLysValTyr 1527
Db 1559 -----GGCGGGGCGCTGCAGAGTG--- 1576
Qy 1528 IleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeuProIleProGly 1547
Db 1577 ATCGATGGCTGGGTGACAGCGGGGGCTTGGATG-----CCTGGC 1618
Qy 1548 GlyGlyAlaLeuValLeu-----GlyGlnGluGlnAspLysGlyGluGly 1563
Db 1619 ACAGCAGGCTCGGGGTGTGGCCCCCATGAGCGCTGCGTCAGCCAGCCAGGGGGCAAC 1678
Qy 1564 PheSerProAla-----GluSerPheValGlySerIleSerGlnLeuAsnLeuTrpAsp 1581
Db 1679 TTTTCTGATCTGTGACAGTGGCTTTACTGTCACCTACTGTCATGAGAACTTGCAGCAC 1738
Qy 1582 TyrValLeuSerPro-----GlnGlnValLysSerLeuAla 1593
Db 1739 TGCTGGCCAGCCCTGCGCAATGGGGGCACATGATGATGAGGTGGAGCCCTTCCGC 1798
Qy 1594 ThrSerCysProGluGluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSer 1613
Db 1799 TGCTTCTGCCCC-----AGC 1813
Qy 1614 GlyIleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg 1633
Db 1814 GGTGGGAGGGCGAGCTC---TGCGACCAACCAATCCACGACTGCTTCCGATCCC--- 1867
Qy 1634 LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653

Db 1868 -----TGCCACAGCCGCGCCCTGCTAGACCTG----- 1897
Qy 1654 ValLeuLeuPheCysAspProGlyPheGlnLeuValGlyAsnProValGlnTyrCysLeu 1673
Db 1898 GTCAATGACTTC-----TACTGTGCG 1918
Qy 1674 AsnGlnGlyGlnTrpThrGlnProLeuProHis-----CysGluArgIle 1688
Db 1919 TCGACGAGCGCTGGAAGGCGCAAGACCTGCCACTCAOGBAGTTCAGTGCAGTGCCTAC 1978
Qy 1689 SerCysGlyValProProLeuGluAsnGly-----PheHisSerAlaAspAsp 1705
Db 1979 ACTTGC-----AGCAACGGTGGCACCCTGTCTACGACAGCGCGACACC 2020
Qy 1706 Phe-----TyrAlaGlySerThr----- 1711
Db 2021 TTCGCTGCGCTGCCCGCCCGCTGGAAGGCGAGCACCCTGCGCCCTGCCCAAGACAGC 2080
Qy 1712 -----ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPhe 1729
Db 2081 AGTGCCTGCCCAACCCCTGTGTGAATGGTGGCACCCTGCTGGTGGGCGAGCGGGCCTCTTC 2140
Qy 1730 -----CysThrAspAsnGlySer----- 1735
Db 2141 TCCTGCATCTGCCGCGAGCGCTGGGAGGGTGTCTACTTGCCTCACAATACCAAGACTGC 2200
Qy 1736 -----TrpAsnGly----- 1738
Db 2201 AACCTCTGCTGTGTACATGCTGGCATCTGTGTGAGCGGCTCAACTGGTTCGCTGC 2260
Qy 1739 -----ValSerProSerCys---LeuAspValAspGluCysAlaVal 1751
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Qy 1752 GlySerAspCysSerGluHisAlaSerCysLeuAsnValAspGlySerTyrIleCysSer 1771
Db 2318 TCCTGCCCTGTGCTACGCGGCGCAGGTGTGGATGAGATCAACGGGTATCGCTGTAGC 2377
Qy 1772 CysValProProTyrThrGlyAspGlyLysAsnCysAlaGluProIle----- 1787
Db 2378 TGCCACCGCGCGAGCC-----GGCCCCCGGTGCCAGAGTGTATCGGTTCGGGAGA 2431
Qy 1788 LysCysValysAlaProGlyAsnPro 1795
Db 2432 TCCTGCTGGTCCCGGGCAGCTCCG 2455

RESULT 23

US-08-882-046-3
; Sequence 3, Application US/08882046
; Patent No. 6136952
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Krantz, Ian D.
; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; COUNTRY: USA
; STATE: California
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,046
; FILING DATE: 25-JUN-1997

CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UW 2637
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4315 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 16..3460
 US-08-882-046-3

Alignment Scores:
 Pred. No.: 6,47e-48 Length: 4315
 Score: 642.50 Matches: 232
 Percent Similarity: 33.68% Conservative: 93
 Best Local Similarity: 24.04% Mismatches: 281
 Query Match: 6.29% Indels: 360
 DB: Gaps: 45

US-09-977-053-6 (1-1842) x US-08-882-046-3 (1-4315)

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 QY 987 PheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThr 1006
 DB 493 TTCTGCGCGCCCGCAACGACTTTTTCGGC----- 522
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 DB 523 -----CACTACACTTC-----GACCAG 540
 QY 1027 GluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluThrIleHisSer 1046
 DB 541 TACGGCAAC-----AAGGCTCATGCGACGCGCTGGATGGGCAAG----- 579
 QY 1047 ArgAsnIleSerAspCysLys-----AlaGlnCysLysGlnGly----- 1059
 DB 580 -----GAGTGCACGAAGCTGTGTGTAAACAAGGGTGTAAATTTGCTCCACGGG 627
 QY 1060 -----ThrTyrSerTyrSerGlyLeuGluThrCys 1069
 DB 628 GGATGACCGCTCGCTGGGAGTGCGAGTGCGAGCTACGCTGCGCAAGGG---AGTTCTGC 684
 QY 1070 GluSerCysProLeuGlyThrTyrGlnProLysPheGlySerArgSerCysLeu----- 1087
 DB 685 GATGAGTGT-----GTCCCTTACCCCGGC-----TGGTGTCATGCG 720
 QY 1088 SerCysProGlu-----AsnThrSerThrValLysArgGlyAlaVal----- 1101
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 DB 829 ACGTGCATCAACCGCGAGCTGACCATCGCTGCACCTGCGCTGACCGGCTACTCGGCG 888
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 QY 1173 SerValValProProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGln 1192
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 DB 1024 GATGAGTGTCTTGAACCGGTGTGCGCGCGTGGCCACTGTGTGGACACAGGTGACGCGC 1083
 QY 1253 PheIleCysGluCysProSerGlyTyrThrGlnArgCysGluGluAsnIleAsnGlu 1272
 DB 1084 TTTGAGTGCATCTGCCCGGAGCAGTGGGTGGGGGCCACCTGCCAGCTGAGCTCAACAGC 1143
 QY 1273 CysSerSerSerProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArg 1292
 DB 1144 TGTGCGGGCGCAG---TGTGAGATGGGGGCACCTGTGCAAGNACCTGTGTGAACGGGTACCAG 1200
 QY 1293 CysThrCysValLysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGln 1312
 DB 1201 TGTGTGTGCCACCGGGCTTTCGGAGGCGCGCATTCGCGAGCTGGAAACGACAGAGTGTGCC 1260
 QY 1313 SerAsnProCysLeuAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLys 1332
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 DB 1381 CCTTGGCGAAACGCGCTGCTGTCTGTAACTTGGAGGTGACTATTACTGCGCTGCCCT 1440
 QY 1360 ----- 1360
 DB 1441 GATGACTTTGTGGCAAGAACTGCTCGTGCCCGCGAGCGGTGCTGCGGGGCGCTGCGAG 1500
 QY 1361 -----LysAspGlyAla----- 1364
 DB 1501 AGTGATGATGGCTGCGGGTTCAGACGCGGGGCTTGGGATGCTGGCACGACGCTCCGCGC 1560
 QY 1365 -----AsnSerPheArgCysLeuCys 1371
 DB 1561 GTGTGTGGCCCCCATGAGCGCTGGTCCAGCCAGCGGGGCAACTTTTCTGTCATCTGT 1620
 QY 1372 AlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnPro 1391
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 QY 1392 CysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnPro 1411
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 QY 1412 GlyPheSerGlyGlnArgCysGluThrGlu-GlnSerThrGlyPheAsnLeuAspPheGln 1431
 DB 1741 GGCTGGAGGCGCGAGCTGTGCGACACCAATCCCAACAGACTGCTCTC----- 1786
 QY 1431 uValSerGlyIleTyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLe 1451
 DB 1787 -----CCGATCCCTGCCACAGCGCGCGC 1809
 QY 1451 uThrCysThrPheTyrMetLysSerSer-----AspAspMetAsnTyrGlyThr 1467

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CITY: New York
STAT8: NY

COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
ACQUISITION METHOD: PG/08/98.392

APPLICATION NUMBER: 03/08/1997
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605

REFERENCE/DOCRST NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864
TELEX: 66141 PENNIE

SEQUENCE CHARACTERISTICS:
LENGTH: 2803 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
1-981-392-3

Document Scores:
No.: 2.336-47
613.00

Local Similarity: 26.44%

Match: 0.134
3
Gap: 0.000

9-977-053-6 (1-1842) x US-08-901-392-3
822 PheGluThrThrLeuGlyLysMetValPro

289 TTCTGCTGACGCTGGCCCTCTCTCTGGG

840 -----IleAspCysArgLeuGluGluGlu
 :: ::|::|::|
249 GCGCTTTCAGCTGGAGCTGCACGACTTT

858 TyrAspTyrGluAsnGlyPheAlaIleGlu

409 AACTGCTGCGGGGGC-----CG

878 asptYtSer-----
|||
457 GACTGCAGAGCCTTCTTCGGGGTCTGCTT

987 -----ThrValGlnGluThrAlaThr

517 CCGCCCTGCACCTACGGCAGGGCCATCAG

504 CYNATGCGAAG
577 CCCGACGGCTCGGGGGGCCGCCTAACCCCGG

9:00 I leThr-----N

537 TTACCTGGCCCGGACCTTCTCTGCTCA
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1000

[illegible]

Search completed: May 11, 2004, 22:21:40
Job Time : 597.768 sec

[illegible]

Search completed: May 11, 2004, 22:21:40
Job Time : 597.768 sec

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 10, 2004, 15:48:01 ; Search time 2199.65 Seconds
(without alignments)
3793.447 Million cell updates/sec

Title: US-09-977-053-6

Perfect score: 10219

Sequence: 1 MWPLAFCCGGLALVSGWAT.....GVTKITLBSGWNHLPYC 1842

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09977053@cgn_1_484@runat 06052004 075944 18296
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPHLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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18:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	10208	99.9	10878	14	US-10-150-821-1
3	10047	98.3	10674	16	US-10-295-027-429
4	10047	98.3	10674	16	US-10-295-027-1080
5	9862	96.5	11152	16	US-10-028-248A-7
6	9862	96.5	11152	16	US-10-107-782-7
7	9812	96.0	11158	16	US-10-028-248A-5
8	9812	96.0	11158	16	US-10-107-782-5
9	8552.5	84.7	11230	9	US-09-911-842-3
10	8552.5	84.7	11230	14	US-10-150-821-3
11	5485	53.7	3448	13	US-10-302-172-34
12	3133	30.7	2064	10	US-09-822-846-55
13	1977	19.3	1408	9	US-09-822-846-54
14	1498	14.7	1892	9	US-09-764-898-49
15	1278	12.5	680	9	US-09-764-853-173
16	1278	12.5	680	9	US-09-764-898-122
17	1278	12.5	680	10	US-09-764-881-14
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22	1237	12.1	3262	13	US-10-466-164-29
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24	914.5	8.9	6728	16	US-10-369-072-3
25	893.5	8.7	7410	16	US-10-190-115-1
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28	872	8.5	8064	15	US-10-004-113-56
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30	869	8.5	7693	13	US-10-072-012-133
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56	727	7.1	3921	15	US-10-303-685-7
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59	716.5	7.0	3786	15	US-10-303-685-8
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DB 1331 CTCGCCAGCCGAACNATGGCCACATCAGCTGTCTACAGGGGNAATGTTATATAGACA 1390
QY 461. ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
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QY 481 GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr 500
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DB 2111 ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATT 2170
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QY 1121 MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
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Qy 1181 GlyHisIleTyrArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn 1200
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Qy 1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
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Db 4031 CGATGTGGAAGAACGTCGATGAGTGTCTCAGTCAGCCATGCAAAATGGAGCTACCTGT 4090
Qy 1361 LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys 1380
Db 4091 AAAGACGGTGGCAATAGCTTCAGATGCCCTGTGTGCAGCTGGCTTCACAGGATCACACTGT 4150
Qy 1381 GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp 1400
Db 4151 GAATGAACATCATGAATGTGAGTCTAATCATGTAGAAATCAGGCCACCTGTGTGGAT 4210
Qy 1401 GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr 1420
Db 4211 GAATTAATTCATACAGTTGTAATGTGAGCCAGGATTTTCAGGCAAAAGGTGTGAACA 4270
Qy 1421 GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet 1440
Db 4271 GAACAGCTTCACAGGCTTTAAACCTGGATTTTGAAGTTTCTGGCATCTATGGATATGTGATG 4330
Qy 1441 LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSer 1460
Db 4331 CTAGATGGCATGCTCCCATCTCTCCATGCTCTAACTGTGATCTTCTGGATGAATTCCTCT 4390
Qy 1461 AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr 1480
Db 4391 GACGACATGAACACTTGAACACCAATCTCTATGCGATGTTGATAACGGCAGCGACCAATACC 4450
Qy 1481 LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThr 1500
Db 4451 TTGCTCTGACTGATTAACGGCTGGGTCTCTTATGTCGAATGGCAGGGGAAAGATAACA 4510
Qy 1501 AsnCysProSerValAsnAspGlyArgTyrHisIleAlaIleThrThrSerAla 1520
|||

Db 4511 AACTGTCCCTCGGTGAATGATGGCAGATGGCATCATATTGCAATCACTTGGACAAAGTGCC 4570
Qy 1521 AsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer 1540
Db 4571 AATGCCATCTGGAAAGTCTATATCGATGGGAAATATATCTGACGGTGGTCTGGCCTCTCT 4630
Qy 1541 ValGlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGluGluAspLysLys 1560
Db 4631 GTTGGTTTGGCCCATACCTCGTGGTGGTGGTGTAGTTCCTGGGCAAGAGCAAGCAAAANA 4690
Qy 1561 GlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTyr 1580
Db 4691 GGAGAGGATTCAGCCAGCTGAGTCTTTTGTGGGCTCCATAAGCCAGCTCAACCTCTGG 4750
Qy 1581 AspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeu 1600
Db 4751 GACTATGTCTGTCTCCACAGCAGTGAAGTCACTGGCTACCTCTGCCCAGAGGAACTC 4810
Qy 1601 SerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGlyIleValGlyLysValLys 1620
Db 4811 AGTAAAGGAACGTGTTAGCATGGCTGATTTCTTGTCAAGNATTTGTGGGAAAGTGAAG 4870
Qy 1621 IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis 1640
Db 4871 ATCGATTTCTAAGAGCATATTTTGTCTGATTCGCCACGCTTAGGAGGGTCACTGCCTCAT 4930
Qy 1641 LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro 1660
Db 4931 CTGAGAACTGCATCTCGAAGATTTAAAGCCAGGTTCCAAAGTCAATCTGTCTCTGTGATCCA 4990
Qy 1661 GlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGln 1680
Db 4991 GCTTCCAGCTGGTCCGGAACCTGTGCAGTACTGTCTGAAATCAAGGACAGTGGACACAA 5050
Qy 1681 ProLeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPhe 1700
Db 5051 CCACCTCTCTCACTGTGAAGCATTTAGTGTGGGTGCCACCTCTCTTGAGAAATGGCTTC 5110
Qy 1701 HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr 1720
Db 5111 CATTCAGCGCATGACTTCTATGCTGGCAGCACAGTAACCTACAGTGCACCAATGGCTAC 5170
Qy 1721 TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTyrAsnGlyValSer 1740
Db 5171 TATCTATTGTGGTGAATCTCAAGGATGTTCTGTACAGATATATGGAGCTGGGAACGGGTTC 5230
Qy 1741 ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer 1760
Db 5231 CCATCTCTGCTTGTATGTCGATGAGTGTGCAGTTGCATTCAGATTTGTAGTGAGCATGCTTCT 5290
Qy 1761 CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGly 1780
Db 5291 TGCCCTGAACGTAGATGGATCTCTACATATGTTCTATGTTGCCCGGTACACAGGATGGG 5350
Qy 1781 LysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer 1800
Db 5351 AAAAACTGTCCAGAACCTTATAAATATGAAGGCTTCAGGAAATCCGGAATAATGGCCACTCC 5410
Qy 1801 SerGlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGln 1820
Db 5411 TCAGGTGAGATTTATACAGTAGGTGCGGAAGTCACATTTTGTGTGTCAGGAAGGATACCAG 5470
Qy 1821 LeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluThrAsnHisLeuIlePro 1840
Db 5471 TTGATGGGAGTAAACCAAAATCAATGTTTGGAGTCTGGGAATGGAAATCATCTAATATCCA 5530
Qy 1841 TyrCys 1842
Db 5531 TATTGT 5536

RESULT 2

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; Sequence 1, Application US/10150821

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GENERAL INFORMATION:
APPLICANT: Welcher, Andrew A.
APPLICANT: Elliott, Gary S.
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES
TITLE OF INVENTION: THEREOF
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CURRENT APPLICATION NUMBER: US/10/150,821
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PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 10878
TYPE: DNA
ORGANISM: Homo sapiens
US-10-150-821-1

Alignment Scores:
Pred. No.: 0 Length: 10878
Score: 10208.00 Matches: 1838
Percent Similarity: 99.95% Conservative: 3
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.89% Indels: 0
DB: 14 Gaps: 0

US-09-977-053-6 (1-1842) x US-10-150-821-1 (1-10878)

QY	1	MetTyrProArgLeuAlaPheCysCysTyrTyrGlyLeuAlaLeuValSerGlyTyrAlaThr	20
DB	11	ATGTGGCCCTCGCTGGCTTTTGTGTGGGTCGTGGCTTGGGGCTGGGGCGACC	70
QY	21	PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro	40
DB	71	TTTTCAGCAGATGTCCTGGCTGGCAATTCAGCTTCCGCTCTTCCCGGAGCGCGCCC	130
QY	41	GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg	60
DB	131	GGGGCCCCGGGAGTATCCCGCGCCCGCTCTCTGGCGAGCAAGCGCGGGGAGCAGA	190
QY	61	ValGluArgLeuGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu	80
DB	191	GTGGAGCGGCTGGCGCCAGCGCTTCCCGCGAGCGCTGGCTGGCGGAGCTCAGCGAG	250
QY	81	ArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGluValAlaAsnPheArg	100
DB	251	CGCTGGAGCTGTGTCTTCTGGTGAGTATTCCTCGAGCGTGGCGGAGTCACTTCGCG	310
QY	101	SerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThr	120
DB	311	AGCGAGCTCATGTTCGTCGCAAGCTCTGTCCGACTTCCCGCTGGTGGCGCCCAAG	370
QY	121	ArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIle	140
DB	371	CGGTGGCCCATCGTACCTTCTCTCCCAAGAACTACGTTGGTGGCGCGCTCGATATCAT	430
QY	141	SerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIleProAlaIle	160
DB	431	TCCACCCCGCGCGCGCCGACGACGACGAGTGGCGCTGTCTCTCCAGAGATCCCTGCCATC	490
QY	161	SerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeu	180
DB	491	TCCTACCGAGTGGCGGCACCTACACCAAGGCGCTTCCAGCAAGCGCGCAAAATCTT	550
QY	181	LeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn	200
DB	551	CTTCATGCTAGAGAAACTCACAAAAGTTGTATTTCTCATCATGATGATATTCCAAT	610
QY	201	GlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThr	220

DB	611	GGGGAGACCCCTAGACCAATTTGCAGCGCTCACTGCGAGATTTCAGGAGTGGAGATCTTCACT	670
QY	221	PheGlyIleTyrGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu	240
DB	671	TTTGGCATATGGCAAGGCAACATTCGAGAGCTGAATCATGTGCTTCCACCCCAAGAG	730
QY	241	GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgArgAlaLeu	260
DB	731	GAGCAGCTGTACCTGCTACACAGTTTGAAGAAATTCAGGCTTTAGCTCGCGGGCATG	790
QY	261	HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu	280
DB	791	CATGAGATCTACCTTCTGGAGTTTATTCAAGATGATATGTTCCACTGCTCTTATCTT	850
QY	281	CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr	300
DB	851	TGTGATGAAGGCAAGGACTCTGTCGACCAATGGGAAGCTGCAATGTGGGACACACACA	910
QY	301	GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys	320
DB	911	GGCCATTTTGTGTCATCTGTGAAGAAGGGGTATTACGGGAAGGTCTGCAGTATGAATGC	970
QY	321	ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys	340
DB	971	ACAGCTTGGCCATCGGGGACATACAAACCTGAAGGCTCACCGAGGGAATCAGCAGTTGC	1030
QY	341	IleProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAspCys	360
DB	1031	ATTCCATGTCTGTGATGAANAATCACCTCTCCACCTGGAAGACATCCCTCTGAAGACTGT	1090
QY	361	ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla	380
DB	1091	GTCTGCAGAGAGGATACAGGCACTTGGCCAGACCTGTGAACCTTGCCTGCCCTGCC	1150
QY	381	LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla	400
DB	1151	CTGAAGCTCTCCGAAATGGTTACTTTATCCAAACACCTTGCAACACCACTTCAATGCA	1210
QY	401	AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuCys	420
DB	1211	GCCTGTGGGTCGATGTCCCTGGATTTGATCTTGTGGGAAGCAGCATCATCTTATGT	1270
QY	421	LeuProAsnGlyLeuTyrSerGlySerGluSerTyrCysArgValArgThrCysProHis	440
DB	1271	CTACCCAAATGGTTGTGGTCCGTTTCAGAGAGCTACTGCAGAGTAAGAACATGCTCTCAT	1330
QY	441	LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr	460
DB	1331	CTCGCCAGCGCAACATGCGCACATCAGCTGTTCTACAGGGGAAATGTTATATAAGACA	1390
QY	461	ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys	480
DB	1391	ACATGTTTGTGTGCTGTGTATGAAGGTACAGACTAGAGGCGATGATGAAGCTTACTTGT	1450
QY	481	GlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGluArgHisCysSerThr	500
DB	1451	CAGGAACAGCCAGTGGGATGGCCAGAACCCCGTGTGTGGAGCGCCACTGTTCACCC	1510
QY	501	PheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys	520
DB	1511	TTTCAGATGCCCAAGATATCATCATATCCCCCACAACCTGTGGCAAGCAGCCAGCAAA	1570
QY	521	PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu	540
DB	1571	TTTGGGACGATCTGCTATGTAAGTTGGCCCAAGGGTTTCAATTTATCTGGAGTCAAGAA	1630
QY	541	MetLeuArgCysThrThrSerGlyLysTyrAsnValGlyValGlnAlaAlaValCysLys	560
DB	1631	ATGCTGAGATGTACCACTTCTGGAAATGGATGTGGAGTTTCAAGGAGCTGTGTGTAAA	1690
QY	561	AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln	580
DB	1691	GACGTGGAGGCTCTCAAAATCAACTGTCTTAAGGACATAGAGGCTTAGACTCTGGAACAG	1750

Qy 581 GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys 600
 Db 1751 CAAGATTCTGCAATGTTACCTGGCAGATTCCAAACAGCTAAGACAACCTCTGGTGAAG 1810
 Qy 601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620
 Db 1811 GTGTGAGTCCAGTTCATCAGCTTTACCCACCTTTACCTTTTCCAGTTGGAGATGT 1870
 Qy 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
 Db 1871 GCTATGTAATACACGGCACTGACCTATCCGCAACACAGGCCAGCTGCAATTTCCATATC 1930
 Qy 641 LysValIleAspAlaGluProProValIleAspTrpCysArgSerProProValGln 660
 Db 1931 AAGGTTATTGATGCAGAACCACTCTGTATAGACTGGTCAGACTCTCCACCTCCCGTCCAG 1990
 Qy 661 ValSerGluLysValHisAlaSerTrpAspGluProGlnPheSerAspAsnSerGly 680
 Db 1991 GTCTGGAGAGGTACATGCCGCAAGCTGGGATGAGCTCAGTTCTCAGACAACTCAGGG 2050
 Qy 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
 Db 2051 GCTGAATGGTCNTTACAGAGTATACACAGGAGACCTTTCCCTCAAGGGGAGACT 2110
 Qy 701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
 Db 2111 ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATT 2170
 Qy 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
 Db 2171 GTCATAAAGGTTCCTCCCTGTGAATTCATTCACACCTGTAAATGGGGAATTTATATGC 2230
 Qy 741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
 Db 2231 ACTCCAGATATACCTGGAGTCACTGTACATTAACCTTGGAGGGCTATGATTTTCA 2290
 Qy 761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThrTyr 780
 Db 2291 GAAGGGTCTACTGACAAGTATTATTGTCTTATGAAGATGGCGTCTGGAAACCAACATAT 2350
 Qy 781 ThrThrGluTrpProAspCysAlaLysLysValArgPheAlaAsnHisGlyPheLysSerPhe 800
 Db 2351 ACCACTGAATGGCCAGACTGTGCCAAAACGTTTGTCTAACCCAGGGTTCAAGTCTTT 2410
 Qy 801 GluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGlu 820
 Db 2411 CAGATGTTCTACAAAGCAGCTGTGTGATGACACAGATCTGATCAAGAAGTTTCTGAA 2470
 Qy 821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
 Db 2471 GCATTTGAGACGACCTGGGAAAAATGGTCCCATCATTTTGTAGTGATGACAGACAT 2530
 Qy 841 AspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
 Db 2531 GACTGCAGACTGGAGAGACCTGACCAAAATATTTGCTAGATATTAATTTATGACTAT 2590
 Qy 861 GluAsnGlyPheAlaIleGlyProGlyGlyTrpGlyAlaAlaAsnArgLeuAspTyrSer 880
 Db 2591 GAAATGGCTTTGCAATTTGGACCACTGGCTGGGGTGCAGCTAAATAGGCTGGATTA 2650
 Qy 881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 900
 Db 2651 TACGATGATCTTCTGGACACTGTGCAGAAACAGCCACAGCAATCGCAATGCCAAGTCC 2710
 Qy 901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920
 Db 2711 TCACGGATTAAGAAGTGGCCCATATCTGACTATTAATAATTAAGTTAATTTTAAACATC 2770
 Qy 921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGln 940
 Db 2771 ACAGCTAGTGTGCCATTACCCGATGAAGAAATGATACCTTGTGATGGGAAATCAGCAA 2830

Qy 941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
 Db 2831 CGACTCCTTCAGACATTCGAAACATATCAATAATAAGAAAGGACTCTCAACAAAGAC 2890
 Qy 961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGlu 980
 Db 2891 CCCATGATTTCTTCAGCTTGCATCAGAAATACCTTATAGCCGACAGCAATTCATTAGAA 2950
 Qy 981 ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal 1000
 Db 2951 ACMAAAAGGCTTCCCTCTTCGACAGCAGGCTCAGTGTCTGAGAGGGGTATGTGTCTC 3010
 Qy 1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
 Db 3011 AATTGGCCCTTTGGGAACCTATTATTAATCTGGAACATTTTCACTGTGAAAGCTGCCCGATC 3070
 Qy 1021 GlySerTyrGlnAspGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr 1040
 Db 3071 GGATCTATCAAGATGAGAGGGCACTTGAGTGCAGCTTTGCCCTCTGGGATGTAC 3130
 Qy 1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr 1060
 Db 3131 ACAGGAATATATCCATTCAAGAAACATCTCTGATTTGTAAGCTCAGTGTATAACAGGCAAC 3190
 Qy 1061 TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLys 1080
 Db 3191 TACTCATACAGTGGACTTGGAGCTTGTGATTCGTCTCCATCTGGGCACTTATCAGCCAAA 3250
 Qy 1081 PheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAla 1100
 Db 3251 TTTGGTTCGCGAGCTGCTCTGCTGTCCAGAAAACACCTCACTGTGAAAAGAGAGGCC 3310
 Qy 1101 ValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeu 1120
 Db 3311 GTGAACATTTCTGCATGTGGAGTTCCTTGTCCAGAAAGGAAATTTCTCGCGTTCTGGGTTA 3370
 Qy 1121 MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
 Db 3371 ATGCCCTGTACCCCATGCTCTGCTGACTATTAACCACTTAATGCAGGGAAGGCTTCTGC 3430
 Qy 1141 LeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCys 1160
 Db 3431 CTGGCCTGTCTCTTTTATGGAATACCTCCCATTTGCTGGTTCAGATCCATCAAGAATGT 3490
 Qy 1161 SerSerPheSerSerThrPheSerAlaAlaGluGluSerValValProProAlaSerLeu 1180
 Db 3491 TCAAGTTTTAGTTCAACTTTCTCAGCGCAGAGGAAGTGTGGTGGCCCTCTCTCTT 3550
 Qy 1181 GlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn 1200
 Db 3551 GGACATATTTAAAAGAGGCAATGAAATCAGCACTCAGTTTTCATGATGCTTCTTTAAC 3610
 Qy 1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
 Db 3611 CTTGGCCCAATAGTAGGAACCTGCCAGCACTTGGCGGTGTGTATGTTGTCTCTCTCCA 3670
 Qy 1221 LeuGlyTyrThrGlyLysCysGluThrAspIleAspGluCysSerProLeuProCys 1240
 Db 3671 CTTGGATATACAGGCTTAAAGTGTGAAACAGACATCATGATGAGTGCAGCCACTTCTGC 3730
 Qy 1241 LeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGly 1260
 Db 3731 CTCACAAATGGGTTGTGAAAGACCTAGTTGGGGAATTCATTTGTGAGTGGCCATCAGGT 3790
 Qy 1261 TyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsn 1280
 Db 3791 TACACAGGTCAAGCGGTGTGAAGAAAATATAAATGATGTAGTCTCCAGTCTCTTGTAAAT 3850
 Qy 1281 LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal 1300
 Db 3851 AAAGGAATCTGTGTGATGGTGTGGCTGTATGTTGTGACATGTGTGAAGAGATTTGTA 3910
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Db 3911 GGCCTGCATTTGTGAACAGAGTCAATGAATCCAGTCAACCCATGCTTAAATATGCA 3970
Qy ValCysGluAspGlnValIglyPheLeuCysLysCysProGlyPheLeuGlyThr 1340
Db 3971 GTCTGTGAAGACAGGTTGGGGATTTCTTGTGCAATGCCCCACCTGGATTTTGGGTACC 4030
Qy 1341 ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCys 1360
Db 4031 CGATGTGGAAAGAACGTCGATGAGTGTCTCAGTCAGCCATGCAAAATGAGACTACTGT 4090
Qy 1361 LysAspGlyValAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys 1380
Db 4091 AAAGACGGTCCCAATAGCTTCAGATGSCCTGTGTGACAGTGGCTTCACAGGATCACACTGT 4150
Qy 1381 GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp 1400
Db 4151 GAATTTGAACATCAATGAATGTCAATGATGCTTAATCCATGATAGAAATCAGGCCACCTGTGTGGAT 4210
Qy 1401 GluLeuAsnSerThrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr 1420
Db 4211 GAATTAATTTTACAGTGTGTAATGTGAGCCAGGATTTTCAGGCCAAAGGTGTGAACA 4270
Qy 1421 GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet 1440
Db 4271 GAACAGTCTACAGGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGGATATGTCATG 4330
Qy 1441 LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSer 1460
Db 4331 CTAGATGGCATGCTCCCATCTCTCCATGCTCTAACTGCTAACTGCTGATGTAATCTCT 4390
Qy 1461 AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr 1480
Db 4391 GAGCAGATCAATGATGGAACACCAATCTCTATGTCAGTGTGATAACGGCAGCAATACC 4450
Qy 1481 LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThr 1500
Db 4451 TTGCTCTGACTGATTTATTAACGGCTGGTTCCTTATGTAATGCGAGGGAAGATAACA 4510
Qy 1501 AsnCysProSerValAsnAspGlyArgTrpHisIleAlaIleThrTrpThrSerAla 1520
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Qy 1521 AsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer 1540
Db 4571 AATGGCATCTGGAAAGTCTATATCGATGGGAATTTATCTGACGGTGTGCTGGCTCTCT 4630
Qy 1541 ValGlyLeuProIleProGlyGlyGlyAlaLeuValLeuGlyGlnGlnAspLysLys 1560
Db 4631 GTTGGTTTCCCATACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4690
Qy 1561 GlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrp 1580
Db 4691 GGAGAGGGATTCAGCCAGCTGAGTCTTTTGTGGCTCCATAAGCCAGCTCAACCTCTGG 4750
Qy 1581 AspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeu 1600
Db 4751 GACTATGTCTGTCTCCACAGCAGGTGAAGTCACTGCTTACCTCTGCTCCAGAGGAATC 4810
Qy 1601 SerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLys 1620
Db 4811 AGTAAAGAAAGAGTGTAGCATGGCTGATTTCTTGTGAGAAATTTGGGGAAAGTGAAG 4870
Qy 1621 IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis 1640
Db 4871 ATCGATTTCAAGAGCATATTTTGTCTGATGTCAGTCCACGCTTAGGAGGTTCAGTGCCTCAT 4930
Qy 1641 LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro 1660
Db 4931 CTGAGAACTGCACTGAAAGATTTTAAAGCCAGGTTCCAAAGTCAATCTGTTCTGTATCCA 4990
Qy 1661 GlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGln 1680

Db 4991 GGCTTCACGCTGTCGGGAACCCCTGTGCAGTACTGTCTGAATCAAGACAGTGGACACAA 5050
Qy 1681 ProLeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPhe 1700
Db 5051 CCATCTCTCCATCTGTGAGCCATTAAGTGTGGGGTGCCACTCTCTTTGGAGAAATGGCTTC 5110
Qy 1701 HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr 1720
Db 5111 CATTCAGCCGATGACTTCTATGCTGGCAGCACAGTAACCTACCAGTGCACAAATGGCTTAC 5170
Qy 1721 TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSer 1740
Db 5171 TATCTATGGGTGACTCAAGGATGTTCTGTACAGATAATGGAGCTGGAAACGGGTTTCA 5230
Qy 1741 ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer 1760
Db 5231 CCATCTGCTTGTGATGTCAGTGTGTCAGTGTGATGTCAGATGTAGTGTAGTGTCTTCT 5290
Qy 1761 CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGly 1780
Db 5291 TGCTGACGCTAGATGATCTCATATATGTTCAATGTGTCACCGTACACAGAGATGGG 5350
Qy 1781 LysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer 1800
Db 5351 AAAAATCTGTCAGAACCTATAAAATGTAAGGCTCCAGGAAATCCGGAATGGCCACTCC 5410
Qy 1801 SerGlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGlyTyrGln 1820
Db 5411 TCAGGTGAGATTTATACAGTAGGTGCGGAAGTTCATTTTGTGTCAGGAAGTATACCAG 5470
Qy 1821 LeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluTrpAsnHisLeuIlePro 1840
Db 5471 TTGNTGGAGTACCAAAATCACATGTTTGGAGTCTGAGAAATGGAATCATCTAATACCA 5530
Qy 1841 TyrCys 1842
Db 5531 TATTTGT 5536

RESULT 3

US-10-295-027-429

; Sequence 429, Application US/10295027

; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

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; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/10/295,027

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; PRIOR APPLICATION NUMBER: US 09/663,733

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; PRIOR APPLICATION NUMBER: US 60/350,666

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; PRIOR APPLICATION NUMBER: US 60/332,464

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; PRIOR APPLICATION NUMBER: US 60/334,393

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/340,376

; PRIOR FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: US 60/347,211

; PRIOR FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 60/347,349

; PRIOR FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 60/355,250
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 429
 ; LENGTH: 10674
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-295-027-429

Alignment Scores:

Pred. No.: 0 Length: 10674
 Score: 10047.00 Matches: 1812
 Percent Similarity: 98.86% Conservative: 9
 Best Local Similarity: 98.37% Mismatches: 13
 Query Match: 98.32% Indels: 8
 DB: 16 Gaps: 2

US-09-977-053-6 (1-1842) x US-10-295-027-429 (1-10674)

Qy 1 MetTrpProArgLeuAlaPheCysCysTrpGlyLeuAlaLeuValSerGlyTrpAlaThr 20
 Db 1 ATGTGGCCCTCGCCCTGGCCCTTTGTTGGCTGGGGTCTGGGGCTCGTTTCGGGGCTGGGGGACC 60
 Qy 21 PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro 40
 Db 61 TTTTCAGAGAGTGTCCCGTGGCGCAATTCAGTTCCGGCTCTTCCCGGAGACCCTGGGCC 120
 Qy 41 GlyAlaProGlySerIleProAlaProProAlaProGlyAspGluAlaAlaGlySerArg 60
 Db 121 GGGGCCCTCGGAGTATCCCGCGCGCGCTCTCTGGCGACGAGCGCGGGAGCAGAGA 180
 Qy 61 ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu 80
 Db 181 GTGGAGCGGCTGGGCGAGCGTTCGGCGACGCGTGGCGCTGCTCGGGAGCTCAGCGAG 240
 Qy 81 ArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArg 100
 Db 241 CGCTGGAGCTTGCTTCTGTGTGATGATTCGTCCAGCGTGGGCGAAGTCAACTTCGCG 300
 Qy 101 SerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThr 120
 Db 301 AGCGAGCTCATGTTCTGTCGCAAGCTGCTGTCGACATCCCGTGGTCCCGCGCCACG 360
 Qy 121 ArgValAlaIleValThrPheSerSerLysSerValValProArgValAspTyrIle 140
 Db 361 CGCTGGCCATCGTGACCTTCTGTCGCAAGAACTACGTGGTGGCGCGCTCGATTTACATC 420
 Qy 141 SerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuGlnGlnIleProAlaIle 160
 Db 421 TCCACCGCGCGCGCGCAGCAGCANGTGGCGCTGCTCTCCAGAGATCCCTGCCATC 480
 Qy 161 SerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaGlnIleLeu 180
 Db 481 TCCTACCGAGGTGGCGGACCTTACACCAAGGCGCTTCCAGCAAGCGCGCAAAATCTCT 540
 Qy 181 LeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn 200
 Db 541 CTTTCATGCTAGAGAAATCTCAACAAAGTTGTATTTCTCATCATCATGATGATTTCCAA 600
 Qy 201 GlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValIlePheThr 220
 Db 601 GGGGAGACCTTAGACCAATTCAGCGTCACTGCGAGATTCAGGAGTGGAGATCTTCACT 660
 Qy 221 PheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu 240
 Db 661 TTTGGCATATGGCAAGGAAACATTCCAGAGCTGAAATGATGCTTCCACCCCGCAAGGAG 720
 Qy 241 GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeu 260

Db 721 GAGCACTGTACCTCTCTACAGATTTTGGAAATTTGAGCTTTAGCTTCCCGGATTC 780
 Qy 261 HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu 280
 Db 781 CATGAAGATCTACCTTCTGGGAGTTTATTTCAAGATGATATGTCCTCACTGCTCATATCTT 840
 Qy 281 CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr 300
 Db 841 TGTGATGAAGGCAAGGACTGCTGTGACCGAAATGGGAAGCTGCANAATGTGGGACACACACA 900
 Qy 301 GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys 320
 Db 901 GGCCATTTTGTGTGATCTGTGAAAGGGGTATTCGGGAAGGCTTCAGATATGATATGTC 960
 Qy 321 ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys 340
 Db 961 ACAGCTCTCCCATCGGCGACATACAACTGAAGGCTCACACGAGGAGAAATCAGCAGTTC 1020
 Qy 341 IleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCys 360
 Db 1021 ATTCCATGTCTGATGAAATTCACACCTCTCCACTGGGAAGCACATCCCTCGAAGACTGT 1080
 Qy 361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
 Db 1081 GTCTCAGAGAGGATACAGGCACTCTGCCAGACTGTGAACCTGTCCACTGCTGCTGCC 1140
 Qy 381 LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla 400
 Db 1141 CTGAAGCCTCCCGAAATGTTACTTTATTCAAACACTTGCACCAACCACTTCAATGCA 1200
 Qy 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys 420
 Db 1201 GCCTGTGGGGTCCGATGTACCTCGATTTGATCTTGTGGGAAGCAGCATCATCTTATGT 1260
 Qy 421 LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
 Db 1261 CTACCAATGTTTGTGTGCTCGGTTCCAGAGACTACTGCAGAGTAAGAATGTTATATAAGACA 1320
 Qy 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
 Db 1321 CTCCGCCACCGAATGTCGCATCAGCTGTTCTTACAAAGGGAATGTTATATAAGACA 1380
 Qy 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
 Db 1381 ACATGTTTGTGTGCTGTGATGAGGTTACAGACTAGAGGCGAGTGTATGACTTACTTGT 1440
 Qy 481 GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr 500
 Db 1441 CAAGGAACAGCCAGTGGGATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
 Qy 501 PheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys 520
 Db 1501 TTTTCAGATGCCCAAGATGTCATCATATATATATATATATATATATATATATATATATAT 1560
 Qy 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
 Db 1561 TTTGGAGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Qy 541 MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLys 560
 Db 1621 ATGCTGAGATGTACCACTTCTGGAATAATGGAATGTCGAGTTCAGGAGCTGTGTGTAA 1680
 Qy 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln 580
 Db 1681 GACGTGGAGGCTCTCAATCAACTGTCCTAAGGACATAGAGGCTAAGACTCTGGAAACAG 1740
 Qy 581 GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys 600
 Db 1741 CAAGATTCGCCCATGTTTACCTGGCAGATTCACAGAGCTAAGACCACTCTGTGTGAAG 1800
 Qy 601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620

1801 GTGTCACTCCAGCTTCATCCAGCTTTTCCACCCACCTTACCTTTTCCCAATGAGATGTT 1860
Qy
621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
Qy
1861 GCTATCGTATACAGCGCACTGACCTATCCGGCAACAGCGCCAGCTGCACTTTTCCATATC 1920
Db
641 LysValIleAspAlaGluProProValIleAspTyrCysArgSerProProValGln 660
Qy
1921 AGGTTATTGATGCAGAACCACTGTTCATAGACTGGTGAGACTCCACCTCCGCTCCAG 1980
Db
661 ValSerGluLysValHisAlaIleSerTyrAspGluProGlnPheSerAspAsnSerGly 680
Qy
1981 GTCTCGAGAGGATACATGCCAGCTGGGATGAGCTCAGTCTCTCAGACAACTCAGGG 2040
Db
681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
Qy
2041 GCTGAATGGTCAATACCAAGTCTATACCAAGGAGACCTTTTCCCTCAAGGGGAGACT 2100
Db
701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
Qy
2101 ATAGTACAGTATACAGCCACTGACCTCAGGCAATAACAGGACATGTGATATCCATATT 2160
Db
721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
Qy
2161 GTCATAAAAGGTTCTCCCTGTGAAATTCATTCACACCTGTAAATGGGATTTTATATGC 2220
Db
741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
Qy
2221 ACTCCAGATAAATCTGGAGTCAACTGTACATTAATCTGTGGAGGCTATGATTTTCA 2280
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761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyr 780
Qy
2281 GAAGGCTCTACTGACAGATATTATTGTGCTTATGAGATGGCTCTGGAACCAACATAT 2340
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781 ThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
Qy
2341 ACCACTGAATGGCAGACTGTGCAAAAACGTTTTCGCAAAACCAACGCGTTTCAAGTCTCTT 2400
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801 GluMetPheTyrIlysalAlaArgCysAspAspThrAspLeuMetIlyLysPheSerGlu 820
Qy
2401 GAGATGTTCTACAAAGCAGCTCTGTGTGATGACACAGATCTGATGAAGAGTATTTCTGAA 2460
Db
821 AlaPheGluThrThrLeuGluLysLysMetValProSerPheCysSerAspAlaGluAspIle 840
Qy
2461 GCATTTGACAGCACCTCGGAAAATGGTCCCATCAITTTGTAGTGTATGACAGGACATT 2520
Db
841 AspCysArgLeuGluLeuAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
Qy
2521 GACTGCAGACTGGAGGAGAACCTGACCAAAAATATTTGCCAGAAATATAATTTATGACTAT 2580
Db
861 GluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyValAlaAsnArgLeuAspTyrSer 880
Qy
2581 GAAATGGCTTTTGCAATTTGACACAGTGGCTGGGGTGCAGCTAATAGGCTGGATTAATCT 2640
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881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 900
Qy
2641 TAGCATGACTTCTGACACTGTGCAAGAAACAGCCACAGCAATCGGCAATGCAAGTCC 2700
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901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920
Qy
2701 TCACGGATTTAAAGAAAGTGCCTTATCTGACTATATAAATTAAGTTAATTTTAAACATC 2760
Db
921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnGln 940
Qy
2761 ACAGCTAGTGTGCTATTCGCGATGAAGAAATGATACCTTGAATGGGAAATATCAGCAA 2820
Db
941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
Qy
2821 CGACTCTTCAGACATGGAACTATACAAATAAATGAAAGGACTCTCAACAAGAC 2880
Db
961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGlu 980
Qy
2881 CCCATGTATTCTCTTTCAGCTTGCATCAGAAATACTTATAGCCGACAGCAATTCATTAGAA 2940
Db

Qy 981 ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal 1000
Db 2941 ACAAAAAGAGCTTCCCTCTTTCGACACAGGCTCAGTGTCTGAGAGGGCGTATGTGTCTC 3000
Qy 1001 AspCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
Db 3001 AATTGGCCCTTTGGGACCTATTATAATCTGGAACTTTTCACTGTGAAAGCTGCGGATC 3060
Qy 1021 GlySerTyrGlnAspGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr 1040
Db 3061 GGAATCTTATCAGATGAAGAGGCAACTTGAGTGCAGGCTTTGCCCTCTCGGAGTGTAC 3120
Qy 1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr 1060
Db 3121 ACAGATATATCAATTCAGAAACATCTCTGATTTGTAAAGCTCAGTGTAAACAGGAC 3180
Qy 1061 TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGluProLys 1080
Db 3181 TACTCATACAGTGGACTTGAGACTTGTGAATCGTGTCCACTGGGCACTTATCAGCCAAA 3240
Qy 1081 PheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAla 1100
Db 3241 TTTGGTTCCCGAGCTGCTCTCGTGTCCAGAAAACACCTCAACTGTGAAAAGAGGACC 3300
Qy 1101 ValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeu 1120
Db 3301 GTGAACATTTCTGCATGTGGAGTTCTCTGTCCAGAGGAAATTTCTCGGTTCTGGGTTA 3360
Qy 1121 MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
Db 3361 ATGCCCTGTCAACCATGCTCTCTGTGACTATTACCAACTAATGAGGAGAGGCTTCTGC 3420
Qy 1141 LeuAlaCysProPheTyrGlyThrThrProPhealaglySerArgSerIleThrGluCys 1160
Db 3421 CTGCGCTGTCTCTTTTATGGAACCTACCCCATTTGCTGGTTCCAGATCCATCAGCAATGT 3480
Qy 1161 SerSerPheSerSerThrPheSerAlaAlaGluGluSerValValProProAlaSerLeu 1180
Db 3481 TCACCT-----TCAGTCTGAAATATTAATTTTTCGGTGGATTT 3519
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Db 3520 GGGCATCTGGAGTTGTTAAAT---TGTCTCTCTGAGGTTTTTCCATGAATGCTTCTTTAAC 3576
Qy 1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
Db 3577 CCTTGGCAATAGTGGAACTCTGCCAACAATTTGGGGCTGGTTATGTTTGTCTCTGTCCA 3636
Qy 1221 LeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCys 1240
Db 3637 CTTGATATACAGCTTAAAGTGTGAACACAGACATCGATGAGTGCAGCCCACTGCTTGC 3696
Qy 1241 LeuAsnAsnGlyValCysLysAspLeuValGlyLysPheIleCysGluCysProSerGly 1260
Db 3697 CTCAACAAATGGAGTTTGTAAAGACCTAGTTGGGGAATTCATTTGTGAGTGGCCATCAGT 3756
Qy 1261 TyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsn 1280
Db 3757 TACACAGGTGAGCGGTGTGAAGAAATATAAATGAGTGTAGCTCCAGTCTCTGTTAAAT 3816
Qy 1281 LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal 1300
Db 3817 AAGGAATCTGTGTGTATGTGTGGCTGTGCTGTATGTTGCACATGTGTGAAGGATTTGTA 3876
Qy 1301 GlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAla 1320
Db 3877 GGCCTGCAATTTGAAACAGAGAGTCAATGAATGCCAGTCAAAACCCATCTCTAAATAATGCA 3936
Qy 1321 ValCysGluAspGlnValGlyPheLeuCysLysCysProProGlyThrPheLeuGlyThr 1340
Db 3937 GTCTGTGAAGACAGGTTGGGGATTTCTTGTGTCAAAATGCCACCTGGAATTTTGGGTACC 3996

Qy 1341 ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyValThrCys 1360
Db 3997 CGATGTGGAAAGACGTCGATGTCCTCAGTCAGCCATGCAAAAATGGAGCTACCTCT 4056
Qy 1361 LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys 1380
Db 4057 AAGACGGTGCCTAGCTTCAGATGCTGCTGTGTGAGCTGCTTCACAGGATCACTCT 4116
Qy 1381 GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp 1400
Db 4117 GAATGAACATCAATGAATGTCAGTCTTAATCATATAGAAATCAGGCCACCTGTGTGGAT 4176
Qy 1401 GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGlnThr 1420
Db 4177 GAATTAATTCATACAGTTGTAAATGTGCGCAGGATTTTCAGGCAAAAGGTGTGAACA 4236
Qy 1421 GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet 1440
Db 4237 GAACAGCTCTACAGGCTTTAACTGGAATTTTGAAGTTTCTGGCATCTATGGATATGTCATG 4296
Qy 1441 LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetIysSerSer 1460
Db 4297 CTAGATGGCATGCTCCCATCTCTCCATGCTTAACCTGTACCTTTCTGGATGAATCTCTCT 4356
Qy 1461 AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr 1480
Db 4357 GACGACATGAATATGGAACACCAATCTCTATGCGTGTGATTAACGGCAGCGACATAC 4416
Qy 1481 LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThr 1500
Db 4417 TTGCTCTCTGACTGATTAATACCGCTGGGTCTTTATGTGAATGGCAGGAAAGATAACA 4476
Qy 1501 AsnCysProSerValAsnAspGlyArgTrpHisIleIleAlaIleThrTrpThrSerAla 1520
Db 4477 AACTGTCTCTCGTGAATGATGGCAGATGGCATCATATATGCAATCACTTGGACAAAGTCC 4536
Qy 1521 AsnGlyIleTrpLysValTyrIleAspGlyLysLeuSerAspGlyGlyValAlaGlyLeuSer 1540
Db 4537 AATGCACTCTGGAAGTCTATATCATGGAAGATTAATCTGACGGTGTGCTGGCTCTCT 4596
Qy 1541 ValGlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGlnAspLysLys 1560
Db 4597 GTTGGTTTGGCCATACCTGGTGTGTGGTGTAGTTCTTGGGGCAGAGCAAGACAAAAA 4656
Qy 1561 GlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrp 1580
Db 4657 GGAGAGGGAATTCAGCCCACTGAGTCTTTTGTGGGCTCCATAAGCCAGCTCAACCTCTGG 4716
Qy 1581 AspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeu 1600
Db 4717 GACTATGTCCTGTCTCCACAGAGTGAAGTCACTGGCTACTCTCTGCCAGAGGAATCTC 4776
Qy 1601 SerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLys 1620
Db 4777 AGTAAAGGAACGTTGATGATGGCTGCTGATTTCTTGTTCAGGAATTTGTGGGAAGTGAAG 4836
Qy 1621 IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis 1640
Db 4837 ATCGAATTCAGAGCATATTTTGTTCATATGCCACCGCTTAGGAGGGTCAGTGGCTCAT 4896
Qy 1641 LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro 1660
Db 4897 CTGAGACTGATCTGAAGATTTAAAGCCAGGTTCCAAAGTCATCTGCTCTGTGATCCA 4956
Qy 1661 GlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyIleTrpThrGln 1680
Db 4957 GGCCTCCAGCTGGTGGGAACCCCTGTGAGTACTGTCTGAATCAAGGACAGTGGACACAA 5016
Qy 1681 ProLeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPhe 1700
Db 5017 CCACCTCTCTGTCGTGAACGATAGCTGTGGGGTGGCCACTCTCTTGGAGAAATGGCTTC 5076
Qy 1701 HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr 1720

Db 5077 CATTCAGCCGATGACTTCTATGCTGGCAGCAGTAACCTACAGTCGCAACAAATGGCTAC 5136
Qy 1721 TyrIleuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSer 1740
Db 5137 TATCTATTGGGTGACTCAAGGATGTTCTGTACAGATAATGGGAGCTGGAAACGGCGTTTCA 5196
Qy 1741 ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer 1760
Db 5197 CCATCTCCCTTGTATGTCATGATGATGTCAGTTCAGTTGGATTCAGATTGTAGTCAGCATGCTTCT 5256
Qy 1761 CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrTrpThrGlyAspGly 1780
Db 5257 TGCCTGACGTTAGATGGATCTTACATATGTTTCATGTCTCCACCGTACACAGGAGATGGG 5316
Qy 1781 LysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer 1800
Db 5317 AAAAATCTGTGAGAACCTTATAAATGTAAGGCTCCAGGAATCCGGAAATGGCCACTCC 5376
Qy 1801 SerGlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGln 1820
Db 5377 TCAGTGTAGATTATACAGTAGTGGCGAGTCACATTTTGTGTCCAGGAAGATACCAAG 5436
Qy 1821 LeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluTrpAsnHisLeuIlePro 1840
Db 5437 TTGATGGGAGTAACCAAAATCACATGTTTGGAGTCTGGAGATGGAATCATCTAATACCA 5496
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Db 5497 TATTGT 5502

RESULT 4

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; Sequence 1080, Application US/10295027

; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

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; APPLICANT: Hevezi, Peter A.

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; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and

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1921 AAGGTTATGATGAGAACCACTGTCATAGACTGGTGCAGATCTCCACCTCCCGTCAG 1980
661 ValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGly 680
1981 GTCTCGGAGAGGTACATGCCGCAAGCTGGGATGAGCTCAGTCTCTCAGACAACTCAGGG 2040
681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
2041 GCTGAATTGGTCATTACCAAGAGTCATACACAGGAGACCTTTTCCCTCAAGGGGAGACT 2100
701 IleValGlnThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
2101 ATAGTACAGTATACAGCACCTGACCCCTCAGCGCAATACAGACACATGTGATATCCATAT 2160
721 ValIleLysGlySerProCysGluLeuProPheThrProValAsnGlyAspPheIleCys 740
2161 GTCATAAAGGTTCTCCCTGTGAAATTCATTCACACCTGTAAATGGGGATTTATATGC 2220
741 ThrProAspAsnThrGluValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
2221 ACTCCAGATAATACGGAGTCAACTGTATCACTTTCCTGGAGGGCTATGATTTTCA 2280
761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyr 780
2281 GAAGGGTCTACTGACAGTATATGTGCTTATGAGATGGGCTCGAACCACATAT 2340
781 ThrThrGluTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
2341 ACCACTGAATGCCAGACTGTGCCAAAAAAGCTTTGCCAACCAACCGGGTTCAAGTCTCTT 2400
801 GluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGlu 820
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2461 GCATTTGAGACACCTCGGAAATATGTGCCATCATTTTGTAGTATGCAGAGGACAT 2520
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4177 GAATTAATAATCATACAGTTGTAATGTTCAGCCAGGATTTTCAGGCAAAAGGTGTGAACA 4236
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4237 GAACAGTCTACAGGCTTTAACTCTGATTTTGAAGTTTCTGCACTATGATGATGTCATG 4296
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4657 GGAGGGATTCACCCAGCTGAGTCTTTGTGGCTCCATGAGCAGCTCACTCTCTGG 4716
1581 AspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeu 1600
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4777 AGTAAAGGAAACGTGTAGCATGGCTGATTTCTTGTGAGGAATGTGGGGAATGTGAAG 4836
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RESULT 5
US-10-028-248A-7
; Sequence 7, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimketa, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glennnda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchervnev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
; TITLE OF INVENTION: Theoreof
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
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; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
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; PRIOR APPLICATION NUMBER: 60/272408
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; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
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QY	664	LysValHisAlaSerTrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeu	683	QY	1024	GlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyr	1043
DB	2057	AAAGTACATCCGAGCTGGAGTACGCTCAGTTCTCAGACCACTCAGGGCTGAATTG	2116	DB	3137	CAAGATGAAGAGGCAACTTGAGTGCAGAGCTTTGCCCCCTCTGGAGTGTACACGGAATAT	3196
QY	684	ValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGln	703	QY	1044	IleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyr	1063
DB	2117	GTCAATACCAAGAAGTCATACACAAGGAGACCTTTTCCCTCAAGGGAGACTATAGTACAG	2176	DB	3197	ATCCATTCAAGAAACATCTCTGATTGTAAGCTCAGTGTAAACAGGACCCCTACTCATAC	3256
QY	704	TyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLys	723	QY	1064	SerGlyLeuGluThrCysGlySerCysProLeuGlyThrTyrGlnProLysPheGlySer	1083
DB	2177	TATACAGCCACTGACCCCTCAGGTAATACAGGATATGTGATATCCATATGTCCATGAA	2236	DB	3257	AGTGAGCTTGAGACTTGTAATGTGTCCACTGGCAGCTTATCAGCCAAATTTGGTTCC	3316
QY	724	GlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAsp	743	QY	1084	ArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIle	1103
DB	2237	GGTCTCCCTGTGAAATTCATTCACACCTCTGTAATGGGATTTTATATGCACCTCAGAT	2296	DB	3317	CGGAGCTGCCTCTCTGTGCCAGAAAAACACCTCAACTGTGTGAAAAGAGGAGCCGTGAACATT	3376
QY	744	AsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySer	763	QY	1104	SerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCys	1123
DB	2297	AATACTGGAGTCAACTCTACATTAACCTTGTGGAGGGCTACGATTTTCACAGAGGGTCT	2356	DB	3377	TCTGCATGTGGAGTTCTTGTCCAGAAAGAAAAATCTCGCGTCTCGGGTTAATGCGCTGT	3436
QY	764	ThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThrTyrThrGlu	783	QY	1124	HisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCys	1143
DB	2357	ACTCACAAATATATTCTGTCTTATGAAGATGGCGTCTGGAACCAACATATACCCTGAA	2416	DB	3437	CACCATGTCTCTGTGACTATTACCACTAATGCAGGAAGGCCCTTCTGCTCGCCCTGT	3496
QY	784	TrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGluMetPhe	803	QY	1144	ProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSerSerPhe	1163
DB	2417	TGCGCAGACTGTGCAAAAACGTTTTGCAAAACCGGGTTCAAGTCTCTTGAGATGTTTC	2476	DB	3497	CCCTTTATGGAACCTACCCCAATTCCTGGTTCCAGATCCATCACAGAAATGTTCAAGTTT	3556
QY	804	TyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAlaPheGlu	823	QY	1164	SerSerThrPheSerAlaAlaGluGluSerValValProProAlaSerLeuGlyHisIle	1183
DB	2477	TACAAACGACTCGTTGTGATGACTCAGATCTGATGAAGAAGTTTTCTGAAGCAATTTGAG	2536	DB	3557	AGTTCAACTTTCTCAGCGGCAGAGAAAGTGTGGTGGCCCTCTCTCTTGACATATT	3616
QY	824	ThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAspCysArg	843	QY	1184	LysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHis	1203
DB	2537	ACGACCCCTGGGAAAAATGGTCCCATCATTTTTGTAGTGTGACAGAGCAATTGACTGCAGA	2596	DB	3617	AAAAGAGGCATGAATCAGCAGTCAGCAAGTCATGAATGCTCTTTAAACCCCTTGCCAC	3676
QY	844	LeuGluGluAsnLeuThrLysLysCysLeuGluTyrAsnTyrAspTyrGluAsnGly	863	QY	1204	AsnSerGlyThrCysGlnGlnLeuGluArgGlyTyrValCysLeuCysProLeuGlyTyr	1223
DB	2597	CTGAGAGAACCTGACCAAAAAATATTTGCTAGATATATATATGACTATGAANAATGGC	2656	DB	3677	AATAGTGGAACTGCCAGCACTTGGGGTGGTTATGTTTGTCTCTCTCCACTTGGATAT	3736
QY	864	PheAlaIleGlyProGlyTyrTrpGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAsp	883	QY	1224	ThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsn	1243
DB	2657	TTTGCAATTGGTCCAGGTGGCTGGGTGACCTAATAGCTGGATTAATCTTACGATGAC	2716	DB	3737	ACAGGTTTAAAGTGTGAAACACAGATCGATGAGTGCAGCCCACTGCTTGGCTCAACAAT	3796
QY	884	PheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIle	903	QY	1244	GlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGly	1263
DB	2717	TTCTCGACACTGTGCAAGAAACACGACCAAGCATCGCAATCGCAATGCTCAGCGATT	2776	DB	3797	GGAGTTGTAAAGACCTAGTTGGGAATTCATTTGTGAGTGGCCCATCAGTTACACAGT	3856
QY	904	LysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIleThrAlaSer	923	QY	1264	GlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLysGlyIle	1283
DB	2777	AAAAGAAGTGCCTTATCTGACTATATAAATTAAATTAAATTTTAACTACACAGCTAGT	2836	DB	3857	AAGCACTGTGAATTGAAACATCAATGAATGTCAGTCTAATCCATGTAGAATCAGGCCACC	3916
QY	924	ValProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGlnArgLeuLeu	943	QY	1284	CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis	1303
DB	2837	GTGCCATTACCGATGAAGAAATGATACCTTGAATGGGAAATCAGCAACGACTCCTT	2896	DB	3917	TGTGTGGAATGAATTAATTAATTCATACAGTTGTAAATGTGAGCCAGGATTTTCAGGCAAAAGG	3976
QY	944	GlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyr	963	QY	1304	CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGlu	1323
DB	2897	CAGACATTGGAAATATATACAAATAAACTGAAAAAGGACTCTCAACAAGACCCCATGTAT	2956	DB	3977	TGTGAACAGTGTATGATCAACTCAGTGTATTATTAATTAACCTTTAATGTCAGTCTGTGAA	4036
QY	964	SerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLys	983	QY	1324	AspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCysGly	1343
DB	2957	TCCTTTTTCAGCTTGTGATCAGAAATATCTTATAGCCGACAGCAATTCATTAGAAAACAAAAAG	3016	DB	4037	GACCAGGTTGGGGGATTTCTGTGCAAAATGCCACCTGGATTTTGGGTACCCGATGTGGA	4096
QY	984	AlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysPro	1003	QY	1344	LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly	1363
DB	3017	GCTTCCCTTCTGCAGACCCAGGCTCAGTGTGAGAGGGCGTATGTGTCAATTGCGCT	3076	DB	4097	AAGAACGTGATGTAGTGTCTCAGTCAGCATGCAAAAATGGAGCTACCTGTAAAGACCGT	4156
QY	1004	LeuGlyThrTyrThrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyr	1023	QY	1364	AlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn	1383
DB	3077	TTGGAAACCTTATTAATCTGGAAACATTTCACTCTGTAAGAGCTGCCGATCGGATCTCTAT	3136	DB	4157	GCCAAATAGCTTCAGGTGCTGTGTGACGTGCTGTCACAGGATCACACTGTAATTAAC	4216
				QY	1384	IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn	1403

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Db 4337 ACAGGCTTTAACTGGGATTTTGAAGTTTCGCGCATCTATGATATGTCTATGATGGC 4396
Qy 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetLysSerSerAspMet 1463
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Qy 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
Db 4457 AACTATGACACCACTCTCTATGAGTGTATTAACGGCAGCAATACCTTGTCTCTG 4516
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Qy 1524 TrpLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeu 1543
Db 4637 TGGAGGGTCTATATAAATGGGAAATATCTGACGGTGGTACTGGCCCTCTCCATTGGCAA 4696
Qy 1544 ProIleProGlyGlyValAlaLeuValLeuGlyGlnGluGlnAspLysLysGlyGluGly 1563
Db 4697 GCCATACCTGTGGCGGTGCATTTAGTCTTGGGCAAGAGCAGACAAAAGAGAGGGG 4756
Qy 1564 PheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTyrAspTyrVal 1583
Db 4757 TTCACCGCGTGAATCTTTTGTGGCTCCATAGCCAGCTCACTCTGGGACTATGTC 4816
Qy 1584 LeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeuSerLysGly 1603
Db 4817 CTGTCTCCACAGCAGGTGAAGTCACTGGCTACTCTCTGCCAGAGGAACTCAGTAAAGGA 4876
Qy 1604 AsnValLeuAlaTyrProAspPheLeuSerGlyIleValGlyLysValLysIleAspSer 1623
Db 4877 AACGTGTAGATGCGCTGATTTCTGTGAGAAATGTGGGAAAGTGAAGATCATCTCT 4936
Qy 1624 LysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHisLeuArgThr 1643
Db 4937 AAGAGCATATTTTGTCTGATTTGCCACGCTTGGAGGGTCACTGCTCATCTGAGAACT 4996
Qy 1644 AlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGlyPheGln 1663
Db 4997 GCATCTGAAGATTTAAACACAGGTTCCAAAGTCAATCTGTCTGTGAACACAGGCTTCAG 5056
Qy 1664 LeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGlnProLeuPro 1683
Db 5057 CTGTGCGGAACTCTGTCAGTACTGTCTGAATCAAGGACAGTGGACACACCACTCCCTCC 5116
Qy 1684 HisCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPheHisSerAla 1703
Db 5117 CACTGTGAACGATTCGCTGTGGGTGTCACCTCTTTGGAGAAATGGCTTCCATTCAAGCC 5176
Qy 1704 AspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeu 1723
Db 5177 GATGACTTCTATGCTGGCAGCACAGTAACTACCACTGCAACCAATGGCTACTATCTATTG 5236
Qy 1724 GlyAspSerArgMetPheCysThrAspAsnGlySerTyrAsnGlyValSerProSerCys 1743
Db 5237 GGTGACTCAAGGATGTTCTGTACAGTAATGGAGCTGGAACGGGCTTTCACCATCTCTGC 5296
Qy 1744 LeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAsn 1763

Db 5297 TTAGATGTCCGATGAGTGTGCAGTGTGGATCAGATTGTAGTGAGCATGCTCTTTGCCCTGAAC 5356
Qy 1764 ValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyLysAsnCys 1783
Db 5357 GTAGATGGATCTCATATATTTTCATGTGTCCACCGTACACAGGAGATGGGAAACTGT 5416
Qy 1784 AlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGlu 1803
Db 5417 GCAGACCTATAAATGTAAAGCTCCAGGAATCCGGAATCGCCACTCTCTCAGGTGAG 5476
Qy 1804 IleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeuMetGly 1823
Db 5477 ATTTATACAGTAGTGTCCGAAAGTCACTTTTGTGTCTCAGGAGGATACCACTTGTGAGGA 5536
Qy 1824 ValThrLysIleThrCysLeuGluSerGlyGluTyrAsnHisLeuIleProTyrCys 1842
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US-10-107-782-7
; Sequence 7, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Coleman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Paturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zernusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 7
; LENGTH: 11152
; TYPE: DNA
; ORGANISM: Homo sapiens

QY 664 LysValHisAlaAlaSerThrAspGluProGlnPheSerAspAsnSerGlyAlaGluLeu 683
DB 2057 AAGGTATCATGCCCAAGCTGGATGAGCTCAGTCTTCAGACAACTCAGGGGCTGAATTG 2116
QY 684 ValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGln 703
DB 2117 GTCAATTACCAAGAGTCATACACAGGAGACTTTTCCCTCAGGGGAGACTATAGTACAG 2176
QY 704 TyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLys 723
DB 2177 TATACAGCCACTGACCCCTCAGGTAAATAACAGGATATGTGATATCCATATTTGTCAAGAA 2236
QY 724 GlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAsp 743
DB 2237 GGTTCCTCCCTGTGAATTTCCATTACACACCTGTGTAATGGGATTTTATATGACCTCCAGAT 2296
QY 744 AsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySer 763
DB 2297 AATCTGGAGTCAACTGTATACATTACTTGTCTTGAGGGGCTACGATTTTCAACAGAGGTCT 2356
QY 764 ThrAspLysTyrTyrCysAlaIleTyrGluAspGlyValTyrLysProThrTyrThrGlu 783
DB 2357 ACTGACAAGTATTATTGTCTTATGAGATGGCTCTCGAAACCAACATATACCCTGAA 2416
QY 784 TrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGluMetPhe 803
DB 2417 TGGCCAGACTGTGCAAAAAACGTTTTGCAAAACACACGGGTTTCAAGTCTCTTGAGATGTC 2476
QY 804 TyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAlaPheGlu 823
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QY 824 ThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAspCysArg 843
DB 2537 ACCGACCTGGGAAAAATGGTCCCATCTTTGTAGTGTATGATGAGAGGACATTTGACTGCAGA 2596
QY 844 LeuGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGly 863
DB 2597 CTGAGAGAGAACCTGACCAAAAAATATTTGCCCTAGAAATATATATATGACTATGAAAAATGGC 2656
QY 864 PheAlaIleGlyProGlyGlyTyrGlyValAlaAlaAsnArgLeuAspTyrSerTyrAspAsp 883
DB 2657 TTTGCAATTGTCAGGTGGCTGGGTGTCAGCTAATAGCTGGATTAATCTTACGATGAC 2716
QY 884 PheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIle 903
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QY 904 LysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIleThrAlaSer 923
DB 2777 AAAAGAAAGTGGCCCATTTATCTGACTATAAAATTAAGTTTAATTTTAAACATCACAGCTAGT 2836
QY 924 ValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnArgLeuLeu 943
DB 2837 GTGCCATTACCCGATGAAGAAATGATACCTTGAATGGGAAATCAGCAACGACTCCTT 2896
QY 944 GlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyr 963
DB 2897 CAGACATTGGAAACTATACAAATATAACTGAAAAAGGACTCTCTCAACAAAGACCCCATGTAT 2956
QY 964 SerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLys 983
DB 2957 TCCTTTTCAGCTGTGATCAGAAATATCTTATAGCCAGCAATTCATTAGAAACAAANAG 3016
QY 984 AlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysPro 1003
DB 3017 GCCTTCCCTCTTCAGACCAAGGCTCAGTGTGAGAGGGCTATGTGTGCTCAATTTGCCCT 3076
QY 1004 LeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyr 1023
DB 3077 TTGGGAACCTATTATTATCTGGAACATTTTCACTGTGAAAGCTGCCGATCCGATCCTAT 3136

QY 1024 GlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyr 1043
DB 3137 CAGATGAGAGAGGGCAACTTTGAGTGCAGCTTTGCCCTCTGGGATGTACAGGAAATAT 3196
QY 1044 IleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyr 1063
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QY 1064 SerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySer 1083
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QY 1084 ArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIle 1103
DB 3317 CGAGCTGCCCTCTCTGTGTCCAGAAAACACCTCAACTGTGTGAAAAGAGGACCGGTGAACATT 3376
QY 1104 SerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCys 1123
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QY 1124 HisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCys 1143
DB 3437 CACCATGTCTCTGTGACTATTACCACTAATGAGGAAAGGCTTCTGCTGCGCTGT 3496
QY 1144 ProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSerSerPhe 1163
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DB 3557 AGTTCAACTTTCTCAGCGGAGAGGAAAGTGTGGTGGCCCTGCTCTCTTGAGACATATT 3616
QY 1184 LysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHis 1203
DB 3617 AAAAAGAGGCATGAATGAATCAGCAGTCAAGCAAGTCAAGTCAAGTCTTTTAACTTTGCCAC 3676
QY 1204 AsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyr 1223
DB 3677 AATAGTGGAACTGCCAGCAACTTGGGCGTGTATGTTGTCTCTGTCTCCACTTGATAT 3736
QY 1224 ThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsn 1243
DB 3737 ACAGGTTTAAAGTGTGAAACACAGACATCGATGAGTGCAGCCCACTGCTTGGCTCAACAA 3796
QY 1244 GlyValCysLysAspLeuValGlyPheIleCysGluCysProSerGlyTyrThrGly 1263
DB 3797 GGAGTTTGTAAAGACCTAGTTTGGGGAATTCATTTGTGAGTGCCCATCAGTTTACAGGT 3856
QY 1264 GlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLysGlyIle 1283
DB 3857 AAGCACTGTGATTTGAACATCAATGAATGTCACTTCAATCAATGTAGAAATCAGGCCACC 3916
QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
DB 3917 TGTGTGATGAATTAATTTCAATACAGTTGTAATGTCAAGCCAGGATTTTTCAGGCAAAAGG 3976
QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGlu 1323
DB 3977 TGTGAACAGTATGATATCACTCAGTGTATTATAACCTTATAATGACAGTCTGTGAA 4036
QY 1324 AspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCysGly 1343
DB 4037 GACCAGGTTGGGGATTTCTGTGCATAATGCCACCTGGATTTTGGGTACCCGATGTGGA 4096
QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly 1363
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 Db 4877 AAGGTGTACATGCGCTGATTTCTGTGAGAAATGTGGGAAAGTGAAGATGCAATCT 4936
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 Db 4937 AAGAGCATATTTTGTCTGATTTGCCACGCTTGGAGGGTCAGTGCCTCATCTGAGAACT 4996
 Qy 1644 AlaSerGluAspLeuIysProGlySerIysValAsnLeuPheCysAspProGlyPheGln 1663
 Db 4997 GCATCTGAAGATTTAAACACCGGTTCCAAAGTCAATCTGTCTGTGAACAGGCTTCAG 5056
 Qy 1664 LeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrGlnProLeuPro 1683
 Db 5057 CTGGTGGGAACCTGTGCGAGTACTGTCTGAATCAGGACAGTGGACACCACTCCCTCC 5116
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 Db 5177 GATGACTTCTATGCTGCGACACAGTAACCTACAGTGCACCAATGGCTACTATCTATTG 5236
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 Db 5237 GGTGACTCAGAGGATGTCTGTACAGTAATGGAGCTGGAAACGGCTTTCACCATCTCTGC 5296
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Db 5297 TTAGATGTCGATGAGTGTGCAGTTGGATGAGATTTGTAGTGAGCATGCTTCTTGCCTGAAC 5356
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 Db 5417 GCAGAACCTATAAATGTAAGGCTCCAGGAATCCGGAAAAATGGCCACTCTCTCAGGTGAG 5476
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 Db 5477 ATTATACAGTAGGTGCGGAAGTCACATTTTCGTGTGAGGAAGGATACAGTTGATGGGA 5536
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RESULT 7

US-10-028-248A-5
 ; Sequence 5, Application US/10028248A
 ; Publication No. US20030235882A1

GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Gangolli, Bsha
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Taupier Jr, Raymond J
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Colman, Steven
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Si, Jingsheng
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Stone, David
 ; APPLICANT: Sciore, Paul
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Rothenberg, Mark

; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods (

FILE REFERENCE: 21402-222

CURRENT APPLICATION NUMBER: US/10/028,248A

PRIOR FILING DATE: 2001-12-19

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PRIOR FILING DATE: 2001-07-26

PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 211

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5

LENGTH: 11158

TYPE: DNA

ORGANISM: Homo sapiens

US-10-028-248A-5

Alignment Scores:

Pred. No.:	0	Length:	11158
Score:	9812.00	Matches:	1774
Percent Similarity:	97.23%	Conservative:	16
Best Local Similarity:	96.36%	Mismatches:	47
Query Match:	96.02%	Indels:	4
DB:	16	Gaps:	2

US-09-977-053-6 (1-1842) x US-10-028-248A-5 (1-11158)

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Qy	24	MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro	43
Db	143	ATGTCCCGCTCGCGCAATTTTCAGCTTTCGGCTCTTCGCCGAGACCGCGCCCGGGGCCCC	202
Qy	44	GlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArgValGluArg	63
Db	203	GGGAGTATCCCGCGCCCGCGCTCTCGGACGAGGCGGGGCGGAGTGGGCGG	262
Qy	64	LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu	83
Db	263	CTGGGCCAGGGCTTC-----CGCGTGGCGCTCTCGGGAGCTCAGCGAGCGCTGGAG	316
Qy	84	LeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArgSerGluLeu	103
Db	317	CTTGTCTTCTGGTGATGATTCGTGTCAGCGTGGCGGAGTCTACATTCGCGAGCGAGCTC	376
Qy	104	MetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThrArgValAla	123
Db	377	ATGTTGTCGCGCAAGCTGCTGTCGACTTCCCGGTGTGCCACGCGCGGTGGCC	436
Qy	124	IleValThrPheSerSerIysAsnTyrrValValProArgValAspTyrrIleSerThrArg	143
Db	437	ATCGTGACTTCTCGTCCAAAGAACTACGTGGTGGCGCGCTCGATTCATATCTCCACCCGC	496
Qy	144	ArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIleProAlaIleSerTyrrArg	163
Db	497	CGCGCGCCGACGACAGATGCGCGCTGCTCTCCAGAGATCCCTGCCATCTCTTACCGA	556
Qy	164	GlyGlyGlyThrTyrrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAla	183
Db	557	GGTGGCGGCACCTACACCAAGGCGCTTCCAGCAAGCGCGCAAAATCTTCTTCATGCT	616
Qy	184	ArgGluAsnSerThrLysValValPheIleuIleThrAspGlyTyrrSerAsnGlyGlyAsp	203
Db	617	AGAGAAAATCTCAACAAAAGTTGTATTTCTCATCTCTGATGGATATTCATGGGGAGAC	676
Qy	204	ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle	223
Db	677	CTTAGACCAATTCGACGCTCACTGCGAGATTTCAGAGTTCAGATCTTCACTTTTGGCA	736
Qy	224	TrpGlnGlyAsnIleArgGlnLeuAsnAspMetAlaSerThrProLysGlnGluHisCys	243
Db	737	TGGCAAGGGAAATTCGAGAGCTGATGCAATGGCTTCCACCCCAAGAGGAGGACACTGT	796
Qy	244	TyrrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArg-----ArgAlaLeuHis	261
Db	797	TACCTGTCTACACAGTTTGAAGAAATTTAGAGCTTTAGTCGCCCTCTGTCAATGTTATT	856
Qy	262	GluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrrLeuCys	281
Db	857	GTAGATCTACCTTCTGGAGTTTATTTCAGATGATGATGTGCTCCACTGCTCATATCTTGT	916
Qy	282	AspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThrGly	301
Db	917	GATGAAGGCAAGGACTGCTGTGACCGAATTTGGAGCTGCAAAATGTGGGAAACACACAGGC	976
Qy	302	HisPheGluCysIleCysGlnLysGlyTyrrTyrrGlyLysGlyLeuGlnTyrrGluCysThr	321
Db	977	CATTTTGAGTCATCTGTGAAAGGGGTATACGGGAAAGGCTGTCAGTATGATCTGCACA	103

Db 2117 GAATTTGGTCATTACAGAGAGTCATACAGAGAGACCTTTTCCCTCAAGGGGAGACTATA 21176
Qy ValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleVal 721
Db 2177 GTACAGTATACAGGCACCTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATTGTC 2236
Qy IleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThr 741
Db 2237 ATAAAAGGTTCTCCCTGTGAAATTTCCATTTCAACCTGTAAATGGGGATTTTATATGCACT 2296
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Db 2297 CCAGATATACTGAGTCACTGATCAATTAATCTTGGAGGGCTATGATTTACAGAA 2356
Qy GlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyrThr 781
Db 2357 GGGTCTACTGACAAATTAATTTGCTTATGAGTCTTATGAGATGGCTCTGGAAACCAACATATACC 2416
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Qy MetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAla 821
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Qy PheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAsp 841
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Qy ArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIleThr 921
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Db 3257 TCATACAGTGTGACTTGAATCTGTGTCACCTGGGCACCTTATCAGGCCAAATTT 3316
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DB 5177 TCAGCCGATGACTTCTATGCTGGCAGCAGATAACCTACAGTGCACCAATGGCTACTAT 5236
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RESULT 8
US-10-107-782-5
; Sequence 5, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Perenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shencoy, Suresh,
; APPLICANT: Shinkete, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 5
; LENGTH: 11158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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Db 1256 TGGTGTGCGAGAGGGATACAGAGATCTGGCCAGACCTGTGAGGTGTGCTGCT 1315
Qy 380 AlaLeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsn 399
Db 1316 GGCCTGAAGCCTCCTGAAATGTTTTTTTATACAAACACTTGCAGAAACTACTTCAAT 1375
Qy 400 AlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeu 419
Db 1376 GCGGCTGTGGGTCCGATGTCCCGGGCTTGACCTGTGGGAGAGCAGCATCATTTG 1435
Qy 420 CysLeuProAsnGlyLeuTyrPheSerGlySerGluSerTyrCysArgValArgThrCysPro 439
Db 1436 TGTCAACCAATGTTGTGTTGTCGGACAGAAAGCTTTCGACAGATGAGAACGTGCCCC 1495
Qy 440 HisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLys 459
Db 1496 CACCTCCGACAGCCCAACAGGCCACATCAGCTGCTCCACTCGGAAATGCTCTCAAC 1555
Qy 460 ThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThr 479
Db 1556 ACCCTGTGTTGTTACCTGCATGAGGATACAGATTAGAGGACAGCTAGGCTTACC 1615

Qy 480 CysGlnGlyAsnSerGlnTyrPheGlyProGluProArgCysValGluArgHisCysSer 499
Db 1616 TGTCAAGGAAATGCCCAGTGGGATGGCCAGAGCCCGGTGTGTAGACGCCATTTGCC 1675
Qy 500 ThrPheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAla 519
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Db 1736 AGGCTTGGGATGACCTGTCAGCTAAGCTGCCCGCAGGATACATTTATCCGGGTGAGA 1795
Qy 540 GluMetLeuArgCysThrThrSerGlyLysTyrAsnValGlyValGlnAlaValCys 559
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Qy 560 LysAspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGlu 579
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RESULT 10

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; Sequence 3, Application US/10150821
; Publication No. US20020192758A1
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; APPLICANT: Elliott, Gary S.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/10150,821
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; PRIOR APPLICATION NUMBER: US 60/222,438

; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11230
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-150-821-3

Alignment Scores:

Pred. No.: 0 Length: 11230
Score: 8652.50 Matches: 1532
Percent Similarity: 90.56% Conservativeness: 137
Best Local Similarity: 83.13% Mismatches: 171
Query Match: 84.67% Indels: 3
DB: 14 Gaps: 3

US-09-977-053-6 (1-1842) x US-10-150-821-3 (1-11230)

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700 ThrIleValGlnTyrThrAlaThrAspProSerGlyAenAenArgThrCysAspIleHis 719
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720 IleValIleLysGlySerProCysGluIlePhePheThrProValAenGlyAspPheIle 739
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2333 ATTGTCATAAAGGTTCTCCCTGTGAGTCCCTTCAACCTGTGTAAACGGGGACTTTTATC 2392
Qy
740 CysThrProAspAenThrGlyValAenCysThrLeuThrCysLeuGluGlyTyrAspPhe 759
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760 ThrGluGlySerThrAspLysTyrCysAlaTyrGluAspGlyValTyrLysProThr 779
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2453 ACGAAGGGTCACTGAGAAGTACTACTGTGCTTTTGNAGATGTATCTGGAGACCA 2512
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780 TyrThrThrGluTyrProAspCysAlaLysLysArgPheAlaAenHisGlyPheLysSer 799
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800 PheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSer 819
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880 SerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLys 899
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900 SerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAen 919
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Qy
940 GlnArgLeuLeuThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAenLys 959
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QY 1020 IleGlySerTyrrGlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMet 1039
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QY 1040 TyrThrGluTyrrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysIleGlnGly 1059
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QY 1080 LysPheGlySerArgSerCysLeuSerCysProGluAenThrSerThrValLysArgGly 1099
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QY 1180 LeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePhe 1199
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QY 1700 PheHisSerAlaAspAspPheTyrrAlaGlySerThrValThrTyrrGlnCysAsnAsnGly 1719
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QY 758 AspPheThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLys 777
DB 1321 GATTTTCACAGAAGGCTTACTGACAAATTAATTTGCTTATGAAGATGGCGTCTCGAAA 1380
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DB 1501 TTTTCTGAAGCATTTTGACAGACCTTGGGAAAATGGTCCCATCATTTTGTAGTGATGCA 1560
QY 838 GluAspIleAspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsn 857
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DB 1741 GCCAGGTCTCTACCGATTAAGAGAGTGGCCCATTTATCTGACTATAAATAATTAAGTTAAT 1800
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QY 978 SerLeuGluThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArg 997
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DB 2101 TGCCGGATCGGATCTATCAGATGAGAGGGCACTTGAATGACAGCTTGGCCCTCT 2160
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DB 2161 GGGATGTACAGGAATATATCATTCAGAAACATCTCTGATTTGAAGCTCAGTGTAAA 2220
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DB 2401 TCTGGGTAAATGCCCTGTCCCATGTCTCTCGTACTATTACCACTAATGACGGAAG 2460
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DB 2461 GCTTCTGCTGGCTGTCTCCCTTTATGAACTACCCCATTCGCTGTTCCAGATCCATC 2520
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QY 1178 AlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCys 1197
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RESULT 12

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; Sequence 55, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
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; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-55

Alignment Scores:
Pred. No.: 1,848-306 Length: 2064
Score: 3133.00 Matches: 557
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.66% Indels: 0
DB: 10 Gaps: 0

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QY 331 GluGlySerProGlyGlyLysSerSerCysIleProCysProAspGluAenHisThrSer 350
DB 1982 GAAGGCTCACCAGGAGGAATCAGCAGTTGCATTCATGCTCCATGATGAAATCACCCTCT 1923

QY 351 ProProGlySerThrSerProGluAspCysValCysArgGluGlyTyrArgAlaSerGly 370
DB 1922 CACCTGGGAAGCACATCCCTCGAAGCTGTGTCTGACGAGAGGATACAGGCAATCTGGC 1863

QY 371 GlnThrCysGluLeuValHisCysProAlaLeuLysProProGluAenGlyTyrPheIle 390
DB 1862 CAGACCTGTGAACTTGTCCACTGCGCTGCGCTGAGCCCTCTCGAATGCTTACTTTATC 1803

QY 391 GlnAenThrCysAenAenHisPheAenAlaCysGlyValArgCysHisProGlyPhe 410
DB 1802 CAAAACACTTGCACAAACCACTTCAATGACGCTGTGGGGTCCGATGTCAACCTCGGATTT 1743

QY 411 AspLeuValGlySerSerIleLeuCysLeuProAsnGlyLeuTyrSerGlySerGlu 430
DB 1742 GATCTGTGGGAAGCAGCATCATCTTATGTCTACCCAAATGTTTGTGTCCTCGGTTCAAG 1683

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QY 491 ProArgCysValGluArgHisCysSerThrPheGlnMetProLysAspValIleIleSer 510
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QY 571 LysAspIleGluAlaLysThrLeuGluGlnAspSerAlaAenValThrTyrGlnIle 590
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DB 602 CGTTTTGCAAAACCAACCGGTTCAAGTCTTTGAGATGTTCTACAAAGCAGCTCGTTGTGAT 543

QY 811 AspThrAspLeuMetLysLysPheSerGluAlaPheGluThrThrLeuGlyLysMetVal 830
DB 542 GACACAGATCTGATGAAGAGTCTTCTGAAGCATTTTGAGACGACCTTGGGAAATATGTC 483

QY 831 ProSerPheCysSerAspAlaGluAspIleAspCysArgLeuGluGluAenLeuThrLys 850
DB 482 CCATCATTTTGTAGTGTGACAGGACATTTGCTGCAGACTGGGAGAGAACCTGACCAAA 423

QY 851 LysTyrCysLeuGluTyrAenTyrAspTyrGluAenGlyPheAlaIleGly 867
DB 422 AAATATTGCTAGATATAATATGATCATGATAAATGGCTTTGCAATTTGGT 372

RESULT 13

US-09-822-846-54
; Sequence 54, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice


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; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Pechtel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulkota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-54

Alignment Scores:
Pred. No.: 1,21e-189 Length: 1408
Score: 1977.00 Matches: 362
Percent Similarity: 99.72% Conservatative: 0
Best Local Similarity: 99.72% Mismatches: 1
Query Match: 19.35% Indels: 1
DB: 10 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-822-846-54 (1-1408)

QY 505 LysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPheGlyThrIle 524
DB 2 AARGATGTCATCATATCCCCCACAACTGTGGCAGCAGCCAGCCAAATTTGGGACGATC 61
QY 525 CysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGluMetLeuArgCys 544
DB 62 TGTATGTAAAGTTGCGCCAGAGGTTTCATTTTATCTGGAGTCAAGAAATGCTGAGATGT 121
QY 545 ThrThrSerGlyLysTyrPasnValGlyValGlnAlaLysValCysIleAspValGluAla 564
DB 122 ACCACTTCTGGAATGGAATGTCGAGTTTCAGGAGCTGTGTGTAAGACGTGGAGGCT 181
QY 565 ProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGlnGlnAspSerAla 584
DB 182 CTTCAATCAACTGTCCTAAGGACATAGAGGCTAGAGCTCTGGACAGCAAGATTCTGCC 241
QY 585 AsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysValSerValHis 604
DB 242 AATGTTACTTGCAGATTCACAGCTCAAGCAACTCTGGTGAAGAGGTGTCAGTCCAC 301
QY 605 ValHisProAlaPheThrProProTyrLeuPheProIleGlyAspValAlaIleValTyr 624
DB 302 GTTCATCCAGCTTTCACCCCACTTACCTTTTCCCAATTTGGAGATGTTGCTATCGTATAC 361
QY 625 ThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIleAsp 644
DB 362 ACGGCAACTGACCTATCCGGCAACACAGGCCAGCTGCTATTTTCATATCAGGATTATGAT 421
QY 645 AlaGluProProValIleAspTyrCysArgSerProProProValGlnValSerGluLys 664
DB 422 GCAGAACCACTGTCATAGACTGGTGACATCTCCACCTCCCTCCAGGCTCGGAGAG 481
QY 665 ValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeuVal 684
DB 482 GTACATGCCGCAAGCTGGGATGAGCTCAGTCTCTCAGACAACTCAGGGCT-GAATTTGGTC 540
QY 685 IleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGlnTyr 704

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DB 541 ATTACCAAGAGTCATACACAGGAGACCTTTTCCCTCAAGGGGAGACTATAGTACAGTAT 600
QY 705 ThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLysGly 724
DB 601 ACAGCCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATTTGTCTAAGAAGT 660
QY 725 SerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAspAsn 744
DB 661 TTTCCCTGTGAATTTCCATTCACCTGTAAATGGGGATTTTATATGCACTCCAGATAT 720
QY 745 ThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySerThr 764
DB 721 ACTGGAGTCAACTGTACATTAACCTTGGCTTGGAGGGCTATGATTTTCACAGAGGGTCTACT 780
QY 765 AspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThrTyrThrThrGluTrp 784
DB 781 GACAAATATTATTGTGCTTATGAAGATGGCGTCTGGAAACCAACATATATACCACTGAATGG 840
QY 785 ProAspCysAlaLysLysAspPheAlaAsnHisGlyPheLysSerPheGluMetPheTyr 804
DB 841 CCAGACTGTGCCAAAAACGGTTTTTGCAAACCCACGGGTTCCAGTCTTTGAGATGTTCTAC 900
QY 805 LysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAlaPheGluThr 824
DB 901 AAAGCAGCTCGTTGTGATGACACAGATCTGTATGAAGAGGTTTTTCTGAAGCATTTGAGACG 960
QY 825 ThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAspCysAspGlu 844
DB 961 ACCCTGGGAAAAATGCTCCCATCATTTTGTAGTATGACAGAGACATTCACCTGCAGACTG 1020
QY 845 GluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe 864
DB 1021 GAGGAGAACCTTCGACCAAAAAATATTGCTTGAATATATATATGACTATGAAATGCGCTTT 1080
QY 865 AlaIleGly 867
DB 1081 GCANTTGGT 1089

RESULT 14
US-09-764-898-49
; Sequence 49, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0201
; CURRENT APPLICATION NUMBER: US/09/764,898
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-49

Alignment Scores:
Pred. No.: 6,26e-141 Length: 1892
Score: 1498.00 Matches: 263
Percent Similarity: 100.00% Conservatative: 1
Best Local Similarity: 99.62% Mismatches: 0
Query Match: 14.66% Indels: 0
DB: 9 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-764-898-49 (1-1892)

QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
DB 2 TGTGTGTAGTGGTGTGGCTGCTGCTATGCTTGCACATGTGTGAAAGANTTTGTAGCGCTGCAT 61
QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGlu 1323

```


Db 62 TGTGAACAGAGTCAATGAATGCGAGTCAACACCATGCTTAATTAATGAGTCTGTGAA 121
 Qy 1324 AspGlnValGlyGlyPheLeuLeuCysGlyCysProGlyPheLeuGlyThrArgCysGly 1343
 Db 122 GACCAGGTGGGGATTCATGCAAAATGCCACCTGGATTTTGGGTACCCGATGTGA 181
 Qy 1344 LysAsnValAspGluCysLeuSerGlnProCysValAsnGlyAlaThrCysValAspGly 1363
 Db 182 AAGAACGTGATGAGTGTCTCAGTCAGCCATGCAAAATGAGGCTACCTGTAAAGACGGT 241
 Qy 1364 AlaAsnSerPheArgCysLeuCysAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 Db 242 GCCAATAGCTTCAGTGCCTGTGTGAGCTGCTTCACAGGATCACACTGTGAATGAAC 301
 Qy 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
 Db 302 ATCAATGAATGTCAGTCTTAATCCATGTAGAAATCAGGCCACCTGTGTGATGAATTAAT 361
 Qy 1404 SerTyrSerCysGlyCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer 1423
 Db 362 TCATACAGTGTGTAATGTACAGCCAGGATTTTCAGGCCAAAGGTGTGAACAGAACAGTCT 421
 Qy 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
 Db 422 ACAGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGATGATGATGATGATGATGATG 481
 Qy 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSerAspMet 1463
 Db 482 ATGCTCCCATCTCTCCATGCTCTAACCTGTATACCTTCTGGATGAATTCCTCTGACGACATG 541
 Qy 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAsnAsnThrLeuLeuLeu 1483
 Db 542 AACTATGGAACCAACATCTCTATGAGTTGATTAACGCGACGCAATACCTTGTCTCTCTG 601
 Qy 1484 ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLeuIleThrAsnCysPro 1503
 Db 602 ACTGATTAACAGCGCTGGTCTCTTATGTGATGCGAGGAAAGATAACAACATGCTGCC 661
 Qy 1504 SerValAsnAspGlyArgTyrPheHisIleAlaIleThrThrPheThrSerAlaAsnGlyIle 1523
 Db 662 TCGGTGAATGATGCGAGATGCGATCATATTTGCAATCACTTGGACAAAGTGGCAATGGCATC 721
 Qy 1524 TrpLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeu 1543
 Db 722 TGGAAAGTCTATATCGATGGGAAATATCTACGCGTGTGTGCTGCTCTCTGTGTTGTTG 781
 Qy 1544 ProfileProGly 1547
 Db 782 CCCATACCTGGT 793

RESULT 15
 US-09-764-853-173
 ; Sequence 173, Application US/09764853
 ; Patent No. US20020090672A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: FJ206
 ; CURRENT APPLICATION NUMBER: US/09764,853
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 939
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 173
 ; LENGTH: 680
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-853-173

Alignment Scores: 2.4e-119 Length: 680
 Pred. No.: 1278.00 Matches: 224
 Score:

Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 12.51% Indels: 0
 Db: 9 Gaps: 0
 US-09-977-053-6 (1-1842) x US-09-764-853-173 (1-680)
 Qy 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
 Db 3 TGTGTTGATGTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 62
 Qy 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGlu 1323
 Db 63 TGTGAACAGAGTCAATGAATGCGAGTCAACCCATGCTTAATTAATGAGTCTGTGAA 122
 Qy 1324 AspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThrArgCysGly 1343
 Db 123 GACCAGGTGGGGATTCATGCAAAATGCCACCTGGATTTTGGGTACCCGATGTGA 182
 Qy 1344 LysAsnValAspGluCysLeuSerGlnProCysValAsnGlyValAlaThrCysValAspGly 1363
 Db 183 AAGAACGTGATGAGTGTCTCAGTCAGCCATGCAAAATGAGGCTACCTGTAAAGACGGT 242
 Qy 1364 AlaAsnSerPheArgCysLeuCysAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 Db 243 GCCAATAGCTTCAGTGCCTGTGTGAGCTGCTTCACAGGATCACACTGTGAATGAAC 302
 Qy 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
 Db 303 ATCAATGAATGTCAGTCTTAATCCATGTAGAAATCAGGCCACCTGTGTGATGAATTAAT 362
 Qy 1404 SerTyrSerCysGlyCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer 1423
 Db 363 TCATACAGTGTGTAATGTACAGCCAGGATTTTCAGGCCAAAGGTGTGAACAGAACAGTCT 422
 Qy 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
 Db 423 ACAGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGATGATGATGATGATGATGATG 482
 Qy 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSerAspMet 1463
 Db 483 ATGCTCCCATCTCTCCATGCTCTAACCTGTATACCTTCTGGATGAATTCCTCTGACGACATG 542
 Qy 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAsnAsnThrLeuLeuLeu 1483
 Db 543 AACTATGGAACCAACATCTCTATGAGTTGATTAACGCGACGCAATACCTTGTCTCTCTG 602
 Qy 1484 ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLeuIleThrAsnCysPro 1503
 Db 603 ACTGATTAACAGCGCTGGTCTCTTATGTGATGCGAGGAAAGATAACAACATGCTGCC 662
 Qy 1504 SerValAsnAspGlyArg 1509
 Db 663 TCGGTGAATGATGCGAGA 680

RESULT 16
 US-09-764-898-122
 ; Sequence 122, Application US/09764898
 ; Patent No. US20020090673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: FJ201
 ; CURRENT APPLICATION NUMBER: US/09764,898
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 311
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 122
 ; LENGTH: 680
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-898-122

Alignment Scores:
 Pred. No.: 2.4e-119 Length: 680
 Score: 1278.00 Matches: 224
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 12.51% Indels: 0
 DB: 9 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-764-898-122 (1-680)

QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
 DB 3 TGTGTTGATGGTGGCTGCTATCTTCACATGTCGTAAGGATTTGTAGCCCTGCAT 62
 QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGlu 1323
 DB 63 TGTGAAACAGAGTCAATCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 122
 QY 1324 AspGlnValGlyPheLeuCysLysCysProGlyPheLeuGlyThrArgCysGly 1343
 DB 123 GACCAAGTGGGGGATTCATGTCGCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 182
 QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly 1363
 DB 183 AAGAACGTGCAGTGTCTCAGTACGCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 242
 QY 1364 AlaAsnSerPheArgCysLeuCysAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 DB 243 GCCAATAGCTTCAGATGCTGTGTGCGAGTTCACAGGATCACACTGTGAAATGGAAC 302
 QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
 DB 303 ATCAATGATGTGAGTGTCTCAGTACGCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 362
 QY 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlnSer 1423
 DB 363 TCATACAGTTGTAAATGTGAGCAGGATTTTCAGGCMAAAGGTGTGAAACAGACAGTCT 422
 QY 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
 DB 423 ACAGGCTTTTAACTGGATTTTGAGTTTCGGCATCTATGCAATCTATGCTAGATGCG 482
 QY 1464 AsnTyrGlyThrProLeuSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
 DB 543 AACTATGGAAACCAATCTCTATGCAATGCCAGTGTGAAACAGACAGTCTTCTGCTGCTG 602
 QY 1484 ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
 DB 603 ACTGATTATAACGGCTGGGTTCTTTATGCAATGCCAGGCMAAAGATACAAACTGTGCC 662
 QY 1504 SerValAsnAspGlyArg 1509
 DB 663 TCGGTGAATGATGGCAGA 680

RESULT 17
 US-09-764-881-14
 ; Sequence 14, Application US/09764881
 ; Publication No. US20030125246A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT207
 ; CURRENT APPLICATION NUMBER: US/09/764,881
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 192
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14

LENGTH: 680
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-764-881-14
 Alignment Scores:
 Pred. No.: 2.4e-119 Length: 680
 Score: 1278.00 Matches: 224
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 12.51% Indels: 0
 DB: 10 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-764-881-14 (1-680)

QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
 DB 3 TGTGTTGATGGTGGCTGCTATCTTCACATGTCGTAAGGATTTGTAGCCCTGCAT 62
 QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGlu 1323
 DB 63 TGTGAAACAGAGTCAATCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 122
 QY 1324 AspGlnValGlyPheLeuCysLysCysProGlyPheLeuGlyThrArgCysGly 1343
 DB 123 GACCAAGTGGGGGATTCATGTCGCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 182
 QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly 1363
 DB 183 AAGAACGTGCAGTGTCTCAGTACGCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 242
 QY 1364 AlaAsnSerPheArgCysLeuCysAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
 DB 243 GCCAATAGCTTCAGATGCTGTGTGCGAGTTCACAGGATCACACTGTGAAATGGAAC 302
 QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
 DB 303 ATCAATGATGTGAGTGTCTCAGTACGCAATGCCAGTCAACCCATGCTTAAATAATGCAGTCTGTGAA 362
 QY 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlnSer 1423
 DB 363 TCATACAGTTGTAAATGTGAGCAGGATTTTCAGGCMAAAGGTGTGAAACAGACAGTCT 422
 QY 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
 DB 423 ACAGGCTTTTAACTGGATTTTGAGTTTCGGCATCTATGCAATCTATGCTAGATGCG 482
 QY 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspMet 1463
 DB 483 ATGCTCCCATCTCTCCATGCTCTAACTGTACCTTCTGGATGAAATCCTCTGACGACATG 542
 QY 1464 AsnTyrGlyThrProLeuSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
 DB 543 AACTATGGAAACCAATCTCTATGCAATGCCAGTGTGAAACAGACAGTCTTCTGCTGCTG 602
 QY 1484 ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
 DB 603 ACTGATTATAACGGCTGGGTTCTTTATGCAATGCCAGGCMAAAGATACAAACTGTGCC 662
 QY 1504 SerValAsnAspGlyArg 1509
 DB 663 TCGGTGAATGATGGCAGA 680

RESULT 18
 US-09-764-881-14
 ; Sequence 14, Application US/09764881
 ; Publication No. US20020086821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT207
 ; CURRENT APPLICATION NUMBER: US/09/764,881
 ; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 192

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 680

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-764-881-14

Alignment Scores:

Pred. No.: 2,4e-119 Length: 680
Score: 1278.00 Matches: 224
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 12.51% Indels: 0
DB: 13 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-764-881-14 (1-680)

```
QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
DB 3 TGTGTTGATGGTGGCTGCTATCGTTGCACATGTTGTGAAGGATTTGTAGGCGCTGCAT 62
QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGlu 1323
DB 63 TGTGAACACAGAGTCATGATGCCAGTCAGTCAACCCATGCTTAATATGACGCTCTGTGA 122
QY 1324 AspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThrArgCysGly 1343
DB 123 GACCAAGTTGGGGGATTCATGTGCAATGCCAGTCAGTCAACCCATGCTTAATATGACGCTCTGTGA 182
QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly 1363
DB 183 AAGAAGCTCGATGAGTGTCTCAGTCAGCCATGCCAAATGGAGCTACCTGTAAAGACGGT 242
QY 1364 AlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
DB 243 GCCAATAGCTTCAGATGCTGAGTGTGTCAGCTGCTTCCAGAGATCACACTGTGATTAAT 302
QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
DB 303 ATCAATGATGTCAGTCTTAATCCATGTAGAAATCAGGCCACCTGTGTGGATGAATTAAT 362
QY 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyAlaArgCysGluThrGlnSer 1423
DB 363 TCATACAGTTGTAAATGTCCAGCCAGGATTTTCAGGCGAAAGGTGTGAACAGACAGTCT 422
QY 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
DB 423 CAGGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGGATATGTCTAGTGTAGATGGC 482
QY 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspMet 1463
DB 483 ATGCTCCCATCTCTCCATGCTCTAACCTGTACCTTCTGGATGAATCTCTGACGACATG 542
QY 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
DB 543 AACTATGGAACCAATCTCTATGTCAGTTGTATACCGCAGCGACATACCTTGTCTCTG 602
QY 1484 ThrAspTyrAsnGlyTrpValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
DB 603 ACTGATTATACGGCTGGGTTCTTTATGTGATGTCAGGCGGGAAGATACAACTGTCTCC 662
QY 1504 SerValAsnAspGlyArg 1509
DB 663 TCGGTGAATGATGGCAGA 680
```

RESULT 19

US-09-764-893-37

; Sequence 37, Application US/09764893

; Publication No. US20020086330A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJ209

; CURRENT APPLICATION NUMBER: US/09/764,893

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 37

; LENGTH: 680

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-764-893-37

Alignment Scores:

Pred. No.: 2,4e-119 Length: 680
Score: 1278.00 Matches: 224
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 12.51% Indels: 0
DB: 13 Gaps: 0

US-09-977-053-6 (1-1842) x US-09-764-893-37 (1-680)

```
QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
DB 3 TGTGTTGATGGTGGCTGCTATCGTTGCACATGTTGTGAAGGATTTGTAGGCGCTGCAT 62
QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGlu 1323
DB 63 TGTGAACACAGAGTCATGATGCCAGTCAGTCAACCCATGCTTAATATGACGCTCTGTGA 122
QY 1324 AspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThrArgCysGly 1343
DB 123 GACCAAGTTGGGGGATTCATGTGCAATGCCAGTCAGTCAACCCATGCTTAATATGACGCTCTGTGA 182
QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly 1363
DB 183 AAGAAGCTCGATGAGTGTCTCAGTCAGCCATGCCAAATGGAGCTACCTGTAAAGACGGT 242
QY 1364 AlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
DB 243 GCCAATAGCTTCAGATGCTGAGTGTGTCAGCTGCTTCCAGAGATCACACTGTGATTAAT 302
QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
DB 303 ATCAATGATGTCAGTCTTAATCCATGTAGAAATCAGGCCACCTGTGTGGATGAATTAAT 362
QY 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyIleTyrGlyTyrValMetLeuAspGly 1423
DB 363 TCATACAGTTGTAAATGTCCAGCCAGGATTTTCAGGCGAAAGGTGTGAACAGACAGTCT 422
QY 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
DB 423 CAGGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGGATATGTCTAGTGTAGATGGC 482
QY 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspMet 1463
DB 483 ATGCTCCCATCTCTCCATGCTCTAACCTGTACCTTCTGGATGAATCTCTGACGACATG 542
QY 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeu 1483
DB 543 AACTATGGAACCAATCTCTATGTCAGTTGTATACCGCAGCGACATACCTTGTCTCTG 602
QY 1484 ThrAspTyrAsnGlyTrpValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
DB 603 ACTGATTATACGGCTGGGTTCTTTATGTGATGTCAGGCGGGAAGATACAACTGTCTCC 662
QY 1504 SerValAsnAspGlyArg 1509
DB 663 TCGGTGAATGATGGCAGA 680
```

RESULT 20

US-10-073-865-37

; Sequence 37, Application US/10073865
; Publication No. US20030044904A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RJ209C1

; CURRENT APPLICATION NUMBER: US/10/073,865

; CURRENT FILING DATE: 2002-02-14

; Prior Application removed - See file Wrapper or Palm

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 37

; LENGTH: 680

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-073-865-37

Alignment Scores:

Pred. No.: 2,4e-119 Length: 680
Score: 1278.00 Matches: 224
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 12.51% Indels: 0
DB: 15 Gaps: 0

US-09-977-053-6 (1-1842) x US-10-073-865-37 (1-680)

QY 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
DB 3 TGTGTTGATGTTGGCTATGTTGCACATGTTGAAGAGGATTTGTAGGCTGCAT 62
QY 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGlu 1323
DB 63 TGTGAACAGAGAGTCAATGAATGCCAGTCAACCCATGCTTAAATATGCACTGTGTGAA 122
QY 1324 AspGlnValGlyPheLeuGlyCysValProGlyPheLeuGlyThrArgCysGly 1343
DB 123 GACCAAGTTGGGGGATTCATGTGCAAAATGCCACCTGGATTTTGGTACCCGATGTGA 182
QY 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyValAlaThrCysLysAspGly 1363
DB 183 AAGAACGTCGATGAGTCTCAGTCAGCCATCAAAATGAGAGTACCTGTAAAGACGCT 242
QY 1364 AlaAsnSerPheArgCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
DB 243 GCCAATAGCTTCAGATGCTGTGTGCAGCTGCTTTCACAGGATCACACTGTGAATTGAAC 302
QY 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
DB 303 ATCAATGATGTCAGTCTAATCCATGTAGAAATCAGGCCACCTGTGTGATGAATTAAT 362
QY 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlnSer 1423
DB 363 TCATACAGTTGTAATGTCAGCCAGGATTTTCAGGCGMAAAGGTGTGMAACAGACAGTCT 422
QY 1424 ThrGlyPheAsnLeuAspGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
DB 423 ACAGGCTTTAACTCGGATTTGGAAGTTTCGCAATCTATGGCATATGTGATGATGATGTC 482
QY 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetLysSerSerAspAspMet 1463
DB 483 ATGCTCCCATCTCTCATGCTCTAACCTGTATCTTCTGATGAAATTCCTCTGACGACATG 542
QY 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeu 1483
DB 543 AACATATGGAACACCAATCTCTCATGTCAGTTGATACGGCAGCGACAATACCTTGTCTCTG 602
QY 1484 ThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
DB 603 ACTGATTATACGGCTGGGTTCTTTATGTGAATGGCAGGAAAGATAACAACTGTCCC 662
QY 1504 SerValAsnAspGlyArg 1509

DB 663 TCGGTGAATGATGGCAGA 680

RESULT 21

US-10-242-747-14

; Sequence 14, Application US/10242747

; Publication No. US20040005577A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PT207C1

; CURRENT APPLICATION NUMBER: US/10/242,747

; CURRENT FILING DATE: 2002-09-13

; Prior Application removed - See file Wrapper or Palm

; Prior Application removed - See file Wrapper or Palm

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303	ATCAATGAATGTCAGTCTTAATCCATGATAGAAATCAGGCCACCTGTGTGGATGAATTAAT	362
1404	SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer	1423
363	TCATACAGTTGTTAAATGTCAGCCAGGATTTTCAGGCMAAAGGTGTGAACACAGACAGTCT	422
1424	ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly	1443
423	ACAGCCTTTAAACCTGGATTTTGAAGATTTCTGGCATCTATGATGATGTCATGCTAGATGGC	482
1444	MetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspAspMet	1463
483	ATGCTCCCATCTCTCCCATGCTCTAACTGTACCTCTCTGGATGAATTCCTCTGACGACATG	542
1464	AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeu	1483
543	AACTATGGACACCAATCTCTATGCGAGTTGTAACGGCAGCGCAATACCTTGTCTCTGT	602
1484	ThrAspTyrAsnGlyTyrValLeuTyr-ValAsnGlyArgGluLysIleThrAsnCysPro	1503
603	ACTGATTATAACGGCTGGTCTCTTTATGTGAATGCGAGGGAAGAATACAACTGTCTCC	662
1504	SerValAsnAspGlyArg	1509
663	TCGGTGAATGATGCAGA	680

RESULT 22

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US-10-466-164-29
; Sequence 29, Application US/10466164
; Publication No. US20040058365A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; PANZER, Scott R.;
; APPLICANT: LINCOLN, Stephen E.; ALTUS, Christina M.;
; APPLICANT: DUFOUR, Gerard E.; JACKSON, Jennifer L.;
; APPLICANT: JONES, Anissa L.; DAM, Tam C.;
; APPLICANT: LRU, Tommy F.; HARRIS, Bernard;
; APPLICANT: FLORES, Vincent Z.; DAPFO, Abel;
; APPLICANT: MARWAHA, Rakesh; CHEN, Alice J.;
; APPLICANT: CHANG, Simon C.; GERSTIN, Jr., Edward H.;
; APPLICANT: PERALTA, Careyna H.; DAVID, Marie H.;
; APPLICANT: LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1215 PCT
; CURRENT APPLICATION NUMBER: US/10/466,164
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/US02/01008
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/263,065
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/263,329
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/262,209
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,326
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,063
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 29
; LENGTH: 3262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058365A1 LI:202943.4:200
US-10-466-164-29

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Alignment Scores:				
Pred. No.:	4e-114	Length:	3262	
Score:	1237.00	Matches:	240	
Percent Similarity:	93.13%	Conservative:	4	
Best Local Similarity:	91.60%	Mismatches:	9	
Query Match:	12.10%	Indels:	9	
DB:	13	Gaps:	2	
US-09-977-053-6 (1-1842) x US-10-466-164-29 (1-3262)				
Qy	1590	LysSerLeuAlaThrSerCysProGluGluLeuSerIysGlyAsnValLeuAlaTrpPro	1609	
Db	289	GAGTCACTGCTACCTCCCTGCCCAGAGGAACCTCAGTAAAGGAAACGTGTAGCATGCGCT	348	
Qy	1610	AspPheLeuSerGlyIleValGlyIysValIysAlaAspSerIysSerIlePheCysSer	1629	
Db	349	GAITTCITGTCAGGAATTGTGGGGAAGTGAAGATCGATTCTAAGAGCATATTTGTCT	408	
Qy	1630	AspCysProArgLeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuIys	1649	
Db	409	GCTTGCCCAACGCTTAGAGGGGTCACTCTCAGAACTGCACTCGAAGATTAAAG	468	
Qy	1650	ProGlySerIysValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProVal	1669	
Db	469	CCAGGTTCCAAAGTCAATCTGTTCTGTGATCCAGGGCTTCGAGCTGTGCGGAACCCCTGTG	528	
Qy	1670	GlnTyrCysLeuAsnGlnGlyGlnTrpGlnProLeuProHisCysGluArgIleSer	1689	
Db	529	CAGTACTGTCGAATCAAGACAGTGGACACACCACTTCTCTCCTGACGTGACCGATTAGC	588	
Qy	1690	CysGlyValProProLeuGluAsnGlyPheHisAlaAspAspPheTyrAlaGly	1709	
Db	589	TGTGGGTGGCCACTCCTTTGGAGATGCGCTTCCATTGACCGATGACTTCTATGCTGCGC	648	
Qy	1710	SerThrValThrTyrGlnCysAsnAsnGlyTyrTyrIleuLeuGlyAspSerArgMetPhe	1729	
Db	649	AGCACAGTAAACTACCAGTGCACAAATGGCTACTATCTATTGGGTGACTCAGGGATGTTTC	708	
Qy	1730	CysThrAspAsnGlySer-TrpAsnGlyValSerProSerCysLeuAspValAspGluCys	1749	
Db	709	TGTACAGATANTGGGAGCTAGGAACGGCGTTTACCATCTCTCGGTGATGTCATGAGTG	768	
Qy	1749	SalValAlGlySerAspCysSerGluHisAlaSerCysLeu-AsnValAspGlySerTyrI	1769	
Db	769	TGCAGTTGGATCAGATTGATGAGCATGCTCTTCTGCTGAAACGTAGATGGATCCTACA	828	
Qy	1769	IeCysSerCysValProProTyrThrGlyAspGlyIysAsnCysAlaGluProIleIysC	1789	
Db	829	TATGTTTCATGTGCCCAACCGTACACAGGAGATGGGAAAAAATGTGCAAGAACCTTATAAAAT	888	
Qy	1789	ys-LysAlaProGly---AsnProGluAsnGlyHisSerSerGlyIleIleTyrThr-Va	1807	
Db	889	GCTAAGGCTCCACGGCAGAAATCCGGAAATGGGCCACTCTCTCAGGTGAGATTTATACAGT	948	
Qy	1807	lGlyAla---AlaValThrPheSerCysGlnGluGlyTyr-GlnLeuMetGlyValThrL	1826	
Db	949	AGGTGCGCGAGTCACTATTACGTGTGAGBAGGATACCCAGTGTGATGGGAGTAACCA	1008	
Qy	1826	ysIleThrCysLeuGlu-SerGlyGluTrpAsnHisLeuIlePro-TyrCys	1842	
Db	1009	AAATCACTGTTGGAGTACTGGAGAAATGGAATCATCTAATACCAATATGTT	1060	

RESULT 23

US-10-190-115-3
; Sequence 3, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: ALSBROOK, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Grosse, William M.

; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Mezick, Amanda J.
 ; APPLICANT: Padigar, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shen, Lei
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Szekeres, Edward S. Jr.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Voss, Edward Z.
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-050 CIP
 ; CURRENT APPLICATION NUMBER: US/10/190,115
 ; PRIOR FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: 60/303,168
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: 60/368,996
 ; PRIOR FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 60/386,816
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: 60/215,854
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 60/215,856
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 60/215,902
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 60/216,585,
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/216,586
 ; PRIOR FILING DATE: 2001-07-07
 ; PRIOR APPLICATION NUMBER: 60/216,722
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/218,622
 ; PRIOR FILING DATE: 2000-07-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: Curoseq version 0.1
 ; SEQ ID NO 3
 ; LENGTH: 6728
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (13)..(4431)
 ; US-10-190-115-3

Alignment Scores:
 Pred. No.: 5,728-81 Length: 6728
 Score: 914.50 Matches: 355
 Percent Similarity: 34.59% Conservative: 174
 Best Local Similarity: 24.01% Mismatches: 529
 Query Match: 8.95% Indels: 550
 DB: 16 Gaps: 86

US-09-977-053-6 (1-1842) x US-10-190-115-3 (1-6728)

QY 281 CysAspGluGly-----LysAspCys 287
 DB 169 TGTCCAGAGGGCTTCTGGGGGAATATTGTCAACATCGAGACCCCTGTGAGAGAACCCG 228
 QY 288 CysAspArgMetGlySerCysGlyThrHisThrGlyHisPheGluCysIleCys 307
 DB 229 TGCCAGAAATGGTGGGACTTGTGGGCCAGGCCATGTCGGGGAAAGCCACGTCGCCGATGT 288
 QY 308 GluLysGlyTyTyTyGlyLysGlyLeuGlnTyGluCysThrAlaCysProSerGlyThr 327

DB 289 GCTCAGGTTTACAGAGGAGGACTGCCAGTACTCA---ACATCTCATCATGCTTTGTG 345
 QY 328 TyrLysProGluGlySerProGlyGlyIleSerSerCysIleProCysProAspGluAsn 347
 DB 346 TCTCGACCC-----TGCTG-----AATGGC 366
 QY 348 HisThrSerProGlySerThrSerProGluAspCysValCysArgGluGlyTyArg 367
 DB 367 GGCACATGTCATATGCTCAGCGGGATACCTATGAGTCACCTGTCACTGCGGGTTT--- 423
 QY 368 AlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuLysProProGluAsnGly 387
 DB 424 ---ACAGTAAGAGGTGCAATGCGAGGATGCTGCTGTCTCATCCCTGTCAAATGGA 480
 QY 388 TyrPheIleGlnAsnThrCysAsn-----AsnHisPheAsnAlaCysGlyVal 404
 DB 481 -----AGTACTGTATACCACTGTGGCCACAGCTTCTCTGCAAAATGC----- 522
 QY 405 ArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuProAsnGly 424
 DB 523 -----CTCAGAGC----- 531
 QY 425 LeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHisLeuArgGlnPro 444
 DB 532 ---TTCACAGGCGCAGAAATGTCAGACTGATGTCATGAGTGTGACATTCACGAGCACACTGC 588
 QY 445 LysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThrThrCysLeuVal 464
 DB 589 CAGCATGGT-----GTCACAGCCCTGCTC-----GTCACCTGCTC----- 609
 QY 465 AlaCysAspGluGlyTyArgLeuGluGlySerAspLysLeuThrCys---GlnGlyAsn 483
 DB 610 -----AACCTGCTGTTTCTACCACTGTCAGTGCAGTGCCTCTCAGGGC--- 648
 QY 484 SerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThrPheGlnMet 503
 DB 649 -----TTCACAGGCGCAGTACTGTGTCACAGCTGTATGTG 681
 QY 504 ProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaPheGlyThr 523
 DB 682 CCC-----TGTCACCCCTCACCCTTGTGTCAATGAGGCG 714
 QY 524 IleCys-----TyrValSerCysArgGlnGlyPheIleLeu 535
 DB 715 ACCTGTGGCAGACTGGTGACTTCACTTTTGTAGTGCACCTGCTCCAGGTTTGAAGGG 774
 QY 536 SerGlyValLysGluMetLeu-----ArgCysThrThrSerGlyLys 549
 DB 775 AGCAGCTGTGAGAGGAATATTGATGACTGCCCTAACCCACAGGTGTGAGATGAGGGGTT 834
 QY 550 TrpAsnValGlyValGlnAlaValCysLysAspValGluAlaProGlnIleAsn--- 568
 DB 835 TGTGTGATGGGGTCAACACTTACACTGCCCTGT-----CCCCCAATGAGCAGGA 888
 QY 569 -----CysProLysAspIleGluAlaLysThrLeuGlnGlnGlnAspSerAlaAsnVal 586
 DB 889 CAGTTCTGACAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 927
 QY 587 ThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysValSerValHisValHis 606
 DB 928 -----CCCAATGCTGTGCAAAATGGGGC----- 951
 QY 607 ProAlaPheThrProProTyrLeuPheProIleGlyAspValAlaIleValTyrThrAla 626
 DB 952 -----ACCTGT 957
 QY 627 ThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIleAspAlaGlu 646
 DB 958 GCCACCGCATGAGGCTAT---GCCTGTGTATGT----- 990
 QY 647 ProProValIleAspTrpCysArgSerProProValGlnValSerGluLysValHis 666

[illegible]

Qy	989	gProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThrTyrTyrAs	1009
Db	1800	TCCGGGTACATG-----GGCGCCATCTGCAGTGC-----CAGATTGATGAATGTTACAG	1850
Qy	1009	nLeuGluHisPheThrCysGluSerCys-----ArgIleGlySerTyrGlnAspGluG	1027
Db	1851	CAGCCCTTGCTGCATGACCATGGTGGCTGCATTGACCTGGTCAATGGCTAC-----	1899
Qy	1027	uGlyGlnLeuGluCysIleLeuCysProSerGlyMetTyrThrGlnTyrIleHisSerAr	1047
Db	1900	-----CAGTGCACTGCAGCCAGCCAGCAGCTCAGGGGTAAATTGTGGAATT-----	1944
Qy	1047	gAsnIleSerAspCysIleValGln-----CysIysGlnGlyThrTy	1061
Db	1945	AAATTTGATGACTGTGCAAGTAACCTCTGTATCCATGAATCTGTATGATGGCATTAA	2003
Qy	1061	rSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProIysPh	1081
Db	2004	TGCTACAGT-----TGTTCTGCTCACCAGGATTACCA-----	2037
Qy	1081	eGlySerArgSerCysLeuSerCysProGluAsnThrSerThr---ValIysArgGlyAl	1100
Db	2038	GGGCAGAGATGAACATTGACATTGATGAGTGTGCCTCCAACTCCCTGTCGCAAGGGTGC	2096
Qy	1100	aValAsnIleSerAlaCysGlyValPro-----CysProGluGlyIysPh	1115
Db	2097	AACATGTATCAAC-----GGTGTGAATGTTTCGGCTGTATATGCCCCAGGGA-----	2145
Qy	1115	eSerArgSerGlyLeuMetProCysHisPro---CysProArgAspTyrTyrGlnProAs	1134
Db	2146	-----CCCCATCACCCCAGCTGC-----TACTTCACAGGTGAA	2177
Qy	1134	nAlaGlyIysAlaPheCysLeuAlaCysPro---PheTyrGlyThrThrProPheAlaGl	1153
Db	2178	CGAA-----TGCTTGAGCAATCCCTGCATCCATGGA-----	2208
Qy	1153	ySerArgSerIleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluGluSe	1173
Db	2209	-----NACTGTACTGGAGCTCTCAGTGGATATAAGTGTCTC-----	2244
Qy	1173	rValValProProAsrLeuGluHisIleLysLysArgHisGluIleSerSerGlnVa	1193
Db	2245	-----TGTGATCAGCGCTGGTGTGGCATCAACTGTGAAAGTGACAAA-----	2286
Qy	1193	lPheHisGluCysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyAr	1213
Db	2287	-----AATGAATGCTTTTCGAATCCATGCCAGATGAGGAACCTGTGACAACTGTGTGAA	2342
Qy	1213	gGlyTyrValCysLeuCysProLeuGlyTyrThrGlyLeuIysCysGluThrAspIleAs	1233
Db	2343	TGGATACAGTGTACTTGGCAAGAGGGCTTTAAGGCTATTACTTGCAGGTGAATATTGA	2402
Qy	1233	pGluCysSerProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPh	1253
Db	2403	TGAATGTGCTCAAAATCCATCCTCGAACCAAGGAACCTGCTTTGATGCATAAGTGGCTA	2462
Qy	1253	eIleCysGluCysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCy	1273
Db	2463	CACTTGGCACCTGTGTGTCGCATACACAGACAGAAATTTGCACACAGATATGTGCTCCCTG	2522
Qy	1273	sSerSerSerProCysLeuAsnLysGlyIleCysValAsp-----GlyValAlaGlyTy	1291
Db	2523	TTCCCCAAACCTTGTGGAATGCTGCTGTTCGAAGAGTACCAAAATTTTCAGAGTTA	2582
Qy	1291	rArgCysThrCysValIysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCy	1311
Db	2583	TACTTGTCTGTGCTCTCTGCTGGCAAGTCCAGCGGTGTACCATTGCACATTGACCGAGTG	2642
Qy	1311	gGlnSerAsnProCysLeuAsnAsnAlaValCysGluAspGlnValGlyGlyPheLeuCy	1331
Db	2643	TATCTCAAGCCCTGATCAACATGTTCTCTGTCATTAACCCAGCGGAGCTACATGTCG	2702

1331 slycCysProProGlyPheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSe 1351
1351 rGlnProCysLysAsnGlyAlaThrCysLysAsnGlyAlaAsnSerPheArgCysLeuCy 1371
2703 TGAATGTCACAGGCTTCAGTGATGAGTCTGAGGAGACATTCATGATGAGTCTTCG 2762
1351 rGlnProCysLysAsnGlyAlaThrCysLysAsnGlyAlaAsnSerPheArgCysLeuCy 1371
2763 CAATCTTGCCAGAAATGAGGTTCTGTATGATGAGTGAATATCTTCTCTGCTCTG 2822
1371 sAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnPr 1391
2823 CTTCCGGGTTTCACTGGGATAAGTCCAGACAGACATGATGATGATGATGATGATG 2882
1391 oCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerThrSerCysLysCysGlnPr 1411
2883 CTGTGAAGATGAGGAGGAGCTCTGCTGACTACGTCACAGATTACACTTGCAGATGCCAGC 2942
1411 oGlyPheSerGlyGlnArgCysGluThrGlu-----GlnSerThrGlyPh 1426
2943 AGGATTGATGAGTCCATTGTGAGACACATCAATGATGATGATGATGATGATGATG 3002
1426 eAsnLeuAspPheGluValSerGlyIleTyrglyTyrglyValMetLeuAsp-GlyMetLeuP 1446
3003 CAAT-----GGTGACATGCTGTGATGATGATGATGATGATGATGATGATG 3035
1446 roSerLeuHiAlaLeuThrCysThrPheThrMetLysSerSerAspAspMetAsnTyrg 1466
3036 CTTCCT-----CTTGCTTGCCCTGTGGGTT----- 3061
1466 lyThrProIleSerTyraAlaValAspAsnGlySerAspAsnThrLeuLeuThrAspT 1486
3062 -----TCACTGGATTCCTTCTGCTCCATGATGATCA 3092
1486 yrAsnGlyTrpValLeuTyraValAsnGlyArgGluLysIleThrAsnCysProSerVala 1506
3093 TGAATGACGCTCTCATCCATGCTCAATGAGGAGAGCT----- 3130
1506 sAspGlyArgTrpHisIleAlaIleThrTrp-----ThrSerAlaAsnGlyIleT 1524
3131 -----GTGTGATGGCTGGGTACCTACCTCCGCTGCGCTGCCCCCT 3170
1524 rLyseValTyraIleAspGly-LysLeuSerAspGlyGlyAlaGlyLysSerValGlyLeu 1543
3171 GGGCTACACTG-----GGAAAACTGTGAGACCCCTGGTGAATCTCTGCA-GTGGTCT- 3222
1544 ProfileProGlyGlyAlaLeuValLeuGlyGlnGluAsnLysLysGlyGlu---- 1562
3223 CCATGTAAAAACAAGGTACTTGTGT-----CAGAAAAAGCAGAGTCC 3267
1563 -----GlyPheSerProAlaGluSerPheValGlySerIleSerGln 1576
3268 CAGTGCCTATGTCATCTGGATGGCTGGTGGCTATTGTGACGTGCCCAATGTC----- 3321
1577 LeuAsnLeuTrpAspTyraValLeuSerProGlnGlnValLysSerLeuAlaThrSerCys 1596
3322 -----TCTGT 3327
1597 ProGluGluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleVal 1616
3328 GACATAGCAGCCTCCAGGAGAGGTGTCTGTT-----GAACACTTGTGCCAGCACTCA 3381
1617 GlyLeValLysIleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGly 1636
3382 GGT---GTCTGATCAATGCTGCACACAGCATTTACTGTGAGTGCCCC---CTGGGCTAT 3435
1637 SerValProHisLeu-----ArgThrAlaSerGluAspLeuLysProGly 1651
3436 ACTGGAGACTATGTGAGGAGGAGACTGATGATGATGATGATGATGATGATGATGATG 3495
1652 SerLysValAsnLeuPhe-----CysAspProGlyPheGlnLeu 1664
3496 GCAACATGAGTCACTTCATTGTGTGATACAGATGAGTGTGTGCCAGGCTATCAGGCT 3555
1665 ValGlyAsnProVal-----GlnTyraCysLeuAsnGlnGlyGln 1677

3556 GTCAACTGTGAGTATGAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 3615
1678 TrpThrGlnProLeuProHisCysGluArgIleSerCysGlyValProProLeuGlu 1697
3616 TGTATTGACCTTGTGACCAT-----TTCAAGTGTCTTGTGCCACCA----- 3657
1698 AsnGlyPheHisSerAlaAspAspPheTyraAlaGlySerThrValThrGlnCysAsn 1717
3657 ----- 3657
1718 AsnGlyTyraTyraLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsn 1737
3658 -----GGCACTGGGCTTCTCTGTGAAGAGAAC----- 3687
1738 GlyValSerProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGlu 1757
3688 -----ATTGATGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAA 3723
1758 HisAlaSerCysLeuAsnValAspGlySerTyraIleCysSerCysValProProTyraThr 1777
3724 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3783
1778 GlyAspGlyLysAsnCysAlaGluProIleLys-----CysLysAla 1791
3784 GGGGAG-----CGTTGTGAGGAGACATCAAGAGTGTCTTCCAAACCCCTGAGCTCT 3837
1792 ProGlyAsn 1794
3838 GAGGGCAGC 3846

RESULT 24
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; Sequence 3, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alschbrook II, John P
; APPLICANT: Spaderma, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shinkets, Richard
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369, 072
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174, 372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898, 994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215, 854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215, 856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215, 902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216, 585
; PRIOR FILING DATE: 2000-07-07
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; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216, 722
; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 60/218,622
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 60/218,992
 ; PRIOR FILING DATE: 2000-07-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 6728
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-369-072-3

Alignment Scores:
 Pred. No.: 5,72e-81 Length: 6728
 Score: 914.50 Matches: 395
 Percent Similarity: 34.59% Conservative: 174
 Best Local Similarity: 24.01% Mismatches: 529
 Query Match: 8.95% Indels: 550
 DB: 16 Gaps: 86

US-09-977-053-6 (1-1842) x US-10-369-072-3 (1-6728)

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DB 169 TGTCCAGAGGCTTCTTGGGGGAATATTGTCAACATCGAGACCCTGTGTGAGAGAAGACCGC 228
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QY 288 CysAspArgMetGlySerCysLysCysGlyThrHisThrGlyHisPheGluCysIleCys 307
    |||
DB 229 TGCAGAAATGTGGGACTTGTGTGGCCAGCCATGCTGGGGAAAGCAAGTGTCCGATGT 288
    |||
QY 308 GluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCysThrAlaCysProSerGlyThr 327
    |||
DB 289 GCCTCAGGGTTTACAGAGAGAGACTGCCAGTACTCA---ACATCTCATCCATGCTTTGTG 345
    |||
QY 328 TyrLysProGluGlySerProGlyGlyIleSerSerCysIleProCysProAspGluAsn 347
    |||
DB 346 TCTCGACCC-----TGCCTG-----AATGGC 366
    |||
QY 348 HisThrSerProGlySerThrSerProGluAspCysValCysArgGluGlyTyrArg 367
    |||
DB 367 GGCACATGCCATATGCTCAGCGGATACCTATGAGTGCACCTGTCAAGTCGGGTTT--- 423
    |||
QY 368 AlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuLysProProGluAsnGly 387
    |||
DB 424 ---ACAGGTAAAGAGTGCCTCAATGACGAGTGCCTGCTCATCCCTGTGCATAATGGA 480
    |||
QY 388 TyrPheileGlnAsnThrCysAsn-----AsnHisPheAsnAlaAlaCysGlyVal 404
    |||
DB 481 -----AGTACCTGTACCATCTGTGGCCACACAGTCTCTCTGCAATGC----- 522
    |||
QY 405 ArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuProAsnGly 424
    |||
DB 523 -----CTCAGAGC----- 531
    |||
QY 425 LeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHisLeuArgGlnPro 444
    |||
DB 532 ---TTCCAGAGGGCAGAAATGTGAGACTGATGTCAATGAGTGTGCACATTCCTCAGGACACTGC 588
    |||
QY 445 LysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThrCysLeuVal 464
    |||
DB 589 CAGCATGGT-----GGCAGCTGCTC----- 609
    |||
QY 465 AlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys---GlnGlyAsn 483
    |||
DB 610 -----AACCTGCTGTGTTCTTACAGTGCAGTGCCTCAGGCG----- 648
    |||
QY 484 SerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThrPheGlnMet 503
    |||
DB 649 -----TTCAGAGGCGAGTACTGTGACAGCCTGTATGTG 681
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QY 504 ProLysAspValIleIleSerProHisAsnGlyLysGlnProAlaLysPheGlyThr 523
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DB 682 CCC-----TGTGCACCCCTCACCTTGTGTCAATGGAGGC 714
QY 524 IleCys-----TyrValSerCysArgGlnGlyPheIleLeu 535
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DB 715 ACCTGTGCGCAGACTGTGTGACTTTCACCTTTGTGAGTGCACACTCCCTTCCAGGTTTGAAGG 774
    |||
QY 536 SerGlyValLysGluMetLeu-----ArgCysThrThrSerGlyLys 549
    |||
DB 775 AGCACCTGTGAGAGGAATATTGATGACTGCCCTAACCCACAGGTGTGCAGAAATGGAGGGTT 834
    |||
QY 550 TrpAsnValGlyValGlnAlaValCysLysAspValGluAlaProGlnIleAsn--- 568
    |||
DB 835 TGTGTGATGGGTCAACACTTCAACTGCGCTGT-----CCCCACAAATGGACAGCA 888
    |||
QY 569 -----CysProLysAspIleGluAlaLysThrLeuGluGlnGlnAspSerAlaAsnVal 586
    |||
DB 889 CAGTTCTGCACAGAGGATGTGGATGATGCTGTCTGCAG----- 927
    |||
QY 587 ThrTrpGlnIleProThrAlaLysAsnSerGlyGluLysValSerValHisValHis 606
    |||
DB 928 -----CCCAATGCTGTCAAAATGGGGC----- 951
    |||
QY 607 ProAlaPheThrProProTyrLeuPheProIleGlyAspValAlaIleValTyrThrAla 626
    |||
DB 952 -----ACCTGT 957
    |||
QY 627 ThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIleAspAlaGlu 646
    |||
DB 958 GCCAACCCGCAATGGAGGCTAT---GGCTGTGTATGT----- 990
    |||
QY 647 ProProValIleAspTrpCysArgSerProProValGlnValSerGluLysValHis 666
    |||
DB 991 -----GTCAACGGCTGGAGTGGAGAT-----GACTGCAGTGCAGACATT--- 1029
    |||
QY 667 AlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeuValIleThr 686
    |||
DB 1030 -----GATGATGTGCTTCCCTCTCTACTCCAGGCTCCACCTGCATCGAC 1077
    |||
QY 687 ArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGlnTyrThrAla 706
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DB 1078 CGTGTGCGCTCTCTCTCTGTCATGTGCCAGAGGGAGGAGGAGGCTCTCTGTGTGTCATCTG 1137
    |||
QY 707 ThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLysGlySerPro 726
    |||
DB 1138 GATGAT-----GCATGCATCATCAATCTTCCACAGGGGCACTG 1179
    |||
QY 727 CysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAspAsnThrGly 746
    |||
DB 1180 TGTGACACC-----AACCCCTAAATGGGCAATATATTTC----- 1215
    |||
QY 747 ValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySerThrAspLys 766
    |||
DB 1216 -----ACCTGCCACAGGCTTACAAGGGGCTGCTGCACAGAGATGTG 1260
    |||
QY 767 TyrTyrCysAlaTyr-----Glu 772
    |||
DB 1261 GATCAATGTGCCATGGCCATAGCAATCTTGTGAGCATGCAGGAAATGTGTGACACG 1320
    |||
QY 773 AspGlyValTrpLysProThrTyrThrThrGluTrpProAspCysAlaLysLysArgPhe 792
    |||
DB 1321 GATGGCGCTTCCAC-----TGTGAGTGTCTCAAGGGT----- 1353
    |||
QY 793 AlaAsnHisGlyPheLysSerPheGluMetPheTyrLysAlaAlaArgCysAspAspThr 812
    |||
DB 1354 -----TATGCAGGACCTCGTTGT---GAGATG 1377
    |||
QY 813 AspLeuMetLysLysPheSerGluAlaPheGlu-----ThrThrLeuGlyLysMet 829
    |||
DB 1378 GACATCAATGATGCCATTGAGCCCTGAGCCCTGAGATGATGCTACTGCTGATAGATT 1437
    |||
QY 830 -----ValProSerPheCysSerAspAlaGluAspIleAspCys 842
    |||
DB 1438 GGAGGCTTCATGTCTGTGTCATGCCAGGTTTC-----AAAGGTGTGCTATTGT 1485
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Db      3171  GGCCTACACTG-----GGAAAACTGTGAGACCTGTGTAATCTCTGCA-GTGGGTCT- 3222
Qy      1544  ProIleProGlyGlyAlaLeuValLeuGlyGlnGlnAspIleLysGlyGlu--- 1562
Db      3223  CCATGTAATAAACAAAGGTACTTGTGTT-----CAGAAAAAGCAGACTCC 3267
Qy      1563  -----GlyPheSerProAlaGluSerPheValGlySerIleSerGln 1576
Db      3268  CAGTGCCTATGTCATCTGATGGCTGGTGGCTTATGTGACGTGCCAATGTC----- 3321
Qy      1577  LeuAsnLeuTrpAspTyrValLeuSerProGlnGlnValIleValLeuAlaThrSerCys 1596
Db      3322  -----TCTGT 3327
Qy      1597  ProGluGluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleVal 1616
Db      3328  GACATAGCAGCTCCAGGAGGTGTGCTGTT-----GAACACTTGTGTCAGCACTCA 3381
Qy      1617  GlyIleValIleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGly 1636
Db      3382  GGT---GTCTGCATCAATGCTGCGCAACAGCATTAATCTGTCAGTGCCTC---CTGGGCTAT 3435
Qy      1637  SerValProHisLeu-----ArgThrAlaSerGluAspLeuLysProGly 1651
Db      3436  ACTGGGAGCTACTGTGAGGAGCAACTCGATGAGTGTGGTCCACCTCCAGCAGCGG 3495
Qy      1652  SerLysValAsnLeuPhe-----CysAspProGlyPheGlnLeu 1664
Db      3496  GCAACATGCAGTGACTTTCATTGTTGGATACAGATGCGAGTGTGTCCAGGCTATCAGGGT 3555
Qy      1665  ValGlyAsnProVal-----GlnTyrCysLeuAsnGlnGlyGln 1677
Db      3556  GTCAACTGTGATGATGAAGTGATGAGTGCCAGATCAGCTCCAGAAATGGAGGCACC 3615
Qy      1678  TrpThrGlnProLeuProHisCysGluArgIleSerCysGlyValProProProLeuGlu 1697
Db      3616  TGTATTGACCTTGAACCAT-----TTCAAGTGCTCTTCCCAACCA----- 3657
Qy      1698  AsnGlyPheHisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsn 1717
Db      3657  ----- 3657
Qy      1718  AsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsn 1737
Db      3658  -----GGCACTCGGGGCCCTACTCTGTGAAGAGAAC----- 3687
Qy      1738  GlyValSerProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGlu 1757
Db      3688  -----ATTGATGACTGTGCCGGGTGCCCATTTGCTTAAT 3723
Qy      1758  HisAlaSerCysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThr 1777
Db      3724  GGTGTCAGTGCATGGATGATGAGGCTACAGTTGTCTGCTTGCCTTGGCTTGTCT 3783
Qy      1778  GlyAspGlyLysAsnCysAlaGluProIleLys-----CysLysAla 1791
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RESULT 25

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; Sequence 1, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.

; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Raestelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 1
; LENGTH: 7410
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7407)
US-10-190-115-1
Alignment Scores:
Pred. No.: 8,91e-79 Length: 7410
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Percent Similarity: 35.02% Conservative: 171
Best Local Similarity: 24.74% Mismatches: 537
Query Match: 8.74% Indels: 550
DB: 16 Gaps: 90
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Db      217  TGCCAGATGTGGGACTTGTGTGGCCCGCCAGGCCATGTGTGGGAAAGCCACGTCGCCATGT 276
Qy      308  GluLysGlyTyrTyrTyrGlyLysGlyLeuGlnTyrGluCysThrAlaCysProSerGlyThr 327

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Db	334	TCTCGACCT						ATGGC	354
Qy	348	HisThrSerProProGlySerThrSerProGluAspCysValCysArgGluGlyTyrArg							367
Db	355	GGCAGATGCCATATGCTCAGCGGATACCTATGAGTGACCTGTCAAGTCGGGTTT						---	411
Qy	368	AlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuIysProGluAsnGly							387
Db	412	---ACAGTAAGAGAGTCCCAATGACGCGATGCCCTGTCTCATCCCTGTGCAAAATGA							468
Qy	388	TyrPheIleGlnAsnThrCysAsn						AsnHisPheAsnAlaAlaCysGlyVal	404
Db	469	---AGTACTCTGTACCACTGTGGCCACCAAGTTCCTGCAAAATGC						---	510
Qy	405	ArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuProAsnGly							424
Db	511	---CTCAGAGC						---	519
Qy	425	LeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHisLeuArgGlnPro							444
Db	520	---TTCACAGCGCAGAAATGTGAGACTGATGTCAATGAGTGTGCATTCAGACGACACTGC							576
Qy	445	LysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrIysThrThrCysLeuVal							464
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Qy	465	AlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys						GlnGlyAsn	483
Db	598	---AACCTGCTGGTTCCTACCACTGCCAGTCCCTCAGGCG						---	636
Qy	484	SerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThrPheGlnMet							503
Db	637	---TTCACAGCGCAGTACTGTGACAGCTGTATGTG							669
Qy	504	ProLysAspValIleIleSerProHisAsnCysGlyIysGlnProAlaLysPheGlyThr							523
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Qy	524	IleCysTyrValSerCysArgGln						Gly	532
Db	703	---ACCTGTGGCAGACTGTGACTTTCATCTTTGAGTGCCATTACCAAGT							750
Qy	533	PheIleLeuSerGlyValLysGluMetLeu						ArgCysThrThr	546
Db	751	TTTGAAGGGAGCACCTGTGAGAGAAATGATGACTGCCCTAACCAACAGGTGTCAAGAT							810
Qy	547	SerGlyLysTrpAsnValGlyValGlnAlaValCysLysAspValGluAlaProGln							566
Db	811	GGAGGGGTTTGTGTGGATGGGGTCAACACTTACAACTGCCCGT						CCCCACAA	864
Qy	567	IleAsn						CysProLysAspIleGluAlaLysThrLeuGluGlnGlnAspSer	583
Db	865	TGGACAGCAGTTCGACAGAGAGATGTGATGAATGCCCTGCTG						---CAGCCCAAT	918
Qy	584	AlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysValSerVal							603
Db	919	GCTGTCAAAACTGG						---GGCACCTGTGTCACCAACCGCAATGGAGCTATGGCTGTGTA	972
Qy	604	HisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspValAlaIleVal							623
Db	973	TGTCACACGGC						---	984
Qy	624	TyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIle							643
Db	985	TGGAGTGGAGATGACTGCAGTGCAGAACATTGATGATTGTGTTTG						---GGCCCTGTACTC	1042
Qy	644	AspAlaGluProProValIleAspTrpCysArgSerProProValGlnValSerGlu							663

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model.

Run on: May 10, 2004, 15:48:01 ; Search time 13847.8 seconds
(without alignments)
3972.182 Million cell updates/sec

Title: US-09-977-053-6
Perfect score: 10219
Sequence: 1 MWFLAPCCWGLALVSGMAT.....GVTKITCLSGEWNHLLPYC 1842

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool_p/US09977053/runat_06052004_075943_18200/app_query.fasta_1.5710
-DB=EST -OPMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09977053.ecgn_1_15412 @runat_06052004_075943_18200 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7

Database :

RST: *
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2: em_esthum: *
3: em_estin: *
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14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_man: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gse1: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5409.5	52.9	3288	29	AY405591	AY405591 Homo sapi
2	5060.5	49.5	3009	29	AY405592	AY405592 Pan trogl
3	4803.5	47.0	3288	29	AY405593	AY405593 Mus muscu
4	4781	46.8	3171	11	BC030816	BC030816 Homo sapi
5	3955	38.7	2736	11	AK052699	AK052699 Mus muscu
6	3011	29.5	3127	14	CB548140	CB548140 AGNNUC1C
7	2023.5	19.8	3242	11	AK035333	AK035333 Mus muscu
8	1793	17.5	3307	11	AK052463	AK052463 Mus muscu
9	1690	16.5	906	13	BX390270	BX390270 BX390270
10	1470.5	14.4	1201	13	EX356254	EX356254 BX356254
11	1407.5	13.8	1201	13	EX356253	EX356253 BX356253
12	1385	13.6	748	13	EX093982	EX093982 BX093982
13	1359	13.3	738	9	ALU706149	ALU706149 DKFZP686E
14	1304	12.8	801	9	ALU137280	ALU137280 ALU137280
15	1295	12.7	756	12	BG620159	BG620159 602618422
16	1188	11.6	829	12	BG434540	BG434540 602506592
17	1176.5	11.5	701	13	B0929100	B0929100 AGNCOURT
18	1145	11.2	719	12	BG436029	BG436029 602508809
19	1125.5	11.0	1887	11	AK045217	AK045217 Mus muscu
20	1050	10.3	2408	11	AK087058	AK087058 Mus muscu
21	1039.5	10.2	2019	11	BC047729	BC047729 Homo sapi
22	1027.5	10.1	1035	12	BG621817	BG621817 602619678
23	1022	10.0	642	10	BBS00305	BBS00305 BBS00305
24	990	9.7	673	10	BBS42219	BBS42219 BBS42219
25	982.5	9.6	998	13	BQ17243	BQ17243 AGNCOURT
26	982	9.6	763	13	B0392790	B0392790 603805162
27	958	9.4	652	13	BQ367139	BQ367139 MR3-GN018
28	922	9.0	503	10	BF367968	BF367968 RC3-GN004
29	898.5	8.8	482	10	BF998780	BF998780 QV0-GN023
30	875.5	8.6	9330	11	AK090118	AK090118 Mus muscu
31	856	8.4	480	10	BG003364	BG003364 RC3-GN004
32	843	8.2	579	10	BF367305	BF367305 MR0-GN002
33	759	7.4	477	10	BG012274	BG012274 RC2-GN028
34	757.5	7.4	5925	29	AY418022	AY418022 Mus muscu
35	745	7.3	415	10	BG005173	BG005173 CM2-GN022
36	739.5	7.2	4131	29	AY418953	AY418953 Homo sapi
37	735.5	7.2	444	10	BG012481	BG012481 RC3-GN027
38	734	7.2	412	10	BF369449	BF369449 RC0-GN009
39	730	7.1	734	13	B0327243	B0327243 603493537
40	728	7.1	433	10	BF999622	BF999622 RC2-GN013
41	721	7.1	4128	29	AY418955	AY418955 Mus muscu
42	718	7.0	452	13	BF693745	BF693745 BY693745
43	718	7.0	3721	11	BC032414	BC032414 Homo sapi
44	713	7.0	398	10	BG009206	BG009206 IL5-GN024
45	711.5	7.0	806	12	BG782985	BG782985 SEAMUC002
46	708	6.9	450	10	BG012275	BG012275 RC2-GN028
47	704	6.9	770	12	BG619827	BG619827 602618001
48	690	6.8	358	10	BF771579	BF771579 IL5-IT002
49	689	6.7	6838	29	AY418021	AY418021 Pan trogl
50	688	6.7	798	12	BG782977	BG782977 SEAMUC002
51	684	6.7	392	10	BF994869	BF994869 QV0-GN021
52	683	6.7	6848	29	AY418020	AY418020 Homo sapi
53	675.5	6.6	369	10	B8181604	B8181604 CM3-HT063
54	670	6.6	770	12	BG780526	BG780526 SEAMUC000
55	665	6.5	412	14	H72144	H72144 YF99C05.r1
56	658	6.4	382	10	BF368046	BF368046 RC5-GN004
57	657.5	6.4	837	12	BG786173	BG786173 SEAMUC006
58	654	6.4	488	14	R92857	R92857 YQ13e07.r1
59	652.5	6.4	410	14	H72132	H72132 YF99a05.r1
60	646	6.3	477	13	BQ366017	BQ366017 RC0-GN009
61	645.5	6.3	4131	29	AY418954	AY418954 Pan trogl
62	635.5	6.2	423	13	BQ366619	BQ366619 MR0-GN017

63	631.5	6.2	1815	29	AY398787	AY398787 Homo sapi
64	630	6.2	792	14	CD351453	CD351453 UI-M-G10-
65	629	6.2	442	13	BY360080	BY360080 BY360080
66	626.5	6.1	733	14	CF540496	CF540496 UI-M-GV07
67	623	6.1	324	10	BF368870	BF368870 RC6-GN00
68	622.5	6.1	1815	29	AY398789	AY398789 Mus muscu
69	618	6.0	2098	11	BC032053	BC032053 Homo sapi
70	614	6.0	755	14	CD351379	CD351379 UI-M-G10-
71	611	6.0	848	13	BF728191	BF728191 BX728191
72	610	6.0	367	14	RG7816	RG7816 Y124f10.r1
73	607.5	5.9	671	14	CD351340	CD351340 UI-M-G10-
74	605	5.9	974	14	CF592712	CF592712 AGENCOURT
75	600	5.9	422	14	R33004	R33004 Yn7h12.r1
76	600	5.9	805	14	CF537892	CF537892 UI-M-G10-
77	599.5	5.9	381	14	R30986	R30986 Yh60d01.r1
78	598	5.9	753	14	CD803516	CD803516 UI-M-GV0-
79	597	5.8	336	14	HL3496	HL3496 Y115f07.r1
80	595	5.8	362	10	BF997406	BF997406 PML-GN018
81	591	5.8	3392	11	AK044597	AK044597 Mus muscu
82	589.5	5.8	779	12	BY523794	BY523794 603052095
83	588.5	5.8	342	10	BG008596	BG008596 PM4-GN030
84	588	5.8	658	9	AL778052	AL778052 AL778052
85	581	5.7	3394	11	AK004739	AK004739 Mus muscu
86	579	5.7	657	13	BU705790	BU705790 UI-M-F00-
87	578.5	5.7	1013	13	BUS19205	BUS19205 AGENCOURT
88	577.5	5.7	742	14	CF744242	CF744242 UI-M-GV0-
89	575.5	5.6	427	10	BG009198	BG009198 RCL-GN019
90	573	5.6	772	14	CB524782	CB524782 UI-M-FY0-
91	573	5.6	834	14	CB523447	CB523447 UI-M-GH0-
92	572	5.6	589	10	BF422341	BF422341 Lr CA12.0
93	571	5.6	310	10	BE181601	BE181601 CN3-HT063
94	571	5.6	1201	13	EX439805	EX439805 BX31808
95	570.5	5.6	1201	13	EX420707	EX420707 BX420707
96	570	5.6	311	12	BI051224	BI051224 CM4-GN036
97	570	5.6	537	13	EX301808	EX301808 BX301808
98	570	5.6	537	13	EX303884	EX303884 BX303884
99	570	5.6	537	13	EX303885	EX303885 BX303885
100	570	5.6	930	13	EX327882	EX327882 BX327882

RESULT 1	AY405591	3288 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	Homo sapiens HCM2275 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION	AY405591.1 GI:39761565				
ACCESSION	AY405591				
VERSION	GSS.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
ORGANISM	1 (bases 1 to 3288)				
REFERENCE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perrieria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
AUTHORS	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
TITLE	Science 302 (5652), 1960-1963 (2003)				
JOURNAL	14671302				
PUBMED	2 (bases 1 to 3288)				
REFERENCE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perrieria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
AUTHORS	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
TITLE	Direct Submission				
JOURNAL	Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				

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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	<1..>3288
	/locus_tag="HCM2275"
ORIGIN	
Alignment Scores:	
Pred. No.:	0
Score:	5409.50
Percent Similarity:	90.42%
Best Local Similarity:	90.33%
Query Match:	52.94%
DB:	29
	Length: 3288
	Matches: 1000
	Conservative: 1
	Mismatches: 87
	Indels: 19
	Gaps: 1
	US-09-977-053-6 (1-1842) x AY405591 (1-3288)
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DB	1 ATGTGGCCTCGCTGGCTTTTGTCTGGGGTCTGGCGCTCGTTTGGGGCTGGCGACC 60
QY	21 PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro 40
DB	61 TTTCAGCAGATGTCCTGGCGCAATTTTCAGCTTCGGCTNNNNNNNNNNNNNNNNNN 120
QY	41 GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg 60
DB	121 NNN 180
QY	61 ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu 80
DB	181 NNN 240
QY	81 ArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArg 100
DB	241 CGCTGGAGCTTGTCTCTCTGGTGGATGATTCGTCCAGCGTGGCGGAGTCACTTCGC 300
QY	101 SerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThr 120
DB	301 AGCGAGCTCATGTTCTGTCGCAAGCTGCTCCGCTCTCCCGTGGTGGCCACGCGCAG 360
QY	121 ArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIle 140
DB	361 CGCGTGGCCTATGTCGACCTTCTGTCACAGAACTACGTGTCGTCGCGCGCGATCATC 420
QY	141 SerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluIleProAlaIle 160
DB	421 TCACCCCGCGCGCGCGCGCAAGTGGCGCTGCTCTCCAGAGATCCCTGCCATC 480
QY	161 SerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeu 180
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DB	601 GGGGGAGACCTTAGACCAATTCAGCGTCACTCGAGATTCAGAGATTCAGATCTTCACT 660
QY	221 PheGlyIleTTPGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu 240
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Qy 281 CysAspGluGlyAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr 300
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Qy 341 IleProCysProAspGluHisThrSerProGlySerThrSerProGluAspCys 360
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Qy 941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
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Qy 961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGlu 980
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DEFINITION Pan troglodytes HCM2275 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION AY405592
VERSION AY405592.1 GI:39761566
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 3009)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3009)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment
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Score: 5060.50 Matches: 928
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Best Local Similarity: 91.52% Mismatches: 64
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DB: 29 Gaps: 1

US-09-977-053-6 (1-1842) x AY405592 (1-3009)

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QY 134 ValProArgValAspTyrIleSerThrArgAlaArgGlnHisLysCysAlaLeuLeu 153
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Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 3288)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

source

1..3288

/organism="Mus musculus"

/mol_type="genomic DNA"

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gene

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 3288

Score: 4803.50 Matches: 879

Percent Similarity: 84.74% Conservative: 76

Best Local Similarity: 77.99% Mismatches: 139

Query Match: 47.01% Indels: 33

DB: 29 Gaps: 5

US-09-977-053-6 (1-1842) x AY405593 (1-3288)

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 Db 1 ATGTGTCGCGCTGGCCCTTTTGTGCTGGCTCTGGCACTGGTGTCTGGCTGGACCAAC 60
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 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3171)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL
 REMARK NTH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcdopaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 37 Row: 9 Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction, Similarity but not identity to protein
This clone has the following problem: retained intron.

FEATURES

source

Location/Qualifiers
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ORIGIN

Alignment Scores:

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.79% Indels: 0
DB: 11 Gaps: 0

US-09-977-053-6 (1-1842) x BC030816 (1-3171)

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QY	61	ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu	80
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QY	181	LeuHisAlaArgGluLeuSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn	200
DB	878	CTTCATGCTAGAGAAAACCTCAACAAAAGTTGTATTTCTCATCTGATGGAATTCAT	937

QY	201	GlyGlyAspProArgProIleAlaSerLeuArgAspSerGlyValGluIlePheThr	220
DB	938	GGGGGAGACCCCTAGACCAATTCAGCGTCACTGCGAGATTTCAGGAGTGAGATCTTCAC	997
QY	221	PheGlyIleTropGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu	240
DB	998	TTTGGCATATGCAAGGGAAACATTCAGAGCTGAAATGACATGCTTCCACCCCAAGGAG	1057
QY	241	GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeu	260
DB	1058	GAGCACTGTTACTGCTACACAGATTTTGAAGAAATTTAGGCTTTAGCTGCGCGGCAATG	1117
QY	261	HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerThrLeu	280
DB	1118	CATGAGATCTACTTCTGGGAGTTTATTTCAAGATGATATGGTCCACTGCTCATATCTT	1177
QY	281	CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr	300
DB	1178	TGTGATGAGGCGAGAGACTGCTGTGACCGATGGGAGCTGCAATGTGGGACACACACA	1237
QY	301	GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys	320
DB	1238	GGCCATTTTGAAGTGCATCTGTCAAAAGGGTATTACGGAAAGCTCTGCAGTATGAATG	1297
QY	321	ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys	340
DB	1298	ACAGCTTGGCCATCGGGGACATCAAACTGAAGGCTCCACGAGGAATCAGCAGTGC	1357
QY	341	IleProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAspCys	360
DB	1358	ATTCCATGCTCTGATGAAATTCACCTCTCCACTGGAGACATCCCTCTGAAGACTGT	1417
QY	361	ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla	380
DB	1418	GTCTGCAGAGGGGATACAGGCGCATCTGCCAGACCTGTGAATCTGTCCACTGCCCTGCC	1477
QY	381	LeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla	400
DB	1478	CTGAGCCCTCCGAAATGGTTACTTTATCCAAACACTTGCACCAACCACTTCATATGCA	1537
QY	401	AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuCys	420
DB	1538	GCCTGTGGGGTCCGATGTACCTCGATTTGATCTTGTGGGAGAGCATCATCTTATGT	1597
QY	421	LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis	440
DB	1598	CTACCCAAATGTTTGTGGTCCGGTTCAGAGAGCTTCTGCAGAGTAAAGAACATGTCTCAT	1657
QY	441	LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr	460
DB	1658	CTCCGCGAGCGGAAACATGGCCACATCAGCTGTCTACAGGGGAATGTTATATAGACA	1717
QY	461	ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys	480
DB	1718	ACATGTTGGTCCCTGTGATGAAGGGTACAGACTAGAGGCGAGTGAAGCTTACTTGT	1777
QY	481	GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr	500
DB	1778	CAAGGAAACAGCCAGTGGGATGGCGCAGAACCCCGGTGTGTGGAGCCCACTGTGTCCACC	1837
QY	501	PheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys	520
DB	1838	TTTCAGATGCCCAAGATGTCATATCCCCCAACCTGTGGCAAGCGAGCCAGCCAAA	1897
QY	521	PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu	540
DB	1898	TTTGGGCGATCTGCTATGTAAGTGGCGCCAGGGTTCAATTTATCTGGAGTCAAGAA	1957
QY	541	MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLys	560
DB	1958	ATGCTGAGATGTACCACTTCTGGAAAAATGGAAATGTCGGAGTTCAGGCGAGCTGTGTAA	2017

Qy	561	AspValGluAlaProGlnIleAsnCysProIysAspIleGluAlaLysThrLeuGluGln	580
Db	2018	GACGTGAGGCTCTCAAAATCAATCTCTTAAGACATAGAGGCTAAGACTCTGGAACAG	2077
Qy	581	GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys	600
Db	2078	CAAGATTCTGCCAATGTTACCTGGCAGATTCCAAACAGCTTAAGACAACTCTGGTGAAGAAG	2137
Qy	601	ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal	620
Db	2138	GTGTCAGTCCACGCTTCATCCAGCTTTTACCCACCTTACCTTTTCCCAATTTGGAGATGTT	2197
Qy	621	AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle	640
Db	2198	GCTATCGTATACAGCGCACTGACTATCCGCAACCCAGGCCAGCTGCAATTTTCATATC	2257
Qy	641	LysValIleAspAlaGluProProValIleAspTrpCysArgSerProProProValGln	660
Db	2258	AAGGTTATTGATGCAGAACCACTGTCTATAGACTGGTGCAGATCTCCACCTCCCGTCCAG	2317
Qy	661	ValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGly	680
Db	2318	GTCTCGGAGAGGTACATGCCGCAAGCTGGGATGAGCTCTAGTCTCTCAGCAACTCAGGG	2377
Qy	681	AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr	700
Db	2378	GCTGAAATGGTCATTACCGAAGTCTATACAGAGACCTTTTCCCTCAGGGGAGACT	2437
Qy	701	IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle	720
Db	2438	ATAGTACAGTATACAGGCACCTGACCCCTCAGCCAAATACAGACATGTGATATCCATATT	2497
Qy	721	ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys	740
Db	2498	GTCTATAAAGGTTCTCCCTCGAAATTCATTCACCTGTAATGGGGATTTTATATATG	2557
Qy	741	ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr	760
Db	2558	ACTCCAGATAATATCTGGTGCATCTGATCACTTAATCTGTTGGAGGCTATGATTCACA	2617
Qy	761	GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyr	780
Db	2618	GAAGGGTCTACTGACAAAGTATTATTTGCTTATGAGATGGCTCTGGAACCAACATAT	2677
Qy	781	ThrThrGluTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe	800
Db	2678	ACCACTGAATGCCAGACTGTGCCAAAAACGTTTTCGAAACCAACGCGGTTCCAGTCCTTT	2737
Qy	801	GluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGlu	820
Db	2738	GAGATGTTCTCAAGACGCTGCTTGATGATGACAGATCTGATGAGAGATTTTCTGAA	2797
Qy	821	AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle	840
Db	2798	GCATTTGAGACGACCTCGGAAAAAATGGTCCCATCTTTTGTAGTGATGCAGAGACATT	2857
Qy	841	AspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr	860
Db	2858	GACTGCGAGACTGGAGGAGAACTGCACCAAAAAATAATTCCTAGATAATATATGACTAT	2917
Qy	861	GluAsnGlyPheAlaIleGly	867
Db	2918	GAATAATGGCTTTGCATTTGGT	2938
RESULT 5	AK052699	2736 bp mRNA linear HTC 20-SEP-2003	
LOCUS	AK052699	Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched	
DEFINITION	AK052699.1	library, clone:D630026K16 product:polydomain protein, full insert	
ACCESSION	AK052699	sequence.	
VERSION	AK052699.1	GI:26342892	
KEYWORDS	HTC; CAP trapper.		

SOURCE ORGANISM

Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

REFERENCE

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

REFERENCE

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsuoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multipipillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2736)

REFERENCE

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

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Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

Location/Qualifiers

1. 2736

FEATURES

source

Qy	1388	GlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyrSerCys	1407	GluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAsnValAspGlySer	1767
Db	482	CAGTCCAAACCCATGACAGGACCCAGGCTGGTGGATGAACATAACATCATACAGTTGT	541	1562	GAGTGTGAGTCGGCTCGGACTGTAGTAGCAGCAGCTCTCTGCTGCAACACCAACGATCC
Qy	1408	LysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSerThrGlyPheAsn	1427	1768	TyrIleCysSerCysValProProTyrThrGlyAspGlyLysAsnCysAlaGluProIle
Db	542	AAATGTTCGGCAGGATTTTCAGGCGCCAGGTTGAGACAGAACAGCCCTTCGGGTTTTAAC	601	1622	TACATATGCTGTGCGAGCCCGCTGACGCGGAGATGGGAAAACCTGTGCAGAACTGTT
Qy	1428	LeuAspPheGluValSerGlyIleTyrValMetLeuAspGlyMetLeuProSer	1447	1788	LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTyrThrVal
Db	602	CTGATTTTGAAGTTTCTGGCATCTACCGGTACGTTCTCTAGATGGAGTGCTTCCAACA	561	1682	AAATGTAAAGGCTCCAGAAAATCCAGAGAAATGCCACTCTTTGGGCAAGATTTATAGCGTG
Qy	1448	LeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspMetAsnTyrGlyThr	1467	1808	GlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeuMetGlyValThrLysIle
Db	662	CTCCATGCCATAACCTGTGCTTCTGGATGAAGTCTCTGATGTCAATCAATACGGAACG	721	1742	GCTGCTGAAGTCACATTTTCTGTGGAAGAAGGCGCACCTGCTGGAGTGGAGAAAATC
Qy	1468	ProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuThrAspTyrAsn	1487	1828	ThrCysLeuGluSerGlyGluTyrAsnHisLeuIleProTyrCys
Db	722	CCCATCTCTATGCACTGGAGGGCAACAAGAACACACCTCTCTCTGACTGATTACAAAT	781	1802	ACGTGTTTGGAGTCTGGCGAGTGGGATCACTCAGACCATCTCTGT
Qy	1488	GlyTrpValLeuTyrValAsnGlyArgGluLysIleThrAsnCysProSerValAsnAsp	1507	AK035333	3242 bp mRNA linear HTC 18-SBP-2003
Db	782	GCTGGGTTCTTATGTGATGGAAGGAAGAAAGATCACCACTGCCCTCTGTAAATCAT	841	AK035333.1	GI:26330611
Qy	1508	GlyArgTrpHisHisIleAlaIleThrTrpThrSerAlaAsnGlyIleTrpLysValTyr	1527	KEYWORDS	HTC; CAP trapper.
Db	842	GGCATTTGGCATCATATATGCAATCATCATGGAACAGCACTGGTGGAGCCTGGAGGCTCTAT	901	SOURCE	Mus musculus (house mouse)
Qy	1528	IleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeuProIleProGly	1547	ORGANISM	Mus musculus
Db	902	ATAGACGGGGAGCTATCTGACAGTGTGTACTGCGCTCTCTGTGGCAAAAGCCATACCTGCT	961	REFERENCE	1 Carninci, P. and Hayashizaki, Y.
Qy	1548	GlyGlyAlaLeuValLeuGlyGlnGluLysLysGlyGlyLysGlyPheSerProAla	1567	AUTHORS	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Db	962	GCTGTGCTATGTTCTTGGCGACAGACGACGACGACGACGACGACGACGACGACGACG	1021	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Qy	1568	GluSerPheValGlySerIleSerGlnLeuAsnLeuTrpAspTyrValLeuSerProGln	1587	MEDLINE	20499374
Db	1022	GAGTCTTTTGGTGGCTCCATAGCCAGCTCAACCTCTGGCACTATGCTCTCTCCACAG	1081	PUBMED	11042159
Qy	1588	GlnValLysSerLeuAlaThrSerCysProGluGluLeuSerLysGlyAsnValLeuAla	1607	REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Db	1082	CAGGTGAAGTCTGCTGGCAGCTCTCCCGCAGAGGAACCTGCTGGGGAACGTTGTAGCA	1141	AUTHORS	Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Qy	1608	TrpProAspPheLeuSerGlyIleValGlyLysValLysIleAspSerLysIlePhe	1627	TITLE	Normalizing and subtracting of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Db	1142	TGGCTCTGATTTGCTATCGGGATCACGGGAGGTGAAGTTGATTCACGACGATCTTC	1201	MEDLINE	20499374
Qy	1628	CysSerAspCysProArgLeuGlyGlySerValProHisLeuArgThrAlaSerGluAsp	1647	PUBMED	11042159
Db	1202	TGCTCTGATTTGCCATCTTTAGAGGGTCCGTGGCTCTACCTGAGACCTGCATCAGGAGAT	1261	REFERENCE	4 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Qy	1648	LeuLysProGlySerLysValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsn	1667	AUTHORS	Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Db	1262	CGAAAGCCAGGTTCANAGTCAAGTCTGTCTGTGACCCCGGCTTCAGATGTCGGGAT	1321	TITLE	Normalizing and subtracting of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Qy	1668	ProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGluArg	1687	MEDLINE	20530913
Db	1322	CCGGTGCAGTATGTTTGAACCAAGGCGAGTGGTCAAGCCACTCTCTCAGTCAACGCG	1381	PUBMED	11076861
Qy	1688	IleSerCysGlyValProProLeuGluAsnGlyPheHisLeuAlaAspPheTyr	1707	REFERENCE	5 The RIKEN Consortium and the RIKEN Genome Exploration Research
Db	1382	ATTGCTGTGGGCTCCCTCCACCTTCGAGATGGCTTCTATTACGCGGAGACCTCCAT	1441	AUTHORS	Group Phase I & II Team.
Qy	1708	AlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArg	1727	TITLE	Functional annotation of a full-length mouse cDNA collection
Db	1442	GCTGCGACGACAGTACCTATCAGTGCACCAAGTGGCTACTACCTGTGGGTGACTCCAGA	1501	MEDLINE	20530913
Qy	1728	MetPheCysThrAspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspValAsp	1747	PUBMED	11076861
Db	1502	ATGTTCTGTACGACCAACCGGAGGCTGGAAAGGCAATTTCTCCATCTCTGCTGATTTGAT	1561	REFERENCE	6 Nature 409, 685-690 (2001)

Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Haramoto, K., Hiroaka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Takagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

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cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

CS

ORIGIN

Alignment Scores:

Argument Scores:					
Pred. No.:	2.88e-158	Length:	3242		
Score:	2023.50	Matches:	370		
Percent Similarity:	90.57%	Conservative:	24		
Best Local Similarity:	85.06%	Mismatches:	40		
Query Match:	19.80%	Indels:	1		
DB:	11	Gaps:	1		

US-09-977-053-6 (1-1842) x AK035333 (1-3242)

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 239 ARGTGGTCGCGCTGGCCCTTTTGTGTGGGCTCTGGCCTGGTGTGAGGCTGGACCAAC 298
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320 CysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSer 339
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2225 GACAGGCTGGCTCAAACTCAATATCTCTGGCTGTGGCTCCAGAGTCTCGAATT 2284
375 ----- 375
2285 AAAATGGTGTGCCACCACTCCAGGCTGGTGTCTTCTTCAATTATTTCAATGTTATCTTAATA 2344
375 ----- 375
2345 AGAGAGAAAAATATTAATTATCTATGGAAGTCAAGAACCAAGGACTAGGGTTATATAGCT 2404
375 ----- 375
2405 TGTGGCAGAGCATGTGCTTAGCATACCTGAGATCTCTGGACTCAGCACCAAGCTGAGGG 2464
375 ----- 375
2465 GCAGGGGAAGGGTGGGAAATCTTACATTTATCTATGCCAGTATCAAAATAAAACTCTTTTG 2524
375 ----- 375
2525 AAGCTTAAAAAGTAGTGTGTAGACTATATTAATTTTAAATGGCTAGTACATATCTTCCAG 2584
375 ----- 375
2585 GAGTCATATGTAAAGGTTCTCCCTCAAAACACTCTTAGAAATCAGATGATCAATATAGGA 2644
375 ----- 375
2645 AAGCTATAGGGAAATATGATGATAAATATAGATGTACATATGTAGACAGACAGACAGAT 2704
375 ----- 375
2705 GCATGCTTTGGTAAATAAACTGAAGCAATGCAATTCGTTCCGTAGACAAACATCTGACTT 2764
376 -----ValHisCysProAlaLeuLysProProGluAan 386
2765 TTTTGTCTCTCTCTGTAATTTAGTTGTCACCTGTCTGCTGCTGAGGCTCTGAAAT 2824
387 GlyTyrPheIleGlnAanThrCysAanHisPheAanAlaAlaCysGlyValArgCys 406
2825 GCTTTTTTATACAAACACTTGCAGAAACCACTTCAATGCGCTGTGGGTCGAGTGT 2884
407 HisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuProAsnGlyLeuTrp 426
2885 CGCCCGGGCTTTGACCTTTGTGGGAAGCAGCATTCATTTGTGTCAACCCCAATGGTTGTGG 2944
427 SerGlySerGluSerTyrCysArg 434
2945 TCTGGGACAGAAAGCTTCTGCAGA 2968
```

RESULT 9

BX390270

LOCUS

DEFINITION BX390270 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA

clone CS0D1010V21 5-PRIME, mRNA sequence.

ACCESSION BX390270

VERSION BX390270.1 GI:30463533

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 906)
COMMENT Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4991.r for more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BAG025ZE09_CS02373_1&cluster=4991.r.
 Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0BAG025ZE09_CS02373_1.
FEATURES Location/Qualifiers
 source
 1..906
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1010YG21"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
 Alignment Scores:
 Pred. No.: 3 44e-131 Length: 906
 Score: 1690.00 Matches: 294
 Percent Similarity: 98.01% Conservative: 1
 Best Local Similarity: 97.67% Mismatches: 6
 Query Match: 16.54% Indels: 0
 DB: 13 Gaps: 0
 US-09-977-053-6 (1-1842) x BX390270 (1-906)
 QY 243 CysTyrLeuHisSerPheGluPheGluAlaLeuAlaArgAlaLeuHisGlu 262
 DB 2 TGTACCTGCTACACAGTTTGAAGAAATTGAGGCTTTAGCTCGCGGCAATGTCATGAA 61
 QY 263 AspLeuProSerGlySerPheLeuGlnAspMetValHisCysSerTyrLeuCysAsp 282
 DB 62 GATCTACCTTCTGGGAGTTTATTCAAGATGATATGGTCCACTCATCTTTGTGAT 121
 QY 283 GluGlyLeuAspCysCysAspArgMetGlySerCysLeuGlnGlyThrHisThrGlyHis 302
 DB 122 GAAGCGAGAGACTGCTGTGACCAATGGAGAGTGCATATGGGACACACAGCCAT 181
 QY 303 PheGluCysLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 322
 DB 182 TTTGAGTGCATCTGTGAAAAGGGGTATTACGGAAAGGCTGTCAGATGATGAAATGCACAGCT 241
 QY 323 CysProSerGlyThrTyrLeuProGluGlySerProGlyGlyLeuSerSerCysLeuPro 342
 DB 242 TGCCCATCGGGGACATACAAACCTGAAGGCTCACAGAGGATCAGAGTTCATTTCCA 301
 QY 343 CysProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCysValCys 362
 DB 302 TGTCTGTATGAAATCACACCTCTCCACTCGGAGACACATCCCTCGAAGACTGTGTCTGC 361
 QY 363 ArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuLys 382
 DB 362 AGAGAGGGATACAGGGGCATCTGGCCAGACCTGTGAACCTGTCCACTGCGCCCTGCGCTGAAG 421

383 ProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAlaLys 402
 DB 422 CTCTCCGAAATGGTTACTTTATCCAAACACTTTCGACACACACCTTCATGCGAGCTGT 481
 QY 403 GlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuPro 422
 DB 482 GGGGTCGATGTCACCCCTGGATTGATCTTGTGGGAAGCAGCATCATCTTATGCTACCC 541
 QY 423 AsnGlyLeuTyrSerGlySerGluSerTyrCysArgValArgThrCysProHisLeuArg 442
 DB 542 AATGGTTTGTGGTCCAGTTTCAGAGAGCTACTGAGAGTAGAACAATGCTCTCATCTCCGC 601
 QY 443 GlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThrThrCys 462
 DB 602 CAGCCGAAACATGGCCACATCAGCTGTTCTACAGGGGAATGTTATATAGACACATGT 661
 QY 463 LeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCysGlnGly 482
 DB 662 TTGGTTGCTGTGATGATGAGGTACAGACTAGAGGCGGTGATAAGCTTACTTGTCAAGGA 721
 QY 483 AsnSerGlnTyrAspGlyProGluProArgCysValGluArgHisCysSerThrPheGln 502
 DB 722 AACAGCCAGTGGATGGGCGCAGAACCCCGGTGTGTGAGCGCCACTGTTCACCTTCAG 781
 QY 503 MetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPheGly 522
 DB 782 ATGCCCAAGATGTTCATATATCCCCACACTGTGGCAGCAGCCAAATTTGGG 841
 QY 523 ThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGluMetLeu 542
 DB 842 AGCATCTGTATGATGAGTTGCGCCAGGTTCATTTATTTTGGAGTCAAAGGATTCGTCG 901
 QY 543 Arg 543
 DB 902 AGA 904

RESULT 10
 BX356254 1201 bp mRNA linear EST 05-MAY-2003
 LOCUS BX356254 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1010YG21 5-PRIME, mRNA sequence.
 ACCESSION BX356254
 VERSION BX356254.1 GI:30380055
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4991.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1010AD11QPI&cluster=4991.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1010AD11QPI.
FEATURES Location/Qualifiers
 source
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1010YG21"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)


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Db      421  GAAATTCATTACACCTGTAAATGGGATTTTATATGCACTCCAGATAATCTGGAGTC 480
Qy      748  AenCysLeuThrCysLeuGluGlyTyrAspPheThrGluGlySerThrAspLysTyr 767
Db      481  AACTGTACATTAATCTGCTTGGAGGGCTATGATTTTACAGAGGGTCTACTGCAAGTAT 540
Qy      768  TyrCysAlaTyrGluAspGlyValTTPlysProThrTyrThrThrGluTTPProAspCys 787
Db      541  TATTGTGCTTATGAGATGGCGTCTGGAAACCAACATATACCACTGATGGCCAGACTGT 600
Qy      788  AlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGluMetPheTyrLysAlaLa 807
Db      601  GCCAAAAACGTTTTCMAAACCAACGGGTTCAAGTCCCTTTGAGATGTTCTACAAAGCAGCT 660
Qy      808  ArgCysAspAspThrAspLeuMetLysLysPheSerCysGluAlaPheGluThrThrLeuGly 827
Db      661  CGTTGTGATGACACACATCTGATGAAGAAGTTTCTGAAGCATTTGAGACGCCCTGGGA 720
Qy      828  LysMetValProSerPheCysSerAsp 836
Db      721  AATATGGTCCCATCATTTTGTAGTGAT 747

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RESULT 13
AL706149
LOCUS   AL706149 738 bp mRNA linear EST 04-SBP-2003
DEFINITION DKF2p686E243 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION DKF2p686E243 5', mRNA sequence.
VERSION AL706149
KEYWORDS AL706149.1 GI:19689504
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 738)
AUTHORS Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
No 81 sequence available.
This clone (DKF2p686E243) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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FEATURES

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source Location/Qualifiers
1..738
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p686E243"
/dev_stage="adult"
/clone_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

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ORIGIN

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Alignment Scores:
Pred. No.: 1.69e-103 Length: 738
Score: 1359.00 Matches: 238
Percent Similarity: 98.36% Conservative: 2
Best Local Similarity: 97.54% Mismatches: 4
Query Match: 13.30% Indels: 0
DB: 9 Gaps: 0

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US-09-977-053-6 (1-1842) x AL706149 (1-738)
Qy      1253  PheLysCysGluCysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGlu 1272
Db      3  TTCAATTTGTGAGTTCAGTTCAGGTTTACAGGTCGCGGTCGTGAGGAAATATATATAG 62
Qy      1273  CysSerSerProCysLeuAsnLysGlyLysCysValAspGlyValAlaGlyTyrArg 1292
Db      63  TGTAGCTCCAGTCCTTGTGTTTAAATAAAGGAATCTGTGTGATGCTGTGGCTGGCTATCGT 122
Qy      1293  CysThrCysValLysGlyPheValGlyLysHisCysGluThrGluValAsnGluCysGln 1312
Db      123  TGCACATGTGTGAAGAGATTTGTAGGCTTCGATTTGTGAAGCAGAAATCNMTGAATGCCAG 182
Qy      1313  SerAsnProCysLeuAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysVal 1332
Db      183  TCAACCATGCTTAAATAATGCGTCTGTGAAGACCAAGGTTGGGGGATTTCTTGTGCA 242
Qy      1333  CysProProGlyPheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGln 1352
Db      243  TGCCCACTCGATTTTGGGTACCGATGTGAAAGAACGTCGATGAGTGTCTCAGTCAG 302
Qy      1353  ProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAla 1372
Db      303  CCATGCAAAATGGAGCTACCTGTAAAGACGTCCTCAATAGCTTCAGATGCTGTGTGCA 362
Qy      1373  AlaGlyPheThrGlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCys 1392
Db      363  GCTGGCTTTCACAGGATCACCTGTGAATTAACATCAATGAATGTCACTCAATCCATGT 422
Qy      1393  ArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGly 1412
Db      423  AGAAATCAGCCACATCTGTGTGATTAATTAATTCATACAGTTGTAAATGTCCAGCAGGA 482
Qy      1413  PheSerGlyGlnArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluVal 1432
Db      483  TTTTCAGGCAAAAGGTGTGAACAGACAGCTACAGGCTTTAAACGCTTTAAGAGTT 542
Qy      1433  SerGlyLysTyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThr 1452
Db      543  TCTGGTATCTATGATGATGATGCTAGTGGCTCTCCATCTCTCATGCTCTTAACC 602
Qy      1453  CysThrPheTrpMetLysSerSerAspMetAsnTyrGlyThrProIleSerTyrAla 1472
Db      603  TGTACCTCTCTGATGAATCTCTGACGACATGAATGATGAAACCAACCAATCTCTATGCA 662
Qy      1473  ValAspAsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyr 1492
Db      663  GTTGATAACGGCAGCAGCAATACCTCTCTGACTGATTATAACGGCTGGGTTCTTTAT 722
Qy      1493  ValAsnGlyArg 1496
Db      723  GTGAATGGCAGG 734

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RESULT 14
AL706149
LOCUS   AL706149 801 bp mRNA linear EST 02-AUG-2002
DEFINITION AL706149 Homo sapiens cDNA clone PLACE1006157 5', mRNA
ACCESSION AL706149
VERSION AL706149.1 GI:10997819
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 801)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai

```


Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5' - & 3' - end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source
 1..801
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="PLACE1006157"
 /tissue_type="placenta"
 /clone_lib="PLACE1"
 /note="Vector: pMB18SFL3"

ORIGIN
 Alignment Scores:
 Pred. No.: 8,31e-99 Length: 801
 Score: 1304.00 Matches: 247
 Percent Similarity: 91.18% Conservative: 1
 Best Local Similarity: 90.81% Mismatches: 16
 Query Match: 12.76% Indels: 8
 DB: 9 Gaps: 0

US-09-977-053-6 (1-1842) x AUI37280 (1-801)

QY 318 TyrGluCysThraAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyLe 337
 DB 1 TATGAATGACACAGCTTGCCTCCGATCGGGACATACAAACCTGAAGCCCTCACCAGGAGGAATC 60
 QY 338 SerSerCysLeuProCysProAspGluAsnHisThrSerProGlySerThrSerPro 357
 DB 61 AGCAGTGTGATCTCCATGTCCTCGATGAATATCACACCTCTCCATCTGGAAGCACATCCCT 120
 QY 358 GluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHis 377
 DB 121 GAAGACTGTCTGACAGAGGAGATACAGGCGATCTGGCAGACCTGTGACTGTGCTCCAC 180
 QY 378 CysProAlaLeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHis 397
 DB 181 TGCCTTGCCTGAAGCTTCCGAAATGTTTACTTTATCCAAACACCTTGCACCAACCCAC 240
 QY 398 PheAsnAlaAlaCysGlyValArgCysHisProGlyPheAsnLeuValGlySerSerIle 417
 DB 241 TTCATGTGACGCTGTGGGGTCCGATGTACCCCTGGATTTGATCTTGTGGAGACGACATC 300
 QY 418 IleLeuCysLeuProAsnGlyLeuTyrSerGlySerGluSerTyrCysArgValArgThr 437
 DB 301 AUCTTATGTCTACCCATGTTTGTGTGTGGTTCAGAGGACTACTGCAGAGTAAGACA 360
 QY 438 CysProHisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeu 457
 DB 361 TGTCTCTCATCTCGCCAGCGAAACATGGCCACATCAGCTGTGTTCTACAGGGAATGTTA 420
 QY 458 TyrLysThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLys 477
 DB 421 TATAAGCAACATGTTTGTGTGCTGTGTATGAAGGGGTACAGACTAGAGGCGATGATAG 480
 QY 478 LeuThrCysGlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGluArgHis 497
 DB 481 CTTACTTGTTCAGGAACACGCTAGTGGATGGCCAGAACCCCGGTGTGTGGAGGCCAC 540
 QY 498 CysSerThrPheGlnMet-ProLysAspValIleIleSerProHisAsnCys-GlyLysG 517
 DB 541 TGTTCACCTTTTCCAGATGCCCAGAAAGATGTTCATCATATCCCCCACAACCTGTGGGCAAGC 600
 QY 517 InProAlaLysPheGlyThrIleCysTyrVal-SerCys-ArgGlnGlyPheIleLeuSe 536

601 ANCCAGCCAAATTTGGACAGATCTGCTATGTTAAGTTGCCCGCAAGGGTTCAATTTATC 660
 QY 536 rGlyValLysGluMetLeuArgCysThrThrSerGlyLys--TrpAsnValGlyValGln 555
 DB 661 TGGAGTCAAGAAATGCTGATATGTACAACTCTCGGAAATTTGGAATGTCGAGTTCAA 720
 QY 556 -AlaAlaVal-CysLysAspValGluAlaProGlnIleAsnCysProLysAspIleGluA 575
 DB 721 GGAGCTGTGTGTAAGACATGGAAGGNCCTCATCACTGCTCTTAGGNCATTANAG 780
 QY 575 lAlysThrLeuGluGlnGln 591
 DB 781 GGTAAAGACTCNGGAACAG 800

RESULT 15
 BG620159 756 bp mRNA linear EST 18-APR-2001
 LOCUS 602618422F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4732181 5',
 DEFINITION mRNA sequence.
 ACCESSION BG620159 GI:13671530
 VERSION BG620159.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 756)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapusb@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCMI591 row: 1 column: 06
 High quality sequence stop: 738.

FEATURES
 source
 1..756
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4732181"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 79"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggccgctcgcc); Site_2: SfiI
 (ggccattatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.3
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 4,29e-98 Length: 756
 Score: 1295.00 Matches: 250
 Percent Similarity: 98.04% Conservative: 0
 Best Local Similarity: 98.04% Mismatches: 1
 Query Match: 12.67% Indels: 5
 DB: 12 Gaps: 0

US-09-977-053-6 (1-1842) x BG620159 (1-756)

QY 476 AspLysLeuThrCysGlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGlu 495

Db 1 GATAAGCTTACTTGTCAAGGAAACAGCCAGTGGGATGGCCAGAACCCCGGTGTGTGGAG 60
 Qy 496 ArgHisCysSerThrPheGlnMetProLysAspValIleLeuSerProHisAsnGlyGly 515
 Db 61 CGCCACTGTGTTCCACTTTCAGATGCCCAAGATGTCATCATATCCCCCAACACTGTGGC 120
 Qy 516 LysGlnProAlaLysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeu 535
 Db 121 AAGCAGCCAGCCCAATTTGGGACGATCTGCTATGTAAGTGGCCCAAGGGTTCATTTTA 180
 Qy 536 SerGlyValLysGlnMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGln 555
 Db 181 TCTGGAGTCAAGAAATGCTCAGATGTACCACTTCTCGAAATGGAATGTGGAGTTCCAG 240
 Qy 556 AlaAlaValCysLysAspValGluAlaProGlnIleAsnCysProLysAspIleGluAla 575
 Db 241 GCAGCTGTGTAAAGAGCTGGAGCTCTCTCAATCAACTGTCTTAAGCATAGAGGCT 300
 Qy 576 LysThrLeuGlnGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAsp 595
 Db 301 AAGACTCTGGACAGCAAGATCTGCCAATGTACCTGGCAGATTCACACAGCTAAAGAC 360
 Qy 596 AsnSerGlyLysValSerHisValHisProAlaPheThrProProTyrLeuPhe 615
 Db 361 AACTCTGTGTAAGAGGTGTCAGTCCAGCTTCATCCAGCTTTCACCCCACTTACCTTTTC 420
 Qy 616 ProIleGlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSer 635
 Db 421 CCAATTGGAGATGTGTCTATCGTATACACGGCAACTGACCTATCCGGCAACGAGCCAGC 480
 Qy 636 CysIlePheHisIleLysValIleAspAlaGluProProValIleAspTyrCysArgSer 655
 Db 481 TGCATTTTCCATATCAAGTTATTGTATGTCAGAACCCCTGTCTATGACTGTGTGAGATCT 540
 Qy 656 ProProValGlnValSerGlyLysValHisAlaAlaSerTrpAspGluProGlnPhe 675
 Db 541 CCACCTCCCGTCCAGGCTCGGAGAGGTATACATCGCGCAAGCTGGGATGAGCCCTCAGTTC 600
 Qy 676 SerAspAsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPhe 695
 Db 601 TCAGACAACCTCAGGGCTGGAATTTGGTCATTACCAAGAGTATACACAGGAGACCTTTTC 660
 Qy 696 ProGln-GlyGluThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgTh 715
 Db 661 CCTCAAGGGGAGACTATGATGATGATATACAGC-ACTGACCCCTCAGGCATTAACAGGAC 719
 Qy 715 r-CysAspIle-HisIleVal-IleLysGlySerPro 726
 Db 720 CATGTGATATCCCATATTGTCCATAAAGGTTCTCCG 756

RESULT 16

EG434540 829 bp mRNA linear EST 14-MAR-2001
 LOCUS 602506592P1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4603823 5',
 DEFINITION mRNA sequence.

ACCESSION EG434540

VERSION EG434540.1 GI:13341046

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 829)

NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: scapbs@email.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCM1338 row: g column: 24

High quality sequence stop: 676.

Location/Qualifiers

FEATURES

source

1..829
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4603823"
 /lab_host="DH10B (TI phage-resistant)"
 /clone_lib="NIH_MGC_79"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 5,08e-89 Length: 829
 Score: 1188.00 Matches: 240
 Percent Similarity: 94.14% Conservative: 1
 Best Local Similarity: 93.75% Mismatches: 5
 Query Match: 11.63% Indels: 11
 DB: 12 Gaps: 2

US-09-977-053-6 (1-1842) x BG434540 (1-829)

Qy 618 GlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIle 637
 Db 1 GGAGATGTTGCTATCGTATACACGGCAACTGACCTATCCGGCAACGAGCCAGCTGCAIT 60
 Qy 638 PheHisIleLysValIleAspAlaGluProProValIleAspTyrCysArgSerProPro 657
 Db 61 TTCCATATCAAGGTTATTGTATGTCAGAACCCCTGTCTATGACTGTGTGAGATCTCCACCT 120
 Qy 658 ProValGlnValSerGlyLysValHisAlaAlaSerTrpAspGluProGlnPheSerAsp 677
 Db 121 CCCTCCAGGCTCTCGAGAGGTATACATCCGCAAGCTGGGATGAGCCTCAGTTCTCAGAC 180
 Qy 678 AsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGln 697
 Db 181 AACTCAGGGCTGGAATTTGGTCAATACCAAGAGTATACACAGGAGACCTTTCCCTCAA 240
 Qy 698 GlyGluThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAsp 717
 Db 241 GGGGAGACTATAGTATACAGTATACAGCCACTGACCCCTCAGGCATTAACAGGACATGTGAT 300
 Qy 718 IleHisIleValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAsp 737
 Db 301 ATCCATATTGTTCATAAAGGTTCTCCCTGTGGAATTCATTCACACCTGTAAATGGGAT 360
 Qy 738 PheIleCysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyr 757
 Db 361 TTTATATGCACTCCAGATAATACTGGAGTCAACTGTACATTAACTTGCTTGGAGGGCTAT 420
 Qy 758 AspPheThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLys 777
 Db 421 GATTTCACAGAGGGTCT---GACAAGTATTATTGTGCTTATGAAGATGGCGTCTGGAAA 477
 Qy 778 ProThrTyrThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPhe 797
 Db 478 CCAACATATACACTGAATGCCAGACTGTGCCAAAAAAGC-TTTGCAAAACACCGGTTTC 536
 Qy 798 LysSerPheGluMet-PhetylLysAlaAlaArgCysAspThrAspLeuMethylsly 817

Db 537 AGTCTTTGAGATGGTCTACAAAGCAGCTGTTGTGATGACACAGATCTGATGAGAA 596
 Qy 817 sPheSerGluAlaPheGluThrThrLeuGly-LysMetValProSerPheCysSerAspa 837
 Db 597 GTTTTCTGAAGCATTTGAGACGACCTCGGAAATAATGGTCCCATCAATTTGTAGTATG 656
 Qy 837 laGlu-AspIleAspCysArgLeuGlu---GluAsnLeuThrLysLysTyr-CysLeuGl 855
 Db 657 CAGAGGACATTTGACTGCGAGCTGAAGAGAGAAACCTGAGCAAAAAAATTTGCTTAGA 716
 Qy 855 u-TyrAsn-TyrAsp-TyrGlu-AsnGlyPhe 864
 Db 717 AATATAATTTAGACTTATGAATAATGGGTTT 748

RESULT 17
 LOCUS BU929100 701 bp mRNA linear EST 18-OCT-2002
 DEFINITION AGENCOURT_10425850 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:5662868
 5', mRNA sequence.
 ACCESSION BU929100
 VERSION BU929100.1 GI:24117830
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 701)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: c9abps-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLCM2928 row: a column: 12
 High quality sequence stop: 627.

FEATURES

Location/Qualifiers
 1..701
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5662868"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 79"
 /note="Organ: Placenta, Vector: pDNR-LTB (Clontech);
 Site 1: SfiI (ggccattatggcc); Site 2: SfiI
 (ggccattatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGACCGGACGCGCCGACATG-DT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.3
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 3,5e-88 Length: 701
 Score: 1176.50 Matches: 219
 Percent Similarity: 99.10% Conservative: 0
 Best Local Similarity: 99.10% Mismatches: 1
 Query Match: 11.51% Indels: 2
 DB: 13 Gaps: 1
 US-09-977-053-6 (1-1842) x BU929100 (1-701)

Qy 737 AspPheIleCysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGly 756
 Db 3 GATTTTATATGACCTCCAGATATATCTGGAGTCAACTGTACATTAATCTTCTTGGAGGCG 62
 Qy 757 TyrAspPheThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyr 776
 Db 63 TATGATTTACAGAGGGTCTACTGACAACTATTAATTTGTCTTATGAAGATGGCGTCTGG 122
 Qy 777 LysProThrTyrThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGly 796
 Db 123 AAACCAACATATACCACTGAATGGCAGACTGTGGCCAAAAAAGCTTTTGCACCAACCGG 182
 Qy 797 PheLysSerPheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLys 816
 Db 183 TTCAGTCTCTTGAGATGTTCTACAAAGCAGCTCGTTGTGATGACACAGATCTGATGAG 242
 Qy 817 LysPheSerGluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAsp 836
 Db 243 AAGTTTCTGAAGCATTTGAGACGACCTGGGAAAAATGGTCCCATCAATTTGTAGTAT 302
 Qy 837 AlaGluAspIleAspCysArgLeuGluAsnLeuThrLysLysTyrCysLeuGluTyr 856
 Db 303 GCAGAGGACATTTGACTGCGAGCTGGGAGGAGAACCTGACCAAAAAAATATGCTGAGAATAT 362
 Qy 857 AsnTyrAspTyrGluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyValAlaAsnArg 876
 Db 363 AATTATGACTATGAATAATGGCTTGCAATTTGGACAGTGGCTGGCGTGCAGCTAATAGG 422
 Qy 877 LeuAspTyrSerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGly 896
 Db 423 CTGGATTACTCTTACGATGACTCTCTCGACACTGTGCAGAAACAGCCACAGCATCGGC 482
 Qy 897 AsnAlaLysSerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeu 916
 Db 483 AATGCCAGTCTCTCAGGATTAAGAAGTGGCCCATTTATCTGACTATAAATAATTAAGTTA 542
 Qy 917 IlePheAsnIleThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyr 936
 Db 543 ATTTTTAATCATCACAGT---GTGCCATTACCCGATGAAGAAGATGATACCTTTGAATGG 598
 Qy 937 GluAsnGlnGlnArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLysLeuArgThr 956
 Db 599 GAAATCAGCAACGACTCTCTTCAGACATTTGGAAACTATCACAATAAATACTGAAAGACT 658
 Qy 957 Leu 957
 Db 659 CTC 661
 RESULT 18
 LOCUS BG436029 719 bp mRNA linear EST 14-MAR-2001
 DEFINITION 602508809P1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4619402 5',
 mRNA sequence.
 ACCESSION BG436029
 VERSION BG436029.1 GI:13342535
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 719)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: c9abps-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

Plate: L10M1379 row: a column: 03
 High quality sequence stop: 696.

FEATURES
 source
 1..719
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4619402"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_79"
 /note="Organ: placenta; vector: pNMR-LIB (Clontech);
 Site 1: SfII (ggcgctcgcc); Site 2: SfiI
 (ggcattatggc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.3
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 1.64e-85. Length: 719
 Score: 1145.00 Matches: 224
 Percent Similarity: 96.58% Conservative: 2
 Best Local Similarity: 95.73% Mismatches: 8
 Query Match: 11.20% Indels: 6
 DB: 12 Gaps: 0

US-09-977-053-6 (1-1842) x BG436029 (1-719)

Qy 630 SerGlyAsnGlnAlaSerCysIlePheHisIleValIleAspAlaGluProVal 649
 Db 2 TCCGGCAACCGAGCGAGCTGCATTTTCCATATCAAGGTTATTGATGCGAAGCCACTGTC 61
 Qy 650 IleAspTrpCysArgSerProProValGlnValSerGluValIleAlaAlaSer 669
 Db 62 ATACGTGTGTCAGATCTCCACCTCCCGTCGAGTCTCGGAGAGTACATGCCCAAGC 121
 Qy 670 TrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeuValIleThrArgSerHis 689
 Db 122 TGGGATGAGCTTCAGTTCTCAGACAACTCAGGGCTGAATTGGTCAATACCAAGAGTCAT 181
 Qy 690 ThrGlnGlyAspLeuPheProGlnGlyThrIleValGlnTyrThrAlaThrAspPro 709
 Db 182 ACACAAGGAGACCTTTTCCCTCAAGGGGAGACTATAGTACAGTATACAGCCACTGACCCC 241
 Qy 710 SerGlyAsnAsnArgThrCysAspIleHisIleValIleValGlySerProCysGluIle 729
 Db 242 TCAGCATAACAGACAGCATGTATCTCATATGTCATAAAGGTTCTCCCTGTGAATTT 301
 Qy 730 ProPheThrProValAsnGlyAspPheIleCysThrProAspAsnThrGlyValAsnCys 749
 Db 302 CCATTACACCTGTAAATGGGGAATTTATATGCACTCCAGATATATCTGGAGTCAACTGT 361
 Qy 750 ThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySerThrAspLysTyrCys 769
 Db 362 ACATTAACCTCTCTGGAGGGCTATGATTCACAGAAAGGGTCTACTGCAAGTATTATTGT 421
 Qy 770 AlaTyrGluAspGlyValTrrPLeuProThrTyrThrThrGluTrrProAspCysAlaLys 789
 Db 422 GCTTATGAAGATGGCGTCTGAAACCAACATATACCTGAATGCGCAGATGTGCCAANA 481
 Qy 790 LysArgPheAlaAsnHisGlyPheLysSerPheGluMetPheTyrLysAlaAlaArgCys 809
 Db 482 AAACGTTTGCACCAACCGGGTCTCAAGTCTCTTGAAGTGTCTCAAAAGCAGCTCGTTGT 541
 Qy 810 AspAspThrAspLeuMetLysGlyPheSerGluAlaPheGluThrThrLeuGlyLysMet 829
 Db 542 GATGACACAGATCTGATGAAGAGTGTCTGAAGCATTTTGAGCGACCTG-GGAAAAATG 600

Qy 830 ValProSerPheCysSerAspAlaGluAspIleAspCysArgLeuGluGluAsnLeuThr 849
 Db 601 GTCCCATCATTT-TGTAGTGATGCGAGGACATGATGG-AAGATGCGAGGAACTG-AAC 657
 Qy 850 LysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGly 863
 Db 658 AAAAAATATGG-CTAGAATATAATTAATGGA-TATGAAATGGT 697

RESULT 19
 AK045217 1887 bp mRNA linear HTC 20-SEP-2003
 LOCUS Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
 DEFINITION enriched library, clone: B130048F05 product: polydomain protein, full
 insert sequence.
 ACCESSION AK045217
 VERSION AK045217.1 GI:26090780
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
 Suno, N., Ishii, Y., Nakamura, S., Hazama, M., Nishie, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multipillar sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 1887)
 6
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tgami, M., Tagawa, A., Tanaka, T., Takahashi, P., Takaku-Akashira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 JOURNAL

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. Tomohiro Kono (Department of Animal Science, Tokyo University of Agriculture, 1737 Hunko Atsugi City, Kanagawa Prefecture, Japan) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

source
1. .1887
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM DB:B130048F05"
/db_xref="MGI:2410576"
/db_xref="taxon:10090"
/clone="B130048F05"
/tissue types="parthenogenote"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="9.5 days embryo"
misc_feature
1. .1887
/notes="polydomain protein (MGI:1928849, GB|NM_022814, evidence: BLASTN, 100%, match=1346)"

ORIGIN

Alignment Scores:
Pred. No.: 3,97e-83 Length: 1887
Score: 1125.50 Matches: 220
Percent Similarity: 88.97% Conservative: 14
Best Local Similarity: 83.65% Mismatches: 28
Query Match: 11.01% Indels: 1
DB: 11 Gaps: 1

US-09-977-053-6 (1-1842) x AK045217 (1-1887)

QY 1 MetTTPProArgLeuAlaPheCysCysTTPGlyLeuAlaLeuValSerGlyTTPAlaThr 20
Db 314 ATGTGGTGGCGCTGGCTTTTGTGTGGCTCTGGCACTGGTGTGAGTGGACCAAC 373
QY 21 PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro 40
Db 374 TTCAGCGCGTGGCCCTTCGCTCACTTCAGCTTCGGCTGTTCCTGGAGGCTCTCCG 433
QY 41 GlyAlaProGlySerIleProAlaProAlaProGly---AspGluAlaAlaGlySer 59
Db 434 GGGGCTCTGGGCGAGCTGGCGGTACCTCCCGCTCCAGTGGAGGAGGAGCGAGGAGC 493
QY 60 ArgValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSer 79
Db 494 AAAGTGGAGCGCTGGCGCGCGCTTCGGAGCGCGCTGGCGGAGCTGGGAGCTCAGC 553
QY 80 GluArgLeuGluLeuValPheLeuValAspAspSerSerSerValGlyGluValAsnPhe 99
Db 554 GGCAGCGCTGGAGCTCGCTTCCTCGTGGAGCGAGCTGCTCCAGCGCTGGCGCAACCACTTC 613
QY 100 ArgSerGluLeuMetPheValArgGlyLeuLeuSerAspPheProValProThrAla 119
Db 614 CTCAACGAGCTCAAGTTCGTGGCGGAGCTGTGCTCCGACTTCCCGGTGGTGTCCACGCGC 673
QY 120 ThrArgValAlaIleValThrPheSerSerIlyAsnTyrValValProArgValAspTyr 139
Db 674 ACGGCTGTGGCCATCGTCACCTTCTCATCCCAAGAACCAACGTTGGTGGCGCGGTGATTAC 733

QY 140 IleserThrArgArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluLeuProAla 159
Db 734 ATCTCACACCGCGCGCGCCCAACCAACAGTGGCGCTACTCAGCCCGAGATCCCCGCC 793
QY 160 IleserTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIle 179
Db 794 ATCACTACCGCGTGGTGGCACTATACCAAGGGCGCTTCCAGCAAGCGCGCAATC 853
QY 180 LeuLeuHisAlaArgGluLeuSerThrLysValValPheLeuLeuThrAspGlyTyrSer 199
Db 854 CTTGCTCACTTAGAGAAACTCCACCAAGTCATATTTCTCATCAGCGCGCTATTCC 913
QY 200 AsnGlyGlyAspProArgProIleAlaAlaSerLeuArgPheSerGlyValGluLeuPhe 219
Db 914 AATGGCGGAGACCCCGACCTATTTCAGCAGTCGCTTCGGGATTTCCGAGTGGAGATCTTC 973
QY 220 ThrPheGlyIleTTPGlnGlyAsnIleArgGluLeuLeuAspMetAlaSerThrProLys 239
Db 974 ACCTTCGGGATTTGGCAGGGGGAATATCCGGGAAGTGAATGACATGCTTCCACCCCGAAG 1033
QY 240 GluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAla 259
Db 1034 GAAGACATTTGTTACTGCTCCACAGTTTGAAGATTTGAGGCTTTAGCTTCGAGGCG 1093
QY 260 LeuHisGlu 262
Db 1094 TTGCATGAA 1102

RESULT 20
AK087058
LOCUS
DEFINITION
Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030024D18 product:polydomain protein, full insert sequence.
ACCESSION
AK087058
VERSION
AK087058.1 GI:26103990
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
20499374
PUBMED
11042159
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
MEDLINE
20530913
PUBMED
11076861
REFERENCE
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection

Gene Collection (WGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-WGC Project URL: <http://wgc.nci.nih.gov>

Contact: WGC help desk
Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: {Dickson, Mark} mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

ORIGIN

Alignment Scores:			
Pred. No.:	7.7e-76	Length:	2019
Score:	1039.50	Matches:	184
Percent Similarity:	92.00%	Conservative:	0
Best Local Similarity:	92.00%	Mismatches:	0
Query Match:	10.17%	Indels:	16
DB:	11	Gaps:	1

US-09-977-053-6 (1-1842) x BC047729 (1-2019)

251	Qy	GluPheGluAlaLeuAlaAarArgAlaLeuHisGluAspLeuProSerGlySerPheIle	270	
		1	GAATTTGAGGCTTTAGCTCGCGGGCAATTGCATGAAGATCTACCTTCTGGGAGTTTTATT	60
271	Qy	GlnAspAspMetValHisCysSerTyrIleuCysAspGluGlyAspCysCysAspArg	290	
61	Db	CAAGATGATATGGTCCACTGCTCATATCTTTGTGATGAAGCGAAGACTGCTGTGACCGA	120	
291	Qy	MetGlySerCysLysCysGlyThrHisThrGlyHisPheGluCysIleCysGlnLysGly	310	
121	Db	ATGGGAAGCTCCAAATGTGGGACACACACAGGCCAATTTGAGTGCATCTGTGAAGAAGGGG	180	
311	Qy	TyrTyrGlyLysGlyLeuGlnTyrGluCys	320	
181	Db	TATTACGGGAAGGCTCTGCAGTATGATGATGATGATGCGCATACAGCTGATGCGCCACATAACATGAGCTTC	240	
321	Qy	-----ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGln	335	
241	Db	TCGCGCTTGTCTGCCACAGCTGTGCCCATCGGGGACATACAACTGTGAAGGCTCACCCAGG	300	
335	Qy	YGLYIleSerSerCysIleProCysProAspGluAsnHisThrSerProProGlySerThr	355	
301	Db	AGGAATCAGCAGTTGCATTCCATGTCTGTGATGAAATACACACTCTCCACCTGGGAAGCAC	360	
355	Qy	rSerProGlnAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGlnIle	375	
361	Db	ATCCCTCGAAGACTGTGTCTGCAGAGAGGGATACAGGGCATCTGGCCACAGACTGTGAAC	420	

Qy	375	uValHisCysProAlaIeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAs	395
Db	421	TGTCCATGCGCTGCCCTCGAAGCCTCCGAAATGGTTACTTTATCCAAACACTTTGC	480
Qy	395	nAsnHisPheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySe	415
Db	481	CAACCACTTCATAGTCGAGCCTGTGGGGTCCGATGTACCTTGATTTGATCTTGGG	540
Qy	415	rSerIleIleLeuCysLeuProAsnGlyLeuTrpSerGlySerGlySerTyrCysArg	434
Db	541	CAGCNCATCTTATGTCTACCAATGGTTGTGTGTCGGTTCCAGAGGCTACTGCAGA	598
RESULT 22			
LOCUS	BG621817	602619678P1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4733347	5', linear EST 18-APR-2001
DEFINITION		mRNA sequence.	
ACCESSION	BG621817		
VERSION	BG621817.1	GI:13673188	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM			
REFERENCE			
AUTHORS		Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE		Mammalia; Rutheria; Primates; Catarrhini; Hominidae; Homo.	
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/	
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)	
		Contact: Robert Strausberg, Ph.D.	
		Email: rgapbs-remail.nih.gov	
		Tissue Procurement: CLONTECH Laboratories, Inc.	
		cDNA Library Preparation: CLONTECH Laboratories, Inc.	
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
		DNA Sequencing by: Incyte Genomics, Inc.	
		Clone distribution: MGC clone distribution information can be	
		found through the I.M.A.G.E. Consortium/LLNL at:	
		http://image.llnl.gov	
		Plate: LUCM1994 row: 1 column: 20	
		High quality sequence stop: 600.	
FEATURES			
source		Location/Qualifiers	
		1..1035	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:4733347"	
		/lab_host="DH10B (TI phage-resistant)"	
		/clone_lib="NIH_MGC_79"	
		/notes="Organ: placenta; Vector: pDNR-LIB (Clontech);	
		Site 1: SfiI (ggcgctcgcc); Site 2: SfiI	
		(ggcattatggcc); 5' and 3' adaptors were used in cloning	
		as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'	
		and 3' adaptor sequence:	
		5'-ATTCTAGGCGGCGGCGCGGCGCATG-dT(30)BN-3' (where B = A,	
		C, or G and N = A, C, G, or T). Average insert size 1.3	
		kb (Range 0.5-4.0 kb). 15/15 colonies contained inserts	
		by PCR. This library was enriched for full-length clones	
		and was constructed by Clontech Laboratories (Palo Alto,	
		CA). Note: this is a NIH_MGC Library."	
ORIGIN			
Alignment Scores:			
Pred. No.:	2.41e-75	Length:	1035
Score:	1027.50	Matches:	232
Percent Similarity:	63.84%	Conservative:	24
Best Local Similarity:	57.86%	Mismatches:	63
Query Match:	10.05%	Indels:	82
DB:	12	Gaps:	11
US-09-977-053-6 (1-1842) x BG621817 (1-1035)			
Qy	668	AlaserTrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeuValIleThrArg	687
Db	3	GCAAGCTGGATGAGCTCGATGTTCTCAGACAACTCAGGGGCTGAATGGTCAATTCACGA	62


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688 SerHisThrGlnGlyAspLeuPheProGlnGlnGluThrIleValGlnThrAlaThr 707
63 AGTCATACACAGGAGACCTTTTCCCTCAAGGGAGACTATAGTACAGTATACAGCCACT 122

708 AspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLysGlySerProCys 727
123 GRACCCCTCAGGCANTAACAGGACATGTGATATCCATATTCATATAAAGGTTCTCCCTGT 182

728 GluIleProPheThrProValAsnGlyAspPheIleCysThrProAspAsnThrGlyVal 747
183 GAAATTCATTCACACCTGTAAATGGGGATTTATATATGCACTCCAGATAATACCTGGAGTC 242

748 AsnCysThrLeuThrCysLeuGluGlyTyAspPheThrGluGlySerThrAspLysTyr 767
243 AACTGTACATTAATCTGCTTGGAGGGCTATGATTTACAGAGGGTCTACTGACAGTAT 302

768 TyrCysAlaTyrGluAspGlyValTyrPheProThrThrThrGluThrProAspCys 787
303 TATTGTGCTTATGAGATGGCGTCTGGAAACCAACATATACCACTGAATGGCCAGACTGT 362

788 AlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGluMetPheTyrLysAlaAla 807
363 GCCAAAAACGTTTGCNAACCAACCGGTTCAAGTCTCTTTCAGATGTTCTACAAAGCAGCT 422

808 ArgCysAspAspThrAspLeuMetLysLysPheSerGluAlaPheGluThrThrLeuGly 827
423 CGTTGTGATGACACAGATCTGATGAGAGAGTTTCTGACAGCATTTGAGACGACCTGGGC 482

828 --LysMetValProSerPheCysSerAspAlaGluAspIleAspCysArgLeuGluAla 847
483 ACACATGTGTCCCATCATTTAGTAGTATGATGATGATGATGATGATGATGATGATGAT 542

847 snLeuThrLysLys-TyrCysLeuGluTyrAsn-TyrAspTyr-GluAsnGlyPheAlaI 866
543 ACTTGACCAAAACATTAATGCTTAGATATAATATTCATGACTATGACCAATGGCTTTCGAA 602

866 leGlyProGlyGlyTyrGlyAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuA 886
603 TTGGT-----CAATACACATTTCTGGCGCATCGGTAGTTG- 637

886 spThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgS 906
638 -----CGCAAGACTAATCTGGCACAATCACGACTA 668

906 exAlaProLeuSerAspTyrLysIleLysLeuIlePheAenIleThrAlaSerValProL 926
669 CGTTCCCGAACACA-----GTGAGGGCAACCTACGACCAACATAAATCTTATTATCAT 719

926 euProAspGluArgAsnAspThrLeuGluThrGluAsnGlnArgLeuGlnThrL 946
720 TATCC-----ATCAAGTATT 734

946 euGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyrSerPheG 966
735 TAAGGATGGTACACATTAATGTCGG-----ATTAAAGTGT 770

966 InLeuAlaSerGluIle-----LeuIleAlaAspSerAsnSerLeuGluThr 981
771 GCGTGGCACAAGAAATCACTCTACGTGTGACTTACTCCACATTTCTGCGGTGACGCAAC 830

981 hrllys-----LysAlaSerProPheCysArgProGlySerValLeuArgGlyA 997
831 ATAAGAACTGAGATTCAGCAACAGCTCCACTGTGTGCCCCACCGGAAT----- 877

997 rgMetCysVal-AsnCysProLeuGlyThrTyr---TyrAsnLeuGluHisPheThrCys 1015
878 --TCCTGTACCGATGACCCACACAGTACGAGACAACACAGTACGCTGCCACGTCG 935

1016 GluSerCysArgIleGlySerTyr-GlnAspGluGluGlyGlnLeuGluCysLysLeuCy 1035
936 AGT-----GGTGGGTACACAATCCCAAGATGGT----- 963

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1035 sProSerGlyMetTyrThrGluTyrIleHisSerArgAsnIleSerAsp 1051

964 -----TGGAGATTATCCACACAGAGAGATACCTGTAC 996

RESULT 23

BB500305

LOCUS

DEFINITION

musculus cDNA clone D630026K16 3', mRNA sequence.

ACCESSION

BB500305.2 GI:16442292

VERSION

BB500305.2

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 642)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuura,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)

On Jul 26, 2000 this sequence version replaced gi:9489092.

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp

URL: http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayashizaki,Y., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuura,S., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Location/Qualifiers

1. 642

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="D630026K16"

/tissue_type="kidney"

/dev_stage="0 day neonate"

FEATURES

source

[illegible]

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCGCACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGCGAGTTAATAATTAATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I."

ORIGIN

Alignment Scores:
 Pred. No.: 1.6e-72 Length: 673
 Score: 990.00 Matches: 175
 Percent Similarity: 86.61% Conservative: 19
 Best Local Similarity: 78.12% Mismatches: 28
 Query Match: 9.63% Indels: 2
 DB: 10 Gaps: 0

US-09-977-053-6 (1-1842) x BB542219 (1-673)

QY 1045 HisSerArgAsnIleSer-AspCysLysAlaGlnCysLysGln-GlyThrTyrSerTyrS 1064
 DB 6 CATTCAAGAGGGTTCCTTAATGCAAGCTCAGGTGAGCAGGGCCCTTACTCTTCCA 65
 QY 1064 erGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySerA 1084
 DB 66 GTGGGTGGAGACCTGCGAATCGTCTGGTGGTACTTATCAACGGGAATTCGATCCC 125
 QY 1084 xgSerCysLeuSerCysProGluSerThrValIysArgGlyAlaValAsnIleS 1104
 DB 126 GGAGCTGCTCTCTAATGCCAACCACCAACGGTGAAAGAGAGCGGTGGACATCT 185
 QY 1104 erAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCysH 1124
 DB 186 CTGCTTGGAGTGCCTGCGCCAGTGGAGAAATCTCCGTTCTGGGTACACACCTGCT 245
 QY 1124 isProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysP 1144
 DB 246 ACCCTTGCCCTCGAGACTATTACCAACCAATGCAAGGAGAGTCTTCTGCTCGCTGTC 305
 QY 1144 roPheTyrGlyThrProPheAlaGlySerArgSerIleThrGluCysSerSerPheS 1164
 DB 306 CCTTTTATGGAACCTACCAACCATCTGGCGCCACGTCCTCATCAGAGCTGCTCAAGTTTA 365
 QY 1164 erSerThrPheSerAlaAlaGluSerValProAlaSerLeuGlyHisIleL 1184
 DB 366 GCTCTACTTCTCAGCAGCAGAGAGAGATGATGCGCCCTCGTGGCCCTCGACATTC 425
 QY 1184 ysLysArgHisGluIleSerSerGlnValPheHisGluCysPheAsnProCysHisA 1204
 DB 426 AGAACAAGTACGAAGTACGAGTCTTTCAGAAATGCTTCTTAAACCCCTGCCACA 485
 QY 1204 snSerGlyThrCysGlnGluLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrT 1224
 DB 486 ACAGTGAACCTGCAACAGCTGGGGGTGGTGTGTCTGTCTGCCACCTGGATACA 545
 QY 1224 hrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsnG 1244
 DB 546 CAGGCTTAAGTGTGAACAGATATTGATGAATGCAGCTCTCTGCTTGGCTCAATGGTG 605
 QY 1244 lyValCysLysAspLeuValGlyGluPheLeCysGluCysProSerGlyTyrThrGlyG 1264
 DB 606 GAATTTGTAGACCAAGTGTGGGGGATTCAGTGGCAATGTTCATTGGGCTATTTCAGGTC 665
 QY 1264 lnArgCys 1266

Db 666 AAATATGT 673

RESULT 25

BQ717243

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13604 row: b column: 15

High quality sequence stop: 458.

FEATURES

source

Location/Qualifiers

1..998

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6196142"

/sex="male"

/tissue_type="sympathetic trunk"

/dev_stage="adult, 16 yr"

/lab_host="DH10B"

/clone_lib="Lupski sympathetic trunk"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:

Not1; Site 2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-TCGACCCACGCTCCG-3' and

5'-GACATGTTCTAGATCGAGCGCGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.9 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine); available through Life

Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 1.38e-71 Length: 998

Score: 982.50 Matches: 178

Percent Similarity: 90.05% Conservative: 3

Best Local Similarity: 88.56% Mismatches: 2

Query Match: 9.61% Indels: 18

DB: 13 Gaps: 1

US-09-977-053-6 (1-1842) x BQ717243 (1-998)

QY 252 PheGluAlaLeuAlaArgArgAlaLeuHisGluAspLeuProSerGlySerPheLeuGln 271
 DB 1 TTTGAGGCTTTAGCTGCGCGCATTCATGATGATCTACCTTCTGGAGTTTTTATCAA 60
 QY 272 AspAspMetValHisCysSerTyrIleuCysAspGluGlyLysAspCysAspArgMet 291
 DB 61 GATGATATGGTCCACTGCTCATATCTTTGTGATGAAGCAAGGACTGCTGTGACCAATG 120
 QY 292 GlySerCysLysCysGlyThrHisThrGlyHisPheGluCysIleCysGluLysGlyTyr 311
 DB 121 GGAAGCTGCAATGTGGAGCACACACAGCCCATTTTGTGATGTCATCTGTGAAAGGGGTAT 180


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QY 312 TyrGlyLysGlyLeuGlnTyrGluCys----- 320
Db |||||
181 TACGGAAAGGTCGCAGTATGAATGCACAGCTGATGTGCCACATAACATGGACTTCTCC 240
QY 321 -----ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyG1 336
Db |||||
241 GGTCTTCTGCCCCACAGCTTGCCCATCGGGGACATACAACTGAGGCTCACCAGGAG 300
QY 336 YleSerSerCysIleProCysProAspGluAsnHisThrSerProGlySerThrSe 356
Db |||||
301 AATCAGCAGTTGCATTCCATGTCCTGATGAAATCACACCTCTCCACCTGGAGCACATC 360
QY 356 rProGluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuVa 376
Db |||||
361 CCTGAAGACTGTGTCTGCAGAGAGGATACAGGGCATCTGGCCAGACCTGTGAACCTGT 420
QY 376 lHisCysProAlaLeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAs 396
Db |||||
421 CCACTGCCCTGCCCTGAGGCTCCGAAATGGTTACTTTATCCAAACACTTGGACAA 480
QY 396 nHisPheAsnAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySer-S 416
Db |||||
481 CCACTTCAATGCAGCCTGTGGGTCCGATGTCACTCCCTGGATTGTATCTGTGGGAGCAA 540
QY 416 erIleIleLeuCysLeuProAsnGlyLeuTrpSer-GlySerGluSerTyrCysArg 434
Db |||||
541 GCATCCTCTTATGTCTACCCCAATGGTTGTGGGCCCGGTCCAGCAGCTACTGAAGA 597
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Search completed: May 11, 2004, 21:52:43
Job time : 13946.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 10, 2004, 15:48:01 ; Search time 4264.35 Seconds
(without alignments)
3793.447 Million cell updates/sec

Title: US-09-977-053-4

Perfect score: 19973

Sequence: 1 MPRFLAFCCMGLALVSGMAT.....CHCLSSWTGHCNSKRRKTGP 3571

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DBV=xlp
-Q=/cgn2_1/USPTO.spool_p/US09977053/runat_06052004_075944_18296/app_query.fasta_1.5710
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blotsum62
-TRANS=human40.cdi -LIST=100 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09977053@cgn_1_1_484@runat_06052004_075944_18296
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

Result No.	Score	Query	ID	Description
1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*			
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*			
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*			
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*			
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*			
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*			
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*			
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*			
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*			
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11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*			
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*			
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*			
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19:	/cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	ID	Description
1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*			
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*			
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*			
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16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*			
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*			
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*			
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1	19958	99.9	10878	9	US-09-911-842-1	Sequence 1, Appli
2	19958	99.9	10878	14	US-10-150-821-1	Sequence 1, Appli
3	19769	99.0	10674	16	US-10-295-027-429	Sequence 429, App
4	19769	99.0	10674	16	US-10-295-027-1080	Sequence 1080, App
5	19616	98.2	11152	16	US-10-028-248A-7	Sequence 7, Appli
6	19616	98.2	11152	16	US-10-107-782-7	Sequence 5, Appli
7	19566	98.0	11158	16	US-10-028-248A-5	Sequence 5, Appli
8	19566	98.0	11158	16	US-10-107-782-5	Sequence 3, Appli
9	16707	83.6	11230	9	US-09-911-842-3	Sequence 3, Appli
10	16707	83.6	11230	14	US-10-150-821-3	Sequence 21, Appli
11	8427	42.2	6153	9	US-09-898-570-21	Sequence 21, Appli
12	8427	42.2	6153	10	US-09-839-446-21	Sequence 21, Appli
13	7471	37.4	3991	17	US-10-311-623-24	Sequence 24, Appli
14	6452	32.3	3804	9	US-09-764-853-214	Sequence 214, App
15	6452	32.3	3804	9	US-09-764-898-60	Sequence 60, Appli
16	6452	32.3	3804	10	US-09-764-881-21	Sequence 21, Appli
17	6452	32.3	3804	11	US-09-764-875-275	Sequence 275, App
18	6452	32.3	3804	13	US-09-764-881-21	Sequence 21, Appli
19	6452	32.3	3804	13	US-09-764-893-43	Sequence 43, Appli
20	6452	32.3	3804	15	US-10-073-865-43	Sequence 43, Appli
21	6452	32.3	3804	16	US-10-242-747-21	Sequence 21, Appli
22	5848	29.3	7286	11	US-09-984-429-525	Sequence 525, App
23	5485	27.5	3448	13	US-10-302-172-34	Sequence 34, Appli
24	4930	24.7	3262	13	US-10-466-164-29	Sequence 29, Appli
25	4058	20.3	2437	9	US-09-728-952-93	Sequence 93, Appli
26	4045	20.3	2444	9	US-09-728-952-46	Sequence 46, Appli
27	3596	18.0	1952	9	US-09-898-570-19	Sequence 19, Appli
28	3596	18.0	1952	10	US-09-839-446-19	Sequence 19, Appli
29	3133	15.7	2064	10	US-09-822-846-55	Sequence 55, Appli
30	2758	13.8	1493	9	US-09-764-853-396	Sequence 396, App
31	2758	13.8	1493	9	US-09-764-898-132	Sequence 132, App
32	2758	13.8	1493	10	US-09-764-881-79	Sequence 79, Appli
33	2758	13.8	1493	11	US-09-764-875-556	Sequence 556, App
34	2758	13.8	1493	13	US-09-764-881-79	Sequence 79, Appli
35	2758	13.8	1493	13	US-09-764-893-66	Sequence 66, Appli
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37	2758	13.8	1493	16	US-10-242-747-79	Sequence 79, Appli
38	2638	13.2	1652	15	US-10-146-473-17	Sequence 17, Appli
39	2305	11.5	1709	9	US-09-898-570-17	Sequence 17, Appli
40	2305	11.5	1709	10	US-09-839-446-17	Sequence 17, Appli
41	2032	10.2	7313	15	US-10-037-270-259	Sequence 259, App
42	2032	10.2	7313	16	US-10-117-722-259	Sequence 259, App
43	2027	10.1	6951	17	US-10-641-643-1265	Sequence 1265, App
44	2006	10.0	7028	13	US-10-376-774-802	Sequence 802, App
45	1977	9.9	1408	10	US-09-822-846-54	Sequence 54, Appli
46	1822	9.1	10136	13	US-10-016-248-1	Sequence 1, Appli
47	1606.5	8.0	5420	9	US-09-954-456-1172	Sequence 1172, Ap
48	1498	7.5	1892	9	US-09-764-898-49	Sequence 49, Appli
49	1278	6.4	680	9	US-09-764-853-173	Sequence 173, App
50	1278	6.4	680	9	US-09-764-898-122	Sequence 122, App
51	1278	6.4	680	10	US-09-764-881-14	Sequence 14, Appli
52	1278	6.4	680	13	US-09-764-881-14	Sequence 14, Appli
53	1278	6.4	680	13	US-09-764-893-37	Sequence 37, Appli
54	1278	6.4	680	15	US-10-073-865-37	Sequence 37, Appli
55	1278	6.4	680	16	US-10-242-747-14	Sequence 14, Appli
56	1184	5.9	3934	17	US-10-641-643-1066	Sequence 1066, Ap
57	1182	5.9	8010	13	US-10-016-248-3	Sequence 3, Appli
58	1009	5.1	7693	13	US-10-072-012-133	Sequence 133, App
59	1004	5.0	8091	15	US-10-101-510-86	Sequence 86, Appli
60	1004	5.0	8091	15	US-10-356-625-1	Sequence 1, Appli
61	1004	5.0	8091	16	US-10-159-563-322	Sequence 322, App
62	1001	5.0	7596	15	US-10-004-113-57	Sequence 57, Appli
63	1001	5.0	8064	15	US-10-004-113-56	Sequence 56, Appli
64	1001	5.0	8221	12	US-10-152-319A-2167	Sequence 2167, Ap
65	991	5.0	7693	13	US-10-160-497-11	Sequence 11, Appli
66	991	5.0	7693	13	US-10-348-750-11	Sequence 11, Appli
67	990	5.0	7673	9	US-09-815-925-1	Sequence 1, Appli
68	990	5.0	7673	16	US-10-294-006-1	Sequence 1, Appli
69	986.5	4.9	7615	15	US-10-004-113-59	Sequence 59, Appli
70	984.5	4.9	6728	16	US-10-190-115-3	Sequence 3, Appli
71	984.5	4.9	6728	16	US-10-369-072-3	Sequence 3, Appli
72	983	4.9	7332	9	US-09-944-849-1	Sequence 1, Appli

QY 421 LeuProAsnGlyLeuTrpSerGlySerGlySerTyrCysArgValaIgrThrCysProHis 440
DB 1271 CTACCACATGGTTGGTTCGGGTTACAGAGCTACTCGCAGGTAAAGCATGTCCTCAT 1330
QY 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
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QY 501 PheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys 520
DB 1511 TTTTCAGATGCCCAAGATATCATCATATCCCCCACAACTGTGGCAAGCAGCCAGCCAAA 1570
QY 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
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QY 541 MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCysLys 560
DB 1631 ATGCTGAGATGTACCACTTCTGGAAATGGAATGTGGAGTTCAGGCAGCTGTGTGTA 1690
QY 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln 580
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QY 601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620
DB 1811 GTGTGAGTCACGGTTCATCCAGCTTTTACCCACCTTACCTTTTCCAGTTGGAGTGT 1870
QY 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
DB 1871 GCTATGCTATACACGGCAACTGACCTATCCGCAACCCAGCCAGCTGCAATTTTCCATATC 1930
QY 641 LysValIleAspAlaGluProProValIleAspTrpCysArgSerProProValGln 660
DB 1931 AAGGTTTATTGATGCAGAACCCACTGTCATAGACTGGTGACAGTCTCCACCTCCGTCGAG 1990
QY 661 ValSerGluLysValHisAlaAlaSerTyrAspGluProGlnPheSerAspAsnSerGly 680
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QY 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyThr 700
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QY 701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
DB 2111 ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATTAACAGGACATGTGATATCCATATT 2170
QY 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
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QY 861 GluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSer 880
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5711 GAACCAAGTGAAGTGTCTAGTCCGGAATAATAAATGGAATAATATATTTTGAAGTGG 5770
5712 |
1921 LeuThrTrpLeuSerThrAlaSerTrpSerCysAspThrGlyTrpSerLeuGlnGlyPro 1940
1922 |
5771 CTTACCTACCTTTCTACTGTCATCATATTCATGCGATACAGATACAGCTTACAGGGCCCT 5830
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1941 SerIleLeuGluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeu 1960
1942 |
5831 TCATTTATGATGACAGGCTTCTGGCATCTGGACAGAGCCACCTGCTGTCACTC 5890
5832 |
1961 ValPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThr 1980
1981 |
5891 GTCTTCTGTGGAGAACCCACCTGCCATCAAGATGCTGTCTATTACGGGGAATAACTTCACT 5950
5892 |
1981 PheArgAsnThrValThrTrpThrCysLysGluGlyTrpThrLeuAlaGlyLeuAspThr 2000
1982 |
5951 TTCAGGAACACCCGTCACCTTACCTTGCATTCGAAAGAGGCTATATCTTGTGCTTTGACACC 6010
5952 |
2001 IleGluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnGlnCysLeuAlaValSer 2020
2002 |
6011 ATTGAATGCTGCGCCAGCGCAAGTGAAGTAGAGTGACGACGAGTGCCTTGGCTGTCTCC 6070
6012 |
2021 CysAspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGly 2040
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6071 TGTGATGAGCCACCCATTTGTGGACCAACGCTCTCCAGAGAGTGCCTCCATCGCTTTTGA 6130
6072 |
2041 AsnIleAlaPheTrpThrCysSerAspGlyTrpSerLeuAlaAspAsnSerGlnLeuLeu 2060
2061 |
6131 GACATTTGCCATTTCTACTGCTCTGATGTTTACAGCTTACGACCAATTCCTCCAGCTTCTC 6190
6132 |
2061 CysAsnAlaGlnGlyLysTrpValProProGluGlyGlnAspMetProArgCysIleAla 2080
2081 |
6191 TGCATGCCCAGGGCAAGTGGGTACCCCAAGAGGTCAAGACATGCCCCGTGTGTATAGCT 6250
6192 |
2081 HisPheCysGluLysProProSerValSerTrpSerIleLeuGluSerValSerLysAla 2100
2101 |
6251 CATTTCTGTGAAAAACCTCCATCGGTTTCTATAGCATCTTGAATCTGTGAGCAAGCA 6310
6252 |
2101 LysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThr 2120
2121 |
6311 AAATTTGCAGCTGGCTCAGTTGTGAGCTTTTAAATGCAATGGAAGGCTTTGTACTGAACACC 6370
6312 |
2121 SerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGln 2140
2141 |
6371 TCAGCAAGATTGATGATGAGAGTGGGAGTGGACCTTCCCACTTCCATCCAC 6430
6372 |
2141 CysIleProValArgCysGlyGluProProSerIleMetAsnGlyTrpAlaSerGlySer 2160
2161 |
6431 TGCATCCCTGTGGGTGTGAGAGCCACCAAGCATCATGAATGGCTATGCAAGTGGATCA 6490
6432 |
2161 AsnTrpSerPheGlyAlaMetValAlaTrpSerCysAsnLysGlyPheTrpIleLysGly 2180
2181 |
6491 AACTACAGTTTGTGGAGCCATGTTGGCTTACAGCTGCACCAAGGGGTCTACATCAAGGG 6550
6492 |
2181 GluLysLysSerThrCysGluAlaThrGlyGlnTrpSerSerProIleProThrCysHis 2200
2201 |
6551 GAAGAAGAGGACCTTGGAGAGCCACAGGCGATGGAGTAGTCTTATATACGAGTGGCCAC 6510
6552 |
2201 ProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrThrGly 2220
2221 |
6611 CCGGTATCTTGTGTGAACCCACCTAAGTTGAGATGGCTTCTTGGAGGACATACACTGGC 6670
6612 |
2221 ArgIlePheGluSerGluValAlaGlyTrpGlnCysAsnProGlyTrpLysSerValGlySer 2240
2241 |
6671 AGGATCTTTGAGAGTGAAGTGAAGTATCAGTGTAAACCCGGGGCTATAAGTCAGTCGGAAGT 6730

2241 ProValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysVal 2260
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6731 CCTGTATTTCTGTGCCAAGCCAAATGGCCACTGGCACAGTGAATCCCCTCTCATGTGTGT 6790
6732 |
2261 ProLeuAspCysGlyLysProProIleGlnAsnGlyPheMetLysGlyGluAsnPhe 2280
2281 |
6791 CCTCTCGACTGTGGAAACCTCCCCCGATCCAGATGGCTTCATGAAAGGAGAAACTTT 6850
6792 |
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6972 |
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2361 |
7031 GAGTAGAGGTTGTGACATTTTCTGTAAAGAGGCGATGCTCTGCAAGGCCCTCTCTGTC 7090
7032 |
2361 LeuLysCysLeuProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeu 2380
2381 |
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2481 |
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2521 |
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2541 |
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2561 |
7631 ACAGGTGATTTGGCATGTAGATGCCCATCTTGCATGCAATGCCATCCACTGTGATTCCCAAA 7690
7632 |
2561 ProIleGluAsnGlyPheValGluGlyAlaAspTrpSerTrpGlyAlaIleIleTrp 2580
2581 |
7691 CCATTTGAAATGGTTTGTAGAGGTGCGAGTTTACAGCTATGGTGGCATTAATCATCTAC 7750
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2581 SerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGly 2600
2601 |
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QY 321 ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyLysSerSerCys 340
DB 971 ACAGCTGGCCCATCGGGACATACAACTCAAGGCTCACAGGAGGAATCAGCAGTTGC 1030
QY 341 IleProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAspCys 360
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QY 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys 420
DB 1211 GCCTGTGGGGTCCGATGTCACTGGATTTGATCTGTGGGAAGCAGCATCATCTTATGT 1270
QY 421 LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
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QY 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
DB 1391 ACATGTTTGGTTGGCTGTGATGAAGGGTACACACTAGAAGCGCAGTGATTAAGCTTACTTGT 1450
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QY 541 MetLeuArgCysThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLys 560
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QY 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlalysThrLeuGluGln 580
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QY 641 LysValIleAspAlaGlnProProValIleAspTrpCysArgSerProProValGln 660
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QY 661 ValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGly 680
DB 1991 GTCTCGGAGAGGTATATGTCGCCGACAGCTGGGATGACCTTCAGTTCTTCAGACAACTCAGG 2050

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QY 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
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QY 921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGlnGln 940
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; Sequence 429, Application US/10295027
; Publication No. US2003023350A1
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; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
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; CURRENT APPLICATION NUMBER: US/10/295,027
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; PRIOR APPLICATION NUMBER: US 60/347,211
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 429
; LENGTH: 10674
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-295-027-429
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Alignment Scores:
Pred. No.: 0 Length: 10674
Score: 19769.00 Matches: 3535
Percent Similarity: 99.41% Conservative: 9
Best Local Similarity: 99.16% Mismatches: 13
Query Match: 98.98% Indels: 8
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US-09-977-053-4 (1-3571) x US-10-295-027-429 (1-10674)

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Qy	901	SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle	920	Db	3757	TACACAGGTCAGCGGTGTGAGAAAATATATAATAGTGTAGTCTCCAGTCTCTGTTTAAAT	3816	Db	3757	TACACAGGTCAGCGGTGTGAGAAAATATATAATAGTGTAGTCTCCAGTCTCTGTTTAAAT	3816
Db	2701	TCACGGATTAAAGAAAGTGGCCCATTTCTGACTATATAAATTAAGTTAATTTTAAACATC	2760	Qy	1281	LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal	1300	Qy	1281	LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal	1300
Qy	921	ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrPdluAsnGln	940	Db	3817	AAAGGAATCTGTGTGATGTGTGGCTGTGCTATCGTTGCACATGTGTGAAAGGATTTGTA	3876	Db	3817	AAAGGAATCTGTGTGATGTGTGGCTGTGCTATCGTTGCACATGTGTGAAAGGATTTGTA	3876
Db	2761	ACAGCTAGTGTGCCATTTACCCGATGAAAGAAATGATACCTTGAATGGGAAATCAGCAA	2820	Qy	1301	GlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAla	1320	Qy	1301	GlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAla	1320
Qy	941	ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp	960	Db	3877	GGCCTGCAATTTGAAACAGAAAGTCAATGAATGCCAGTCAACCCATGCTTAAATATGCA	3936	Db	3877	GGCCTGCAATTTGAAACAGAAAGTCAATGAATGCCAGTCAACCCATGCTTAAATATGCA	3936
Db	2821	CGACTCTTTCAGACATTCGAAACTATCAAAATAAACTGAAAGGACCTCTCAACAAAGAC	2880	Qy	1321	ValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThr	1340	Qy	1321	ValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThr	1340
Qy	961	ProMetTyrSerPheGluLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGlu	980	Db	3937	GTCTGTGAAGACACGAGTTGGGGATTTCTGTGCAAAATGCCACCTGGATTTTGGGTACC	3996	Db	3937	GTCTGTGAAGACACGAGTTGGGGATTTCTGTGCAAAATGCCACCTGGATTTTGGGTACC	3996
Db	2881	CCCATGTATTCCTTTGAGCTTGCAATCAGAAATACCTTATAGCCGACAGCAATTCATAGAA	2940	Qy	1341	ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCys	1360	Qy	1341	ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCys	1360
Qy	981	ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal	1000	Db	3997	CGATGTGAAAGAAACCGTGCATGAGTGTCTCAGTCAGCCATGCAAAATGGAGTACTGT	4056	Db	3997	CGATGTGAAAGAAACCGTGCATGAGTGTCTCAGTCAGCCATGCAAAATGGAGTACTGT	4056
Db	2941	ACAAAAAGGCTTCCCTCTTCGACAGACAGGCTCAGTGTGAGAGGGCTATGTGTGTC	3000	Qy	1361	LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys	1380	Qy	1361	LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys	1380
Qy	1001	AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle	1020	Db	4057	AAAGACGTTGCCAATAGCTTCAGATGCCCTGTGTGAGCTGGCTTTCACAGATCACACTGT	4116	Db	4057	AAAGACGTTGCCAATAGCTTCAGATGCCCTGTGTGAGCTGGCTTTCACAGATCACACTGT	4116
Db	3001	AAATGCCCTTTGGGAACCTTATATAATCTGGAACATTTTCACCTGTGAAAGCTGCCGGATC	3060	Qy	1381	GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp	1400	Qy	1381	GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp	1400
Qy	1021	GlySerTyrGlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr	1040	Db	4117	GAATTTGAACATCAATGAATGTCTAGTCTAATCCATGTAGAAATCAGGCCACCTGTGTGGAT	4176	Db	4117	GAATTTGAACATCAATGAATGTCTAGTCTAATCCATGTAGAAATCAGGCCACCTGTGTGGAT	4176
Db	3061	GGATCCTATCAAGATGAAGAGGCACTTGAGTGCAGACTTTTGCCCTCTGGGATGTAC	3120	Qy	1401	GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr	1420	Qy	1401	GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr	1420
Qy	1041	ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr	1060	Db	4177	GAATTTAAATTCATACAGTTGTAAATGTTCAGCCAGGATTTTTCAGGCAAAAGGTTGAAACA	4236	Db	4177	GAATTTAAATTCATACAGTTGTAAATGTTCAGCCAGGATTTTTCAGGCAAAAGGTTGAAACA	4236
Db	3121	ACGGAATATATCCATTCAGAAACATCTCTGATTTGTAAGCTCAGTGTAAACCAAGCCACC	3180	Qy	1421	GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet	1440	Qy	1421	GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet	1440
Qy	1061	TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLys	1080	Db	4237	GAACAGTCTACAGGCTTTTAACTGGATTTTGAGTTTCTGGCATCTATGATATGTCATG	4296	Db	4237	GAACAGTCTACAGGCTTTTAACTGGATTTTGAGTTTCTGGCATCTATGATATGTCATG	4296
Db	3181	TACTCATACAGTGGACTTGGAGACTTGTGAATCGTGTCCACTGGGGCACTTATCAGCCAAAA	3240	Qy	1441	LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSer	1460	Qy	1441	LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSer	1460
Qy	1081	PheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAla	1100	Db	4297	CTAGATGGCATGCTCCCATCTCTCCATGCTCTAACCCTGTACCTTCTGTGATGAAATCCTCT	4356	Db	4297	CTAGATGGCATGCTCCCATCTCTCCATGCTCTAACCCTGTACCTTCTGTGATGAAATCCTCT	4356
Db	3241	TTTGGTTCCCGGAGCTGCTCTGCTGTCAGAAACACCTCAACTGTGAAAGAGGAGGCC	3300	Qy	1461	AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr	1480	Qy	1461	AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr	1480
Qy	1101	ValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeu	1120	Db	4357	GACGACATGAACATATGGAACACCAATCTCTATGAGTTGTATACCGCGCAGCAATACC	4416	Db	4357	GACGACATGAACATATGGAACACCAATCTCTATGAGTTGTATACCGCGCAGCAATACC	4416
Db	3301	GTGAACATTTCTGCATGTGGAGTCTCTGCTCAGAAAGGAAATTCCTGGGTTCTGGGTTA	3360	Qy	1481	LeuLeuLeuThrAspTyrAsnGlyTrpValLeuTyrValAsnGlyArgGluLysIleThr	1500	Qy	1481	LeuLeuLeuThrAspTyrAsnGlyTrpValLeuTyrValAsnGlyArgGluLysIleThr	1500
Qy	1121	MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys	1140	Db	4417	TTGCTCTTGACATGATATTAACGGCTGGGTTCTTTATGTGTAATGGCAGGAGAAAGATACCA	4476	Db	4417	TTGCTCTTGACATGATATTAACGGCTGGGTTCTTTATGTGTAATGGCAGGAGAAAGATACCA	4476
Db	3361	ATGCCCTGTCACCCATGCTCTCGTGAATATACCAACCTTAATGCAATCATCTGGACAGTCC	3420	Qy	1501	AsnCysProSerValAsnAspGlyArgTrpHisIleAlaIleThrTrpThrSerAla	1520	Qy	1501	AsnCysProSerValAsnAspGlyArgTrpHisIleAlaIleThrTrpThrSerAla	1520
Qy	1141	LeuAlaCysProPheThrGlyThrThrProPheAlaGlySerArgSerIleThrGluCys	1160	Db	4477	AACTGTCTCTGGTGAATGATGGCAGATGGCATCATATTGCAATCATCTGGACAGTGCC	4536	Db	4477	AACTGTCTCTGGTGAATGATGGCAGATGGCATCATATTGCAATCATCTGGACAGTGCC	4536
Db	3421	CTGGCTGTGCTTTTATGAAACTACCCCATTTGCTGTGTTCCAGATTCATCAAGATGT	3480	Qy	1521	AsnGlyIleThrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer	1540	Qy	1521	AsnGlyIleThrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer	1540
Qy	1161	SerSerPheSerSerThrPheSerAlaAlaGluGluSerValValProProAlaSerLeu	1180	Db	4537	AATGCGATCTGGAAGTCTATATCGATGGGAAATATATCTGACGGTGGTGTGCGCTCTCT	4596	Db	4537	AATGCGATCTGGAAGTCTATATCGATGGGAAATATATCTGACGGTGGTGTGCGCTCTCT	4596
Db	3481	TCAACT-----TCAGTTCTGAATATTACTATTTTTCGGTGGATTT	3519	Qy	1541	ValGlyLeuProIleProGlyGlyGlyAlaLeuValLeuGlnGlnGlnAspLysLys	1560	Qy	1541	ValGlyLeuProIleProGlyGlyGlyAlaLeuValLeuGlnGlnGlnAspLysLys	1560
Qy	1181	GlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn	1200								

QY 2281 GluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSer 2300
DB 6817 GAAGTAGGCTCAAGGTTTCAGTTTTCTGTAAATAGGGTTATGACCTTTGTTGGTGACAGT 6876
QY 2301 SerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetPro 2320
DB 6877 TCTTGGACATGTGCAAAATCTGGCAANTGGATAGAAAGTCAATCCAAAGTGCATGCT 6936
QY 2321 AlalysCysProGluProProLeuLeuGlnLeuValLeuValLeuLysGluLeuThrThr 2340
DB 6937 GCCAAGTCCGACAGCCGCCCTCTGGAAAACACAGCTAGTATTAAGAGGTTGACCAACC 6996
QY 2341 GluValGlyValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerVal 2360
DB 6997 GAGGTAGGAGTTGTGACAAATTTTCTGTAAAGAGGGCATGCTCTGCAAGGCCCTCTCTGTC 7056
QY 2361 LeuLysCysLeuProSerGlnGlnTrpAsnAspSerPhePheValCysLysIleValLeu 2380
DB 7057 CTGAATGCTTGCCATCCAGCAATGGAAATGACTCTTTCCTGTGTTGTAAAGATTGTTCTT 7116
QY 2381 CysThrProProProLeuIleSerPheGlyValProIleProSerSerAlaLeuHisPhe 2400
DB 7117 TGTACCCCACTCCCTCAATTTCTTGTGTGCTCCCAATTCCTTCTCTCTCTCTCTCTCT 7176
QY 2401 GlySerThrValLysTyrSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrThr 2420
DB 7177 GGAAGTACTGTCAAGTATTTCTTGTGTAGTGGTTTTTCTTAAGAGAAATTTCTATCCACC 7236
QY 2421 LeuCysGlnProAspGlyThrTrpSerProLeuProGluCysValProValGluCys 2440
DB 7237 CTCTGCCAACTGATGGCACTGGAGCTCTCACTGCCAAGATGTTCCAGTAGAATGT 7296
QY 2441 ProGlnProGluGluIleProAsnGlyIleIleAspValGlnGlnGlyLeuAlaTyrLeuSer 2460
DB 7297 CCCCAACTGAGAAATCCCAATGGAATCAATGATGTGCAAGGCTTGGCTATCTCAGC 7356
QY 2461 ThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCys 2480
DB 7357 ACAGCTCTCTATACCTGCAAGCCAGCTTTGAATGGTGGGAAATACTACCACTTGTGT 7416
QY 2481 GlyGluAsnGlyHisTrpLeuGlyLysProThrCysLysAlaIleIleGluCysLeuLys 2500
DB 7417 CGAAGAAATGGTCACTGGCTTGGAGGAAACCAACATGTAAGACCATTGAGTGCCTGAAA 7476
QY 2501 ProLysGluIleLeuAsnGlyLysPheSerTyrThrAspLeuHisTyrGlyGlnThrVal 2520
DB 7477 CCCAAGGAGATTTGAAATGGCAATTTCTTACACGGACCTACACTATGGACAGACCGTT 7536
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QY 2541 ThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGln 2560
DB 7597 ACAGGTGATGGAGTAGATGCCCATCTTGCATGCCATCCATGTCATGTCATGCCACAA 7656
QY 2561 ProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIleIleTyr 2580
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QY 2581 SerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGly 2600
DB 7717 AGTTGCTCTCCCTGGGTTTTGAGTGGCTGTGTCATGCCATGACAGCTGTGAGAGATCAGA 7776
QY 2601 TrpSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAsp 2620
DB 7777 TGTCAAGTTCCATCCCAACATGATGCCAATAGACTGTGGCTCTCTCTCATATAGAT 7836
QY 2621 PheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspMet 2640
DB 7837 TTTGGAGACTGTACTAAATCAAAAGATGACCGGGATATTTTGGACAAAGACGACATG 7896
QY 2641 MetGluValProTyrValThrProHisProProTyrHisLeuGlyAlaValAlaLysThr 2660

DB 7897 ATGGAGTTCCATATGTGTGCTCTCTCACCTCTCTATCATTTTGGAGCAGTGCTAAACCC 7956
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DB 7957 TGGGAAAATACAAAGGAGTCTCTGTCTACACATTCAAACTTTCTGTATGTGATGACCATG 8016
QY 2681 ValSerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCysGln 2700
DB 8017 GTTTCATACACTGTAATCCAGGATATGAATCTTGGGGAAACCTGTGTCTGATCTGCCAG 8076
QY 2701 GluAspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuPro 2720
DB 8077 GAAGATGGAATCTGGAATGGCAGTCACCATCTCTGCATTTCAATTTGAATGTGACTTGCCT 8136
QY 2721 ThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGln 2740
DB 8137 ACTGCTCTGAAAATGGCTTTTGTGGTTTACAGAGACTAGCATGGGAAGTCTGTGTGAG 8196
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DB 8197 TATAGCTGTAAACCTGGACACATTTCTAGAGGCTCTGACTTAAGGCTTTGTCTAGAAAT 8256
QY 2761 ArgLysTrpSerGlyValAserProArgCysGluAlaIleSerCysLysLysProAsnPro 2780
DB 8257 AGAAAGTGGAGTGTGTGCTCTCCACGCTGTGAGGCATTTCAATGCAAAAGGCCAATCCA 8316
QY 2781 ValMetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGlu 2800
DB 8317 GTCATGAATGGATCCATCAAGGAAGCAATACACATACCTGAGCAGCTGTGTATGAG 8376
QY 2801 CysAspProGlyTyrValLeuAsnGlyThrGluArgArgThrCysGlnAspAspLysAsn 2820
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QY 2821 TrpAspGluAspGluProIleCysIleProValAspCysSerSerProProValSerAla 2840
DB 8437 TGGGATGAGGATGAGCCCATTTGCAATCTCTGTGGACTGCGAGTTCACTCCCGCAGTCTCAGCC 8496
QY 2841 AsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIleGluTyrThrCysAsn 2860
DB 8497 AATGGCCAGGTGAGAGAGAGACGAGTACATTTCCAAAAGAGATTGAATACACTTGCAT 8556
QY 2861 GluGlyPheLeuLeuGluGlyValaArgSerArgValCysLeuAlaAsnGlySerTrpSer 2880
DB 8557 GAAGGTTCTTCTTGTAGAGGACGAGAGTGGGTTTGTCTTGCCAAATGGAGTGGAGT 8616
QY 2881 GlyAlaThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGly 2900
DB 8617 GGAGCCACTCCCGACTGTGTGCTGTGCAGATGTGCCACCCGCCCAACTGGCCAAATGGG 8676
QY 2901 ValThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGluGly 2920
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QY 2921 TyrIleLeuHisGlyValaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAlaGlu 2940
DB 8737 TACATCTTGACGGTGTCTCAAAACTCACTGTCTGCTCAGTCAAGTGGCACTGGGATGACAG 8796
QY 2941 IleProLeuCysLysProValAsnCysGlyProProGluAspLeuAlaHisGlyPhePro 2960
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QY 2961 AsnGlyPheSerPheIleHisGlyHisIleGlnTyrGlnCysPheProGlyTyrLys 2980
DB 8857 AATGGTTTTTCTTATTCATGCGGGCCATATACAGTATCAGTGTCTTCTGTGTTTAAAG 8916
QY 2981 LeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerPro 3000
DB 8917 CTCCATGGAAATTCATCAAGAGGTCCTCTCTCCATGGCTCTCTGGAGTGGCAGCTCACCT 8976
QY 3001 SerCysLeuProCysArgCysSerThrProValIleGluTyrGlyThrValAsnGlyThr 3020

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 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1080
 ; LENGTH: 10674
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-295-027-1080

Alignment Scores:

Pred. No.: 0 Length: 10674
 Score: 19769.00 Matches: 3535
 Percent Similarity: 99.41% Conservative: 9
 Best Local Similarity: 99.16% Mismatches: 13
 Query Match: 98.98% Indels: 8
 DB: 16 Gaps: 2

US-09-977-053-4 (1-3571) x US-10-295-027-1080 (1-10674)

QY 1 MetTrpProArgLeuAlaPheCysCysTrpGlyLeuAlaLeuValSerGlyTrpAlaThr 20
 DB 1 ATGTGGCCCTCGCTGGCCCTTTTGTGCTGGGCTCGGCTGGGCTGGGCGACC 60
 QY 21 PheGlnGlnMetSerProSerArgAnnPheSerPheArgLeuPheProGlnThrAlaPro 40
 DB 61 TTTCAGCAGATGTCCCGCTGCGGCAATTTTCAGCTTCCGCTCTTCCCGAGACCCGGCC 120
 QY 41 GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg 60
 DB 121 GGGGCCCCGGGAGATATCCCGGCGCCCGCTCTTGGCGACGAGCGGGGAGCAGA 180
 QY 61 ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu 80
 DB 181 GTGGAGCGGCTGGGCGAGCGTTCGCGACGCGTGGCTGGCGGCTGGCGGAGCTCAGCGAG 240
 QY 81 ArgLeuLeuValPheLeuValAspAspSerSerValGlyGluValAlaPheArg 100
 DB 241 CCGCTGGAGCTTGTCTTCTGTGTGGATGATTCGTCCAGCGTGGCGGCAAGTCAATTCGCG 300
 QY 101 SerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThr 120
 DB 301 AGCGAGCTCATGTTCTGTCGCGAGCTGCTGTCCGACTTCCCGGTGGTGGCCCGGCGCAG 360
 QY 121 ArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIle 140
 DB 361 CGCGTGGCCATCGTGACCTTCTCGTCAAGAACTAGCTGTGCGCGCTCGATTCATCATC 420
 QY 141 SerThrArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluLeuProAlaIle 160
 DB 421 TCCACCCGCGCGGCGGCGCAGCAAGTGGCGGCTCTCTCCAGAGATCCCTGCGCATC 480
 QY 161 SerTyrArgGlyGlyGlyThrTyrThrLysGlyValAlaPheGlnGlnAlaAlaGlnIleLeu 180
 DB 481 TCTACCGAGGTGGCGGCACTTACACCAAGGGCGCTTCCAGCAGCGCGGCAATTCCTT 540
 QY 181 LeuHisAlaArgGlnAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn 200
 DB 541 CTTTCATGTAGAGAACTCAACAAAGTTGATTTCTCATCTCATCTGATGATATTCAT 600
 QY 201 GlyLysProArgProIleAlaSerLeuArgAspSerGlyValGluIlePheThr 220
 DB 601 GGGGAGACCTTAGACCAATTCAGCGCTCAGTGGGATTCAGGAGTGGAGATCTTCACT 660
 QY 221 PheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu 240

DB 661 TTTCGCATATGCAAGGGAACATTCGAGAGCTGAATGATGATGCTTCCACCCCAAGGAG 720
 QY 241 GluHisCysTyrIleLeuHisSerPheGluGluPheGluAlaLeuAlaArgArgAlaLeu 260
 DB 721 GAGCACTGTTACCTGCTACACAGATTTTGAGGAATTTGAGGCTTTAGCTCGCGGCAATTG 780
 QY 261 HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu 280
 DB 781 CATGAGATCTACCTTCTGGAGTTTATTCAGATGATATGTTCCCTCTCTATATCTT 840
 QY 281 CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr 300
 DB 841 TGTGATGAAGGCAAGCACTGCTGTGACCAATGGGAAGCTGCAATGTGGGACACACACA 900
 QY 301 GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys 320
 DB 901 GGCCATTTTGGAGTGCATCTGTGAAAGGGGTATTACGGGAAAGGCTGCGAGTAGAATGC 960
 QY 321 ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys 340
 DB 961 ACAGCTTGGCCATCGGGGACATCAAACTGAAGGCTCACCAAGGAGGATCAGCAGTTGC 1020
 QY 341 IleProCysProAspGluHisThrSerProGlySerThrSerProGluAspCys 360
 DB 1021 ATTCCATGCTCTGATGAAATCACACTCTCCACCTGGAAGCACATCCCTGGAAGACTGT 1080
 QY 361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
 DB 1081 GTCTGCAGAGAGGATACAGGGCATCTGGCGACAGCTGTGAACCTGTCCACTGCGCTGCC 1140
 QY 381 LeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla 400
 DB 1141 CTGAAGCTTCCCGAAATGTTACTTTATCCAAACACTTGCACCAACCACTTCAATGCA 1200
 QY 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuCys 420
 DB 1201 GCCTGTGGGCTCGATGTCACTGATTTGATCTGTGGGAGGAGCAGCATCATCTTATGT 1260
 QY 421 LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
 DB 1261 CTACCAATATGTTGTGTGTCGCGTTCAGAGAGCTACTGCAGAGTAGAAGATGATGCTCAT 1320
 QY 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
 DB 1321 CTCGCGCACCGGAACATGGCCACATCAGCTGTCTCAAGGGAGATGTTATATAGACA 1380
 QY 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
 DB 1381 ACATGTTTGTGCTGCTGATGAAGGCTACAGACTAGAGGCGAGTGTATAGCTTACTTGT 1440
 QY 481 GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr 500
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 QY 501 PheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys 520
 DB 1501 TTTTCAGTCCCAAGATGTCATATATCCCCCACACATGTGGCAGCAGCAGCCAGCAA 1560
 QY 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
 DB 1561 TTTGGGACATCTGCTATGATGTCGCCCAAGGCTTCAATTTATCTGGAGTCAAGAA 1620
 QY 541 MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCysLys 560
 DB 1621 ATGCTGAGATGTACCACTTCTGGAAATGGAATGTGCGAGTTCAGGCGCTGTGTGTA 1680
 QY 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln 580
 DB 1681 GACGTGGAGGCTCTCTCAATCAACTGTCTTAAGACATAGAGGCTAAGACTCTGGAACAG 1740
 QY 581 GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys 600
 DB 1741 CAAGATTCTGCCAATGTTTACCTGGCAGATTCCAACAGCTAAAGACCACTCTGCTGTA 1800

601 ValSerValHisValHisProAlaPheThrProTyrLeuPheProIleGlyAspVal 620
1801 GGTGAGTCCAGCTTCATCCAGCTTCACCCACCTTCTCTTCCCAATTGAGATGT 1860
621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
1861 GCTATCGTATACAGGCAACTGACCTATCCGGCAACAGCCAGCTGCATTTTCCATATC 1920
641 LysValIleAspAlaGluProProValIleAspTyrCysArgSerProProValGln 660
1921 AAGGTTATTGATGCGAACCCACCTGTATAGACTGGTGAGATCTCCACCTCCCGTCCAG 1980
661 ValSerGluLysValHisAlaAlaSerTyrAspGluProGlnPheSerAspAsnSerGly 680
1981 GTCTCGGAGAGGTACATGCCGCACTGGGATGAGCTCTGTTCTCAGCAACTCAGGG 2040
681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
2041 GCTGAATTGTCATTACCAAGAGTCATACACAAGGAGACCTTTTCCCTCAAGGGAGACT 2100
701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
2101 ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATAACAGGACATGTGTATATCCATAT 2160
721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
2161 GTCATAAAAGGTCTCCCTGTGAATTCATTCACACCTGTAAATGGGATTTTATATGC 2220
741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
2221 ACTCCAGATAATACTGGAGTCAACTGTACATTAACTTGCTTGGAGGGCTATGATTTTCA 2280
761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyr 780
2281 GAAGGGTCTACTGACAAGTATTTATGTGCTTATGAGATGGCGTCTGGAAACCAACATAT 2340
781 ThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
2341 ACCACTGAATGGCCAGACTGTGCAAAAACGTTTTCAAACCAACGGGTTCAGTCTCTTT 2400
801 GluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGlu 820
2401 GAGATGTTCTACAAGCAGCTCGTTGTGATGACACAGATCTGATGAAGAAGTTTCTGAA 2460
821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
2461 GCATTTGAGACGACCTCGGCAAAATGGTCCCATCATTTTGTAGTATGATGACAGACAT 2520
841 AspCysArgGluGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
2521 GACTGACAGCTGGAGGAGAACCTGACCAAAAATATTGGCTAGATAATAATTATGACTAT 2580
861 GluAsnGlyPheAlaIleGlyProGlyGlyTyrPheGlyAlaAlaAsnArgLeuAspTyrSer 880
2581 GAAAATGGCTTTGCAATTGGACCGAGTGGCTGGGTGCGAGCTAATAGCTGGATTACTCT 2640
881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 900
2641 TACGATGACTTCTCGACACTGTGCAAGAAACAGCCACAAGCATCGCAATGCCAAGTCC 2700
901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920
2701 TCACGGATTAAGAAGTGGCCCATTTATCTGACTATAAATAAGTTAATTTTAACTC 2760
921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnGln 940
2761 ACAGCTAGTGTGCCATTACCCGATGAAGAAATGATACCTTGAATGGGAAAATCAGCAA 2820
941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
2821 CGACTCCTTCAGACATTTGGAACTATCACAAATAAACTGAAGAGGACTCTCAACAAGAC 2880

961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaSerSerAsnSerLeuGlu 980
2881 CCCATGTTATCTCTTTCAGCTTGCATCAGAAATACTTATAGCCGACAGCAATTCATTAGAA 2940
981 ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal 1000
2941 ACAAAGAAGCTTCCCTCTTCAGACCAAGGCTCAGTGTCTGAGAGGGCGTATGTGTCTC 3000
1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
3001 AATTGCCCTTTGGAACTTATTAATCTGGAACATTTCACTGTGAAGCTGCCGGATC 3060
1021 GlySerTyrGlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr 1040
3061 GGATCTATCAAGATGAAGAAGGCAACTTGAGTGCAGCTTTGCCCTCTCTGGGATGTAC 3120
1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr 1060
3121 ACGGAATATATCCATTCAGAAACATCTCTGATTTGTAAGCTCAGTGTAAACAAGGCACC 3180
1061 TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLys 1080
3181 TACTCATACAGTGGACTTGGAGCTTGTGAATCGTGTCCACTGGGCACCTTATCAGCCAAA 3240
1081 PheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAla 1100
3241 TTTGGTTCCTCGGAGCTGCTCTCGTGTCCAGAAACACCTCAACTGTGAAGAAGGAGGCC 3300
1101 ValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeu 1120
3301 GTGAACATTTCTGCATGTGGAGTTCCTTGTCTCCAGAAGGAAATTTCTCGCGTCTCTGGGTA 3360
1121 MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
3361 ATGCCCTGTCAACCATGCTCTCGTGACTTATACCACTAATGACAGGAGGCCCTTCTGCG 3420
1141 LeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCys 1160
3421 CTGGCTGTCTCTTTATGGAACCTTACCCCATTCGCTGGTCCAGATCCATCACAGATGT 3480
1161 SerSerSerSerThrPheSerAlaAlaGluSerValValProProAlaSerLeu 1180
3481 TCAACT-----TCAGTTCTGAATATTACTATTCTCGTGAGATTT 3519
1181 GlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn 1200
3520 GGGCATCTGCAGTTGTTAAAT---TGTCCTTCTGAGGTTTTCCAGAAATGCTTCTTTAAC 3576
1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
3577 CCTTGCACACANTAGTGGAACTTGGCCAGCACTTGGCGGTGGTTATTTTGTCTCTGTCCA 3636
1221 LeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProleuProCys 1240
3637 CTGTGATATACAGCTTAAAGTGTGAACACACATCGATGAGTGCAGCCCATCGCTTTCG 3696
1241 LeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGly 1260
3697 CTCACAAATGGAGTTTGTAAAGACCTAGTTGGGGAATTCATTGTGAGTGGCCATCAGT 3756
1261 TyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsn 1280
3757 TACACAGCTCAGCGTGTGAAGAAATATAAATCAGTGTAGTCTCCAGTCTCTGTTTAAAT 3816
1281 LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal 1300
3817 AAAGGAATCTGTGTGTGTGTGGTGGCTGGCTATCGTTGCACATGTGTGAAAGGATTTGTA 3876
1301 GlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAla 1320
3877 GGCTGATGTGTGAACAGAGAGTCAATGAATGCCAGTCAAAACCCATGCTTTAATTAATGCA 3936
1321 ValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThr 1340

Db	3937	GTCTGTGAAGACCAAGTGGGGGATTTCTGTGCAAAATGCCACCTCGGATTTTGGGTACC	3996
Qy	1341	ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCys	1360
Db	3997	CGATGTGGAAAGACGTGATGAGTGTCTCAGTCAGCCATGCAAAATGGAGCTACCTGT	4056
Qy	1361	LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys	1380
Db	4057	AAAGACGGTGGCAATAGCTTTCAGATGCCCTGTGTGAGCTGGCTTTCACAGATCACACTGT	4116
Qy	1381	GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp	1400
Db	4117	GAATTTGAACATCAATGAATGTCAATCTTAATCCATGTAGAAATCAGGCCACCTGTGTGGAT	4176
Qy	1401	GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr	1420
Db	4177	GAATTTAAATTCATACATGTTGTAATGTCAAGCAGGATTTTCAGGCAAAAGGTGTGAAACA	4236
Qy	1421	GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet	1440
Db	4237	GAACAGCTACAGGCTTTAAACCTGGATTTTGAAGTTTCTGGCATCTATGGATATGTCAATG	4296
Qy	1441	LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSer	1460
Db	4297	CTAGATGGCATGCTCCCATCTCTCCATGCTCTAAACCTGTACCTTCTGGATGAATCTCT	4356
Qy	1461	AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr	1480
Db	4357	GACGACATGAACATATGGAACACCAATCTCTATGCGAGTTGTAAACGGCAGCACAATACC	4416
Qy	1481	LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThr	1500
Db	4417	TTGCTCTGACTGATTTATAACGGCTGGTGTCTTTATGTGAATGGCAGGCAAAAGATAACA	4476
Qy	1501	AsnCysProSerValAsnAspGlyArgThrHisHisIleAlaIleThrTrpThrSerAla	1520
Db	4477	AACTGTGCTCCCTGGTGAATGATGGCAGATGGCATCATATTTGCAATCATCTTGGACAAGTGCC	4536
Qy	1521	AsnGlyIleTrpLysValTyrIleAspGlyLysLeuSerAspGlyAlaGlyLeuSer	1540
Db	4537	AATGGCATCTGGAAGTCTATATCGATGGGAAATATATCTGACGGTGGTGTCTGGCCTCTCT	4596
Qy	1541	ValGlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGluAspLysLys	1560
Db	4597	GTTGGTTTGGCCATACCTGCTGGTGGTGGTGTAGTTCTGGGGCAAGCAGCAACAAAAA	4656
Qy	1561	GlyGluGlyPheSerProIleGluSerPheValGlySerIleSerGlnLeuAsnLeuTrp	1580
Db	4657	GGAGAGGGGATTCAGCCCACTGAGTCTTTTGTGGGCTCCATAAGCCAGCTCAACCTCTGG	4716
Qy	1581	AspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeu	1600
Db	4717	GACTATGCTCTGTCTCCACAGCAGGTGAAGTCACTGGCTACCTCTGCCCCAGGGAACCTC	4776
Qy	1601	SerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLys	1620
Db	4777	AGTAAAGGAAACGTGTAGCATGGCTGTATTTCTGTGAGGAATGTGGGAAAGTGAAG	4836
Qy	1621	IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis	1640
Db	4837	ATCGATTTCTAAAGGACATATTTTGTCTGATTTGCCACCGCTTAGGAGGGGTCAAGTCCAT	4896
Qy	1641	LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro	1660
Db	4897	CTGAGNACTGCATCTGAAGATTTAAAGCCAGGTTCACAAAGTCAATCTGTTCTGTGATCCA	4956
Qy	1661	GlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTrpThrGln	1680
Db	4957	GGCTTCCAGCTGGTCGGGAACCTGTGTGAGTACTGTCTGAATCAGGACAGCATGACACAA	5016
Qy	1681	ProLeuProHisCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPhe	1700

Db	5017	CCACTTCTCTCACTGTGAACGCATTAAGCTGTGGGTGCCACCTCTCTTTGGAGAAATGGCTTC	5076
Qy	1701	HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr	1720
Db	5077	CATTTCAGCCGATGACTTCTATGCTGGCAGCAGACAGTAACCTTACCAGTGAACAATGGCTAC	5136
Qy	1721	TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSer	1740
Db	5137	TATCTATTGGGTGACTCAAGGATGTTCTGTACAGATAAATGGGAGCTGGAAACGGCGTTCA	5196
Qy	1741	ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer	1760
Db	5197	CAATCTGCTGTGATGTGATGAGTGTGCGATGGATGATGATGATGATGATGATGATGATGAT	5256
Qy	1761	CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGly	1780
Db	5257	TGCCTGAACGTAGATGATCTTACATATGTTCAATGTTGCCATGCCAGTACACAGGAGATGG	5316
Qy	1781	LysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer	1800
Db	5317	AAAAACGTGTCAGAACCTTATAAATGTAAGGCTCCAGGAAATCCGAAATATGGCCACTCC	5376
Qy	1801	SerGlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGln	1820
Db	5377	TCAGTGAAGATTTATACAGTAGTGTCCGAGCTCACATTTTGTGTGAGGAGGATACCAG	5436
Qy	1821	LeuMetGlyValThrLysIleThrCysLeuGluSerGlyIleTrpAsnHisLeuIlePro	1840
Db	5437	TTGATGGGAGTAACCAAAATCACATGTTTGGAGTCTGGAGATGGAATCATCTAATACCA	5496
Qy	1841	TyrCysLysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGlu	1860
Db	5497	TATTTGTAAGCTGTTTTCATGTGTAAACCGGCTTATTCAGAAATGGTTCATTTGAGGAG	5556
Qy	1861	LeuAlaPheThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAla	1880
Db	5557	TTAGCATTTACTTTTGGCAGCAAGTGACATATAGTGTATTAAGGATATATCTCTGGCC	5616
Qy	1881	GlyAspLysGluSerSerCysLeuAlaAsnSerSerTrpSerHisSerProProValCys	1900
Db	5617	GGTGAATAAGAAATCATCTCTGTCTTGTCTAACAGTCTTTGGAGTCAATTCCTCTCTGTGT	5676
Qy	1901	GluProValLysCysSerSerProGluAsnIleAsnAsnGlyLysTyrIleLeuSerGly	1920
Db	5677	GAACAGTGAAGTGTCTAGTCCGAAATATAAATAATGGAATAATATATTTTGGTGGG	5736
Qy	1921	LeuThrTyrLeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuGlnGlyPro	1940
Db	5737	CTTACTTACTTCTTACTGCATCATATTCATGCGATACAGGATACAGCTTACAGGGCCCT	5796
Qy	1941	SerIleIleGluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeu	1960
Db	5797	TCCATTTATTTGAATTCACGGCTTCTGGCATCTGGGACAGAGCGCCACTGCTGTGCACCTC	5856
Qy	1961	ValPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThr	1980
Db	5857	GTCCTTCTGTGGAGAACCTGCTGCATCAAGATGCTGTCAATTACGGGGAATAACTTCACT	5916
Qy	1981	PheArgAsnThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThr	2000
Db	5917	TTTCAGGAAACACCGTCACTTACATTCGCAAGAGGCTATATCTCTGTGTCTTGACACC	5976
Qy	2001	IleGluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnCysLeuAlaValSer	2020
Db	5977	ATTGAATGCTGGCCGACGCAAGTGGAGTGAAGTGACAGCAGTGGCTGGCTGTCTCC	6036
Qy	2021	CysAspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGly	2040
Db	6037	TGTGATGAGCCACCATTTGTGGACCAAGCTCTCCAGAGACTGCCCATCGGCTCTTTGA	6096
Qy	2041	AspIleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeu	2060
Db	6097	GACATTTGCTTCTTACTTACTTCTGATGGTTACAGCTAGCAGCAATTCACAGCTTCTC	6156

2061 CysAsnAlaGlnGlyLysTrpValProProGluGlyGlnAspMetProAtqCysIleala 2080
Db TGCATGCCAGGCGAGTGGGTACCCCAAGAGTCAAGACATGCCGCCGTGTATAGCT 6216
2081 HisPheCysGluLysProProSerValSerTyrSerIleLeuGluSerValSerIleAla 2100
Db CATTTCTGTGAAACCTCCATCGGTTCCTATAGCATCTTGGAACTCTGTGAGCAAGCA 6276
2101 LysPheAlaAlaGlySerValIleSerPheLysCysMetGluGlyPheValLeuAsnThr 2120
Db AAAATTGCAGCTGGCTCAGTTGTGAGCTTTAAATGTCATGGAGGCTTTGTACTGAACACC 6336
2121 SerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGln 2140
Db TCACAAGATTTGAATGTATGAGAGGTGGGAGTGGAAACCTTCCCCCATGTCTCATCCG 6396
2141 CysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySer 2160
Db TGCATCCCTGTGCGGTGTGAGAGCCACCAAGCATCATGATGGCTATGCAAGTGGATCA 6456
2161 AsnTyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGly 2180
Db AACTACAGTTTTCGAGCCATGGTGGCTTACAGCTGCAACAAGGGTTCTACATCAAGGG 6516
2181 GluLysLysSerThrCysGluAlaThrGlyGlnTrpSerProIleProThrCysHis 2200
Db GAAAGAGAGACACTCGCGAAGCCACAGGCGAGTGGAGTAGTCTTATACCGACGTGCCAC 6576
2201 ProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrThrGly 2220
Db CCGGTATCTTGTGTGTAACCACTAAGTTGAGATGGCTTCTTGGAGCATACAACCTGGC 6636
2221 ArgIlePheGluSerGluValArgTyrGlnCysAsnProGlyTyrLysSerValGlySer 2240
Db AGGATCTTTCAGAGTGAAGTGAAGTATCAGTGTAAACCGGGCTATAAGTCAAGTGGAGT 6696
2241 ProValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysVal 2260
Db CCTGTATTGTGTGCCAAGCCAACTGCCACCTGGCACAGTGAATCCCTCTCATGTGTGT 6756
2261 ProLeuAspCysGlyLysProProIleGlnAsnGlyPheMetLysGlyGluAsnPhe 2280
Db CCTCTCGACTGTGAAACCTCCCGCATCCAGAAATGGCTTTCATGAAAGGAGAAACCTT 6816
2281 GluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSer 2300
Db GAAGTAGGGTCCAAAGTTTCAAGTTTCTGTAAATGAGGGTTATGAGCTTGTGTGACAGT 6876
2301 SerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetPro 2320
Db TCTTGGACATGTCAAAATCTGGCAATGGAAATGAAGATCAATCCAAAGTGCATGCCCT 6936
2321 AlaLysCysProGluProProLeuLeuGluAsnGlnLeuValLeuLysGluLeuThrThr 2340
Db GCCAAGTGCACAGAGCCGCCCTCTTGGAAAAACCCAGCTAGTATTAAAGGAGTTGACACC 6996
2341 GluValGlyValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerVal 2360
Db GAGTAGGAGTTGTGACATTTCTCTGTAAGAAGGAGCATGTCTCTGCAAGGCCCTCTGTC 7056
2361 LeuLysCysLeuProSerGlnTrpAsnAspSerPheProValCysLysIleValLeu 2380
Db CTGAAATGCTGTCCTCCCAAGCAAGGAATGACTCTTCTCTGTTGTGAAGATTGTTCTT 7116
2381 CysThrProProLeuIleSerPheGlyValProIleProSerSerAlaLeuHisPhe 2400
Db TGTACCCCACTCCCTCAATTTCTTTGGTGTCCCAATTCCTCTCTCTCTCTCAATTTT 7176
2401 GlySerThrValLysTyrSerCysValGlyPhePheLeuArgGlyAsnSerThrThr 2420
Db GGAAGTACTGTCAAGTATCTTGTGTAGGTGGGTTTTTCTTAAGAGGAAATTTCTACCAAC 7236

2421 LeuCysGlnProAspGlyThrTrpSerSerProLeuProGluCysValProValGluCys 2440
Db CTCCTGCCAACTGATGGCACTCTGGAGCTCTCCACTGCCAGATGTGTTCCAGTAGATGT 7296
2441 ProGlnProGluGluIleProAsnGlyIleLeuAspValGlnGlyLeuAlaTyrLeuSer 2460
Db CCCCAACCTGAGGAAATCCCAATGGAATCATTTGATGTGCAAGGCTTGCTCTATCTCAGC 7356
2461 ThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCys 2480
Db ACAGCTCTCTATACCTGCAAGCCAGGCTTTGAATTTGGTGGGAAATACTACCACTCTTGT 7416
2481 GlyGluAsnGlyHisTrpLeuGlyLysProThrCysLysAlaIleGluCysLeuLys 2500
Db GGAGAAATGTGCTACTGCTTGGAGGAAACCAACATGTAAAGCCATTGAGTGCCTGAAA 7476
2501 ProLysGluIleLeuAsnGlyLysPheSerTyrThrAspLeuHisTyrGlyGlnThrVal 2520
Db CCCAAGGAGATTTTGAATGGCAATTTCTTACACGGACCTACACTATGACAGACCGTT 7536
2521 ThrTyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGlu 2540
Db ACCTACTCTTCCAAACCGAGGCTTTGCGCTCGAAGGTCCAGTCCCTTGACCTGTTTAGAG 7596
2541 ThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGln 2560
Db ACAGTGATTTGGATGTAGATGCCCATCTTGCATGTCATCCACTGTGATTTCCCAACA 7656
2561 ProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIleLys 2580
Db CCCATGAAAATGCTTTTGTAGAGGTGCAGATTACAGCTATGTTGGCCATAATCATCTAC 7716
2581 SerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluLysSerGly 2600
Db AGTTGCTTCCCTGGGTTTCAGTGGCTGGTCAAGCATGACAGCTGTGAAAGAGTACAGA 7776
2601 TrpSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAsp 2620
Db TGGTCAAGTTCCATCCCAACATGTATGCCATAGACTGTGGCTCCCTCTCATATAGAT 7836
2621 PheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspMet 2640
Db TTTTGACAGCTGACTAAACTCAAGATGACCAAGGATATTTTGGACAAAGACAGCAGT 7896
2641 MetGluValProTyrValThrProHisProProTyrHisLeuGlyAlaValAlaLysThr 2660
Db ATGGAAGTTCCATATGTGACTCTCCACCTCTTATCAATTTGGGAGAGTGGCTAAAAAC 7956
2661 TrpGluAsnThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMet 2680
Db TGGGAAATACAAAGGAGTCTCTGCTGACATTCATCAAACTTTCTGTATGTTACCATG 8016
2681 ValSerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCysGln 2700
Db GTTTTCATACACTCTGTAATCCAGGATATGAACTTCTGGGGAAACCCCTGTGCTATGCCAG 8076
2701 GluAspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuPro 2720
Db GAAATGGAATCTGGAATGGCGATGACCATCTGCTGCAATTTCAATGAATGTGACTGGCT 8136
2721 ThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGln 2740
Db ACTGCTCTGAAATGGCTTTTGGTTTTTACAGAGACTAGCATGGGAAGTGTGTGTCAG 8196
2741 TyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsn 2760
Db TATAGCTGTAAACCTGGACACATTTCTAGCAGGCTCTGACTTTAAAGGCTTTTGTCTAGAA 8256
2761 ArgLysTrpSerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProAsnPro 2780
Db AGAAGTGGAGTGTGCTCCCGCTGTAAGGCAATTTTATGCAAAAGCAATTCATCA 8316
2781 ValMetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGlu 2800

DB 8317 GTTCATGATGGATCCATCAAGAGGCACTACATACCTGAGCACTGTTACTATGAG 8376
QY CysAspProGlyThrValLeuAenGlyThrGluArgThrCysGlnAspAspLysAen 2820
DB 8377 TGTGACCCCGGATATGTCGTAATGCACTGAGAGGAGAACATGCGCAGGATGACAAAAAC 8436
QY TTPAspGluAspGluProIleCysIleProValAspCysSerSerProProValSerAla 2840
DB 8437 TGGGATGAGGATGAGCCCATTTGCTCTGAGACTGCGATTCACCCCGAGTCTGAGCC 8496
QY AenGlyGlnValArgGlyAspGluThrPheGlnLysGluIleGluThrCysAen 2860
DB 8497 AATGCCAGGTGAGGAGAGCGATACATTTCCAAAAGAGATTGAATACACTTGCAT 8556
QY GluGlyPheLeuLeuGluGlyAlaArgSerArgValCysLeuAlaAenGlySerTrpSer 2880
DB 8557 GAAGGGTTCTTGCTTGAGGAGCCAGGAGTGGGTTTGTCTTCCCAATGGAAGTTGGAGT 8616
QY GlyAlaThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAenGly 2900
DB 8617 GGAGCCACTCCCGACTGTGTGCTGTCAGATGTCACCCCGCCCAACTGGCCAAATGGG 8676
QY ValThrGluGlyLeuAspThrGlyPheMetLysGluValThrPheHisCysHisGluGly 2920
DB 8677 GTGACGGAAGGCTGGAATATGGCTTCATGAGGAGTAACTTCACTGTCAAGAGGC 8736
QY TyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGlyAenTrpAspAlaGlu 2940
DB 8737 TACATCTTGACGGTCTCCAAACTCACTGTGCTGAGTGGCAACTGGGATGACAG 8796
QY IleProLeuCysLysProValAenCysGlyProProGluAspLeuAlaHisGlyPhePro 2960
DB 8797 ATTCTCTCTGTAAACCGTCACTGTGACCTCTCGAAGATCTTCCCATGGTTTCCCT 8856
QY AenGlyPheSerPheIleHisGlyGlyHisIleGlnThrGlnCysPheProGlyThrLys 2980
DB 8857 AATGGTTTTCCTTTATTCATGCGGGGCCATATACAGTATCAGTGTCTTCTGGTTATAG 8916
QY LeuHisGlyAenSerSerArgArgCysLeuSerAenGlySerTrpSerGlySerPro 3000
DB 8917 CTCCATGGAAATTCATCAAGAGTGGCTCTCCAAATGGCTCTCGAGAGTGGCAGCTCACT 8976
QY SerCysLeuProCysArgCysSerThrProValIleGluThrGlyThrValAenGlyThr 3020
DB 8977 TCTGCTGCTGCTGCGAGATGTTCCACACAGATTAATGAATATGGAATGTGCAATGGGACA 9036
QY AspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGlyPheLysLeuLeuGly 3040
DB 9037 GATTTTGACTGTGGAAGGCGAGCCCGATTCAGTGTCTCAAGGCTTCAAGCTCTTAGGA 9096
QY LeuSerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGlyPheProHisCysGlu 3060
DB 9097 CTTTCTGAAATCACCTGTGAAGCGGATGGCAGTGGAGCTCTGGGTTCCCCCACTGTGAA 9156
QY HisThrSerCysGlySerLeuProMetIleProAenAlaPheIleSerGlnThrSerSer 3080
DB 9157 CACACTTCTGTGGTTCTCTTCCAAATGATACCAATGGGTTCAATCAGTGGAGACAGCTCT 9216
QY TrpLysGluAenValIleThrThrSerCysArgSerGlyThrValIleGlnGlySerSer 3100
DB 9217 TGGAGGAAATGTGATTAATTAACCTGACGTGCGATGTTGGATATGTCATACAGGCGATTCA 9276
QY AspLeuIleCysThrGluLysGlyValTrpSerGlnProTrpProValCysGluProLeu 3120
DB 9277 GATCTGATTTGTACAGAGAAAGGGTATGAGGCGAGCTTATCCAGTCTGTGAGCCCTTG 9336
QY SerCysGlySerProProSerValAlaAenAlaValAlaThrGlyAlaHisThrThr 3140
DB 9337 TCTGTGGGTCCCCACCGTCTGTGCGCAATGCAAGTGGCAACTGGAGGAGGACACACTAT 9396
QY GluSerGluValLysLeuArgCysLeuGluGlyThrThrMetAspThrAspThr 3160

DB 9397 GAAAGTGAAGTGAACCTCAGATGTCGGAAGGTTATACGATGATACAGATACAGATACA 9456
QY PheThrCysGlnLysAspGlyArgTrpPheProGluArgIleSerCysSerProLysLys 3180
DB 9457 TTCACCTGTGCAGAAAGATGTCGCTGGTTCCCTCGAGAGATCTCTCGCAGTCTCAAAAA 9516
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DB 9517 TGTCTCTCTCCCGGAAAAACATACATATACATATCTGTACATGGGACGATTTCACTGTGAAT 9576
QY ArgGlnValSerValSerCysAlaGluGlyThrPheGluGlyValAenIleSerVal 3220
DB 9577 AGGCAAGTTCTCTGTGTCATGTCAGAAAGGTATACCTTTTGAGGAGATTAAACATATCAGTA 9636
QY CysGlnLeuAspGlyThrTrpGluProProPheSerAspGluSerCysSerProValSer 3240
DB 9637 TGTGAGCTGTGATGGAACTGGGAGGCCCATTTCTCGATGAATCTTTGCGAGTCCAGTTCT 9696
QY CysGlyLysProGluSerProGluHisGlyPheValValGlySerLysThrPheGlu 3260
DB 9697 TGTGGGAACTGTGAAGTCCAGAACATGATTTGTGTGGCAGTAAATACACCTTTGAA 9756
QY SerThrIleIleThrGlnCysGluProGlyThrGluLeuGluGlyAenArgGluArgVal 3280
DB 9757 AGCACAAATTTATTCAGTGTGAGCTGCTGCTATGAATAGAGGGGAACAGGGAACGTGTC 9816
QY CysGlnGluAenArgGlnTrpSerGlyGlyValAlaIleCysLysGluThrArgCysGlu 3300
DB 9817 TCCAGGAGAACAGACAGTGGAGTGGAGGGTGGCAATATGCAAGAGACAGGAGTGTGAA 9876
QY ThrProLeuGluPheLeuAenGlyLysAlaAspIleGluAenArgThrThrGlyProAen 3320
DB 9877 ACTCCACTTGAATTTCTCAATGGGAAAGCTGACATTTGAAACAGGAGCACTGGACCCAC 9936
QY ValValThrSerCysAenArgGlyThrSerLeuGluGlyProSerGluAlaHisCysThr 3340
DB 9937 GTGGTATATTCCTGCAACAGAGGCTACAGTCTTGAAGGGCCATCTGAGGACACACTGCACA 9996
QY GluAenGlyThrTrpSerHisProValProLeuCysLysProAenProCysProValPro 3360
DB 9997 GAAATGGAACTCTGGAGCCACCCAGTCCCTCTCTGCAAAACCAATCCATGCCCTGTTCCT 10056
QY PheValIleProGluAenAlaLeuLeuSerGluLysGluPheThrValAspGlnAenVal 3380
DB 10057 TTTGTGATTTCCCGAGATGCTCTGCTGTCTGAAAGAGGATTTATGTTGATCAGAAATGTG 10116
QY SerIleLysCysArgGluGlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAenPro 3400
DB 10117 TCCATCAATGTAGGGAAGGTTTCTGCTGCGAGGCCACGCGCATCATTTACCTGCAACCCC 10176
QY AspGluThrTrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProProAla 3420
DB 10177 GACGAGACGTGGACACAGACAGCGCCCAATGTGAAAAAATCTCATGTGTGTCCACAGCT 10236
QY HisValGluAenAlaIleAlaArgGlyValHisThrGlnThrGlyAspMetIleThrThr 3440
DB 10237 CAGTAGAATAATGCAATGCTCGAGGGGTACATTTCAATATGAGACATGATCACCTAC 10296
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DB 10297 TCATGTTACATGTCATACATGTTGGAGGGTTTCTGCGAGGAGTGTGTTGTTTAGAAAAATGGA 10356
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DB 10357 ACATGAGCATCACCTCTTATTTGACAGCTGTCTGTGATTTCCATGTGAGATGGGGGC 10416
QY IleCysGlnArgProAenAlaCysSerCysProGluGlyTrpMetGlyArgLeuCysGlu 3500
DB 10417 ATCTGCAACGCCCAATGCTGTTCTGTCCAGAGGGCTGGATGGGGCCCTCTGTGAA 10476
QY GluProIleCysIleLeuProCysLeuAenGlyGlyArgCysValAlaProThrGlnCys 3520
DB 10477 GAACCAATCTGCATTTCTCCCTGCTGCAACGGAGGTGCTGTGTGTGGGCCCTTTACAGTGT 10536

QY 3521 AspCysProGlyTrrpThrGlySerArgCysHisThrAlaValCysGlnSerProCys 3540
Db 10537 GACTGCCCGCTGCTGGAGCGGGTCTCGCTGTCTATACAGCTGTTCAGCTCTCCCTGC 10596
QY 3541 LeuAsnGlyGlyLysCysValArgProAsnArgCysHisCysLeuSerSerTrpThrGly 3560
Db 10597 TTAATGGTGGAAATGTGTAAAGACCAACCGATGTCACTGTCTTCTTGGACGGGA 10656
QY 3561 HisAsnCysSerArg 3565
Db 10657 CATAACTGTTCACGG 10671

RESULT 5

US-10-028-248A-7
; Sequence 7, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangoli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
; FILE REFERENCES: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 11152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-028-248A-7

Alignment Scores:

Pred. No.: 0 Length: 11152
Score: 19616.00 Matches: 3510
Percent Similarity: 98.82% Conservative: 16
Best Local Similarity: 98.37% Mismatches: 40
Query Match: 98.21% Indels: 2

DB: 16 Gaps: 1

US-09-977-053-4 (1-3571) x US-10-028-248A-7 (1-11152)
QY 4 ArgLeuAlaPheCysCysTrrpGlyLeuAlaLeuValSerGlyTrrpAlaThrPheGlnGln 23
Db 83 AGAATTTGCGCGGCTGCTGGGGTCTGGCGCTCGTTTGGGGCTGGCGACCTTTTTCAGCAG 142
QY 24 MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro 43
Db 143 ATGTCCCGCTGGCGCAATTTTCAGCTTTCCTCCGAGACCGCGCCCGGGGCCCC 202
QY 44 GlySerIleProAlaProAlaProGlyAspGluAlaLaGlySerArgValGluArg 63
Db 203 GGGAGTATCCCGCGCGCGCTCTTGGCGACGAGCGCGGGGAGCAGAGTGGAGCGG 262
QY 64 LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu 83
Db 263 CTGGGCCAGCGCTTC-----CGCGTGGCTGCTGGCGGAGCTCAGCGAGCGCTGGAG 316
QY 84 LeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArgSerGluLeu 103
Db 317 CTGTCTTCTCTGGTGGAGTATCTGTCAGCGTGGCGGAAGTCAACTTCGCGAGCGAGCTC 376
QY 104 MetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThrArgValAla 123
Db 377 ATGTTCTGTCGCAAGCTGCTGTCGACTTCCCGTGGTGGCCACCGCCACGCGCGTGGCC 436
QY 124 IleValThrPheSerSerLysAsnTrpValValProArgValAspTyrIleSerThrArg 143
Db 437 ATCTGTGACCTTCTCGTCCAGAACTACGTGTGTGGCGCGCTCGATTACATCTCCACCGC 496
QY 144 ArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluIleProAlaIleSerTyrArg 163
Db 497 CGCGCGCGCCAGCAAGTGGCGCTGCTCTCTCAAGAGATCCCTGCCATCTCTTACCGA 556
QY 164 GlyGlyGlyThrTyrThrLysGlyValaPheGlnGlnAlaLaGlnIleLeuLeuHisAla 183
Db 557 GGTGGCGGCACCTACACACGAGCGCTTCCAGACGCGCGCAAAATCTTCTTTCATGCT 616
QY 184 ArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAsp 203
Db 617 AGAGAAACTCAACAAAAGTTGTATTTCTCATCTACTGATGGATATTCCAAATGGGGAGAC 676
QY 204 ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle 223
Db 677 CCTAGACCAATTGCGAGCTCACTCGAGATTCAGAGTGGAGATCTTCACTTTTGGCAT 736
QY 224 TrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCys 243
Db 737 TGGCAAGGGACATTCGAGAGCTCAATGACATGGCTTCCACCCCAAGGAGGAGCACTGT 796
QY 244 TyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeuHisGluAsp 263
Db 797 TACCTGTCTACACAGTCTTTGAAGAAATTTAGCTCGCGGGCATTTGCATGAAGAT 856
QY 264 LeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeuCysAspGlu 283
Db 857 CTACCTTCTGGGAGTTTATTCAGATGATATGTGTCCTGCTCATATCTTTGTGATGAG 916
QY 284 GlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThrGlyHisPhe 303
Db 917 GGCAGGACCTGCTGTGACCGAATGGGAAGCTGCAAAATGTGGGACACACACAGGCCATTTT 976
QY 304 GluCysIleCysGluLysGlyTyrGlyLysGlyLeuGlnTyrGluCysThrAlaCys 323
Db 977 GAGTGCATCTGTGAAAAGGGGTATTACGGGAAGGCTCTGCAGATGATGATGACACAGCTTGC 1036
QY 324 ProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCysIleProCys 343
Db 1037 CCATCGGGGACATCAAAACCTGGAAGCTTCCACAGAGGAGGATCAGCGATTCATTCATGT 1096
QY 344 ProAspGluAsnHisThrSerProGlySerThrSerProGluAspCysValCysArg 363

1097 CCGGATGAATAATCACACCTCTCCACCTGGAGACACATCCCTCGAGACTGTGTCTGCAGA 1156
364 GluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuLysPro 383
1157 GAGGATACAGGCGATCTGGCCAGACCTGTGAACCTTGTCCACTGCCCTGCCCTGAAGCCT 1216
384 ProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAlaAlaCysGly 403
1217 CCGGAAATGGTTACTTTATCCAAACACTTGCACACACACTTCATATGAGCGCTGTGGG 1276
404 ValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuProAsn 423
1277 GTCCGATGTACCTCGATTGATCTTGTGGAAGCAGCATCATCTTATGTCTACCCAAT 1336
424 GlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHisLeuArgGln 443
1337 GGTTTGTGGTCCGGTTTCAGAGAGCTACTGCAGAGTAAAGACATGTCTCATCTCCGCCAG 1396
444 ProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThrThrCysLeu 463
1397 CCGAAACATGCCACATCAGCTCTGTCTACAGGGAATGTTATATAGACACATGTTTG 1456
464 ValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCysGlnGlyAsn 483
1457 GTTGCTGTGATGAGGGTACAGACTAGAGGCAGTGTATAGCTTACTTGTCAAGGAAC 1516
484 SerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThrPheGlnMet 503
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504 ProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPheGlyThr 523
1577 CCCAAAGATGTCAATCATATCCCCCACTCTGTGGCAGCAGCAGCAAAATTTGGAGCG 1636
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1637 ATCTGTATGTAGTTGCCGCCAAGGGTTCAATTTATCTGGAGTCAAGAAATGCTGAGA 1696
544 CysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCysLysAspValGlu 563
1697 TGTACCACCTTCGGAAATGGAATGTGGAGTTCAGGCAGCTGTGTGTAAAGACGTGGAG 1756
564 AlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGlnGlnAspSer 583
1757 GCTCCTCAATCAACTGTCTCAGGACATAGAGCTTAAGACTCTGGACAGCAAGATTCT 1816
584 AlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysValSerVal 603
1817 GCCAATGTACCTGGCAGATTCCACAGCTAAAGACAACTCTGTGTGAAAGGTGTCAATC 1876
604 HisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspValAlaIleVal 623
1877 CGCGTTTCATCCAGCTTTCCACCCACCTTACCTTTTCCCAATTTGGAGATGTGTATCGTA 1936
624 TyrThrAlaThrAsnLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIle 643
1937 TACCGGCAACTGACCTATCCGCAACCCAGCCAGCTGCATTTTCATATCAAGGTTAT 1996
644 AspAlaGluProProValIleAspTrpCysArgSerProProValGlnValSerGlu 663
1997 GATGCAGAACCACTGTCTAGACTGTGTGAGATCTCCACTCCCGTCCAGGTTCTGGAG 2056
664 LysValHisAlaSerTrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeu 683
2057 AAGGTACATGCGCAAGCTGGATGAGCTTCTCAGCAACTCAGGGGCTGAATTG 2116
684 ValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyThrIleValGln 703
2117 GTCAITACCAAGAGTATACACAGGAGACCTTTCCCTCAAGGGGAGACTATAGTACAG 2176
704 TyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLys 723

2177 TATACAGCCACTGACCCCTCAGGTAAATACAGGATATGTGTATATTCATATGTGTCAATAA 2236
724 GlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAsp 743
2237 GGTTCCTCCCTGTGAATTCATATTCACACCTGTAAATGGGATTTTATATGCACATCCAGAT 2296
744 AsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySer 763
2297 AATCTGGAGTCAACTGTACATTAACCTTGTGGAGGGCTACGATTTTCACAGAGGGTCT 2356
764 ThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThrTyrThrGlu 783
2357 ACTGCAAGATTAATTTGTCTTATAGAGATGGCGTCTGGAACCCACATATACCACCTGAA 2416
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804 TyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAlaPheGlu 823
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2597 CTGGAGAGAACCTGACCAAAAAATATTGCTAGATATTAATATGACTATGAANAATGGC 2656
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2717 TTCTTGACACTGTGCAAGAAACAGCCACCAAGCATCGCAATGCGCAATGCTCCAGGATT 2776
904 LysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIleThrAlaSer 923
2777 AAGAAGTGGCCCATTTATCTGACTATAAATTAAGTTAATTTTAAACATCACAGTAGT 2836
924 ValProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGlnArgLeuLeu 943
2837 GTGCCATTACCCGATGAAGAAATGATACCTTGAATGGGAATTCAGAACGACTCCTT 2896
944 GlnThrLeuGluThrIleThrAsnLysLeuLysLeuArgThrLeuAsnLysAspProMetTyr 963
2897 CAGACATTTGGAACCTATCAAAATAAAGCTGAAAAGGACTCTCAACAAAGACCCCATGTAT 2956
964 SerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLys 983
2957 TCTTTTCAGCTTGCATCAGAAATACCTTATAGCCAGCAGCAATTCATTTAGAAACAAAGAAG 3016
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1004 LeuGlyThrTyrThrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyr 1023
3077 TTGGGAACCTTATTAATCTGGAACATTTTCACTGTGAAAAGCTGCCCGGATCGGATCCTAT 3136
1024 GlnAspGluGluGlnLeuLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyr 1043
3137 CAAGATGAAGAGGGCACTTGATGTGACAGCTTTTCCCTCTGGAATGTACCGAATAT 3196
1044 IleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyr 1063
3197 ATCCATTCAAGAAACATCTCTGATTGTAAAGCTCAGTGTAAACAAGGCACCTTACTATAC 3256
1064 SerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySer 1083
3257 AGTGGACTTGGAGACTTGTGAATCTGTGCCACTTATTCAGCCAAAATTTGGTTCC 3316

Db 5477 ATTTATACAGTAGGTCGGAAGTACATTTTCGGTTCAGGAAGATACAGTTGATGGGA 5536
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 Db 5537 GTAACCAAAATCACATGTTTGGAGTCTGGAGATCGAATCATCATTAATACCATATTGTATA 5596
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 Db 5597 GCTGTTTCATGTTGTAACACCGGCTATTCAGAAATGGTTGATGGAGGTAGCATTTT 5656
 Qy 1864 ThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAlaGlyAspLys 1883
 Db 5657 ACTTTTGGCAGCAAGTAGCATATAGGTGTAATAAGGATATCTCTGGCCGGTGATATA 5716
 Qy 1884 GluSerSerCysLeuAlaAsnSerTrpSerHisSerProValCysGluProVal 1903
 Db 5717 GAATCATCTGCTGTCTTAACAGTTCTTGGAGTCATTCCTCCCTGCTGTGTGACACAGTG 5776
 Qy 1904 LysCysSerProGluAsnIleAsnAsnGlyLysTyrIleLeuSerGlyLeuThrTyr 1923
 Db 5777 AAGTGTTCCTAGTCCGGAAATATAAATAATGGAATAATATATTTTGAGTGGGCTTACCTAC 5836
 Qy 1924 LeuSerThrAlaSerTyrCysAspThrGlyTyrSerLeuGlnGlyProSerIleIle 1943
 Db 5837 CTTTCTACTGCATCATATTCATGCGNTACAGATACAGCTTACAGGGCCCTTCCATTAAT 5896
 Qy 1944 GluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeuValPheCys 1963
 Db 5897 GAATGCACGGCTTCTGGCATCTGGACAGAGCGCCACCTGCTGTCTCACCTGCTCTTCGT 5956
 Qy 1964 GlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThrPheArgAsn 1983
 Db 5957 GGAAACACCATGCTCCATCAAGATGCTGTCTATTACGGGGAATAACTTCACTTTCAGGAAC 6016
 Qy 1984 ThrValThrTyrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThrIleGluCys 2003
 Db 6017 ACCGTCACTTACACTTGCAGAAAGGCTATATCTCTGCTGGTCTTGACACCATTTGATGC 6076
 Qy 2004 LeuAlaAspGlyLysTrpSerArgSerAspGlnGlnCysLeuAlaValSerCysAspGlu 2023
 Db 6077 CTGGCCGACGGCAAGTGGAGTAGAAGTGCACGACAGTGCCTGGCTGTCTCTGTGTATGAG 6136
 Qy 2024 ProProfileValAspHisAlaSerProGluThrAlaHisArgLeuPheGlyAspIleAla 2043
 Db 6137 CCACCCATTGTGGACCAACGCTCTCCAGAGATGCCCCATCGGCTCTTTGGAGACATTCGA 6196
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 Qy 2104 AlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThrSerAlaLys 2123
 Db 6377 GCTGGCTCAGTTGTGAGCTTTAAATGCAATGGAGGCTTTGTACTGACACATCCCTCAGCAAG 6436
 Qy 2124 IleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGlnCysIlePro 2143
 Db 6437 ATTGAATGTATGAGAGGTGGGCGAGTGAACCTTCCCTCCATGTCTCCATCCAGTGCATCCCT 6496
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 Db 6497 GTGCGGTGTGGAGACCCCAAGCATCATGATGGCTATGCAAGTGGATCAAACTACAGT 6556
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Db 6557 TTTGGAGCCATGGTGGCTTACAGCTGCAACAGGGGTTCTTACATCAAGGGCGAAAGAAG 6616
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 Db 6617 AGCACCTCGGAAGCCACAGGGCAGTGGAGTAGTCTCTATACCGACGTGCCACCGGTATCT 6676
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 Qy 2224 GluSerGluValArgTyrGlnCysAsnProGlyTyrLysSerValGlySerProValPhe 2243
 Db 6737 CAGAGTGAAGTGAGCTATCAGTGTAAACCGGGCTATTAAGTCAGTCGGAAGTCTCTGTATTT 6796
 Qy 2244 ValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysValProLeuAsp 2263
 Db 6797 GTCTGCCAAGCCAAATCGCCACTGGCCACAGTGAATCCCTCTGTATGTGTCTCTCGAC 6856
 Qy 2264 CysGlyLysProProIleGlnAsnGlyPheMetLysGlyGluAsnPheGluValGly 2283
 Db 6857 TGTGGAAACCTTCCCCGATCCAGATATGGCTTCATGAAAGGAGAAACCTTTGAAGTAGG 6916
 Qy 2284 SerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSerSerTrpThr 2303
 Db 6917 TCCAAGGTTCAAGTTTCTGTAAATCAGGCTTATGAGCTTGTGTGTCACAGTCTCTTGACA 6976
 Qy 2304 CysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAlaLysCys 2323
 Db 6977 TGTTCAGAAATTCGGCAATGGAATTAAGAGTCAAAATCCAAAGTGCATGCTGCCAAGTGC 7036
 Qy 2324 ProGluProProLeuLeuGluAsnGlnLeuValLysGluLeuThrThrGluValGly 2343
 Db 7037 CGAGAGCGCCCTCTTGGAAACCCAGCTAGTATTAAGAGCTTGACCAACCGAGGTAGGA 7096
 Qy 2344 ValValThrPheSerCysLysGlyGlyHisValLeuGlnGlyProSerValLeuLysCys 2363
 Db 7097 GTTGTGACATTTCTGTAAAGAGGCAATGCTCTGCAAGGCGCCCTCTGCTCTGCAATGC 7156
 Qy 2364 LeuProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeuCysThrPro 2383
 Db 7157 TTGCCATCCCAAGCAATGAATGACTTTTCCCTGTGTGTGAAGATGTTCTTTGTATCCCCA 7216
 Qy 2384 ProProLeuLysSerPheGlyValProIleProSerSerAlaLeuHisPheGlySerThr 2403
 Db 7217 CTTCCCTTAATTTCTTGTGTGCTCCCATTCCTCTCTGCTCTTCTCATTTTGGAGTACT 7276
 Qy 2404 ValLysTyrSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrThrLeuCysGln 2423
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 Qy 2424 ProAspGlyThrTrpSerProLeuProGluCysValProValGluCysProGlnPro 2443
 Db 7337 CTTGATGGACCTGGAGCTCTCCACTGCCAGATGTGTTCAGTAGATGTCTCCAGCAGCTCTC 7396
 Qy 2444 GluGluIleProAsnGlyIleIleAspValGlnGlyLeuAlaTyrLeuSerThrAlaLeu 2463
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 Qy 2464 TyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrLeuCysGlyGluAsn 2483
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 Qy 2524 CysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAsp 2543
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Db 263 |||||CTGGCGCAGGCGTTC-----CGCGTCGCGTCTGTCGGGAGCTCAGCAGCGCCTGGAG 316
Qy 84 LeuValPheLeuValAspSerSerValGlyGluValAenPheArgSerGluLeu 103
Db 317 CTTGTCTTCTCTGTGGTATGATTGCTCAGCGTGGCGAGTCAACTTCOGCAGCGAGCTC 376
Qy 104 MetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThrArgValAla 123
Db 377 ATGTTCTGTCGCGAAGCTGCTCCGACTCTCCCGCTGGTGGCCACGCGCACGCGGTGGCC 436
Qy 124 IleValThrPheSerSerLysSerValValProArgValAspTyrLleSerThrArg 143
Db 437 ATCTGTACCTTCTGTCCTCAAGAACTACGTGTGGTGGCGCGTGGATTAATCTCCACCCGC 496
Qy 144 ArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluLeuProAlaIleSerTyrArg 163
Db 497 CGCGCGCGCCAGCAGTGGCGCTCTCTCCAGAGATCCCTGCCATCTCTCTACCGA 556
Qy 164 GlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaGlnIleLeuLeuHisAla 183
Db 557 GGTGGCGGCACCTACACCAAGGCGCTTCCAGCAGCGCGCAAAATCTTCTTTCATGCT 616
Qy 184 ArgGluAsnSerThrLysValValPheLeuLleThrAspGlyTyrSerAsnGlyGlyAsp 203
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Qy 204 ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle 223
Db 677 CCTAGACCAATTGCAGCGTCACTGCGAGATTTCAGAGTGGAGATCTTCACCTTTGGCATA 736
Qy 224 TrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCys 243
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Qy 244 TyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaLeuAlaLeuHisGluAsp 263
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Qy 264 LeuProSerGlySerPheIleGlnAspMetValHisCysSerTyrLeuCysAspGlu 283
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Qy 304 GluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCysThrAlaCys 323
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Qy 324 ProSerGlyThrTyrLysProGluGlySerProGlyLysSerProGlyLysSerCysValProCys 343
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Qy 344 ProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCysValCysArg 363
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Qy 404 ValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuLeuCysLeuProAsn 423
Db 1277 GTCCGATGTCACTCGGATTTGATCTTGTGGGAGCAGCATCATCTTATGCTTACCCCAAT 1336
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Qy 464 ValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCysGlnGlyAsn 483
Db 1457 GTTGCTCTGTATGAAGGGTACAGACTAGAGCGAGTATAGCTTACTTGTTCAGGAAC 1516
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Qy 504 ProLysAspValIleLeuSerProHisAsnCysGlyLysGlnProAlaLysPheGlyThr 523
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Qy 564 AlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGlnAspSer 583
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Qy 604 HisValHisProAlaPheThrProTyrLeuPheProIleGlyAspValAlaIleVal 623
Db 1877 CGCGTTATCCAGCTTTCACCCCACTTACCTTTTCCCAATTTGGAGATTTGCTATCGTA 1936
Qy 624 TyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIle 643
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Qy 644 AspAlaGluProProValIleAspTrpCysArgSerProProValGlnValSerGlu 663
Db 1997 GATGCAAGCACTGCTATAGACTGTGTGAGATCTCCACCTCCGCTCCAGTCTCGGAG 2056
Qy 664 LysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeu 683
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Qy 684 ValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGln 703
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Qy 724 GlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAsp 743
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QY 1064 SerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySer 1083
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QY 1144 ProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSerSerPhe 1163
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QY 1184 LysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHis 1203
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QY 1504 SerValAsnAspGlyArgTyrHisHisIleAlaIleThrTyrThrSerAlaAsnGlyIle 1523
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Db 6137 CCACCAATTGTGACCAAGCTCTCTCAGAGACTGCCATCGGCTCTTTTGGAGACATTGCA 6196
Qy 2044 PheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeuCysAsnAla 2063
Db 6197 TTTCTACTGCTCTGTAGTGTACAGCTAGCAGCAATTCCTCCAGCTTCTCTGCAATGCC 6256
Qy 2064 GlnGlyLysTrpValProProGluGlyGlnAspMetProArgCysIleAlaHisPheCys 2083
Db 6257 CAGGGCAAGTGGGTACCCCCAGAGGTCAAGACATGCCCGTCTGTATAGCTCATTTCTGT 6316
Qy 2084 GluLysProProSerValSerTyrSerIleLeuGluSerValSerLysAlaLysPheAla 2103
Db 6317 GAAACCTCCATCGGTTTCTATAGCATCTTGGAACTCTGGAGCAAGCAAAATTTGCA 6376
Qy 2104 AlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThrSerAlaLys 2123
Db 6377 GCTGGCTCAGTGTGAGCTTTAATGATGATGGAAGCTTTGTACTGAACACCTCAGCAAG 6436
Qy 2124 IleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGlnCysIlePro 2143
Db 6437 ATTGAATGTATGAGAGGTGGGCAAGTGGAAACCTTCTCCCATGTCCATCCAGTGCATCCT 6496
Qy 2144 ValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySerAsnTyrSer 2163
Db 6497 GTGGGTGTGGAGAGCCACCAAGCATCATGAATGGCTATGCAAGTGGATCAAACTACAGT 6556
Qy 2164 PheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGlyLysLys 2183
Db 6557 TTTGGAGCCATGTGGTTTACAGTGCACAGGGGTTCTACATCAAGAGGGGAAAGAG 6616
Qy 2184 SerThrCysGluAlaThrGlyGlnTrpSerSerProIleProThrCysHisProValSer 2203
Db 6617 AGCACCTGCCAGCCACAGGCGAGTGGAGTAGTCTTATACCGAGTGCACCGCGTATCT 6676
Qy 2204 CysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrGlyArgIlePhe 2223
Db 6677 TGTGGTGAACCACTTAAGGTGAGAAATGGCTTTCTGGAGCATACAACTGGCAGGATCTTT 6736
Qy 2224 GluSerGluValArgTyrGlnCysAsnProGlyTyrLysSerValGlySerProValPhe 2243
Db 6737 GAGAGTGAAGTGAAGTATCAGTGTAAACCCGGCTATAAGTCAAGTGGAGTCTCTGATTT 6796
Qy 2244 ValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysValProLeuAsp 2263
Db 6797 GTCTGCCAAGCCAATCGCCACTGGCAGACGTGAATCCCTCTGTGATGTGTGTCTCTCGAC 6856

2264 CysGlyLysProProPheGlnGlnGlyPheMetLysGlyGluAsnPheGluValGly 2283
6857 TGTGGAAACCTCCCGCATCCAGATGGCTTCATGAAGAGGAAACCTTTGAAGTAGGG 6916
2284 SerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSerTrpThr 2303
6917 TCCAGGTTTCAGTTTTCTGTAAAGGGTATAGCTTTGTGGTACAGTTCTTGGACA 6976
2304 CysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAlaLysCys 2323
6977 TGTGAGAATCTGGCAAAATGGAATAGAAAGTCAATCCAAAGTGCATGCTGCCAAGTGC 7036
2324 ProGluProProLeuLeuGlnGlnLeuValLeuLysGluLeuThrThrGluValGly 2343
7037 CCAGAGCCGCCCTCTTGGAAACCAAGCTAGTATTTAAAGAGGTGACCAAGGAGTAGGA 7096
2344 ValValThrPheSerCysLysGluGlyHisValLeuGlnGlnProSerValLeuLysCys 2363
7097 GTTGTGACATTTTCTGTAAAGAGGGCATGTCTCCAGAGGCCCTCTGTCTGTGAATGC 7156
2364 LeuProSerGlnGlnTrpAsnAspSerPheProValCysLysLeuValLeuCysThrPro 2383
7157 TTGCCATCCAGCAATGGAATGACTCTTCCCTGTTGTGAAGATTGTTCTTTGTACCCCA 7216
2384 ProProLeuLysSerPheGlyValProLysProSerSerAlaLeuHisPheGlySerThr 2403
7217 CCTCCCTCAATTTCTGTGTGCTCCCATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7276
2404 ValLysThrSerCysValGlyPhePheLeuValGlyAsnSerThrThrLeuCysGln 2423
7277 GTCAAGTATTTCTGTGTAGTGGTTTTTCTTAAGAGGAATTTCTACCAACCTCTGCCAA 7336
2424 ProAspGlyThrTrpSerProLeuProGluCysValProValGluCysProGlnPro 2443
7337 CTGTATGGACCTGGAGCTCTCCACTGCCAGAAATGTTCCAGTAGAATGTTCCCAACT 7396
2444 GluGluLeuProAsnGlyLysLeuValGlnGlnGlyLeuAlaTyrLeuSerThrAlaLeu 2463
7397 GAGGAATATCCCAATGGAATCATTTGATGTGAGGCTTTGCCCTATCTCAGCAGCTCTC 7456
2464 TyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsn 2483
7457 TATACCTGCAGCAGGCTTTGATTTGTTGGGAAATACCTACCAACCTTTTGTGGAGAAAT 7516
2484 GlyHisTrpLeuGlyLysProThrCysLysAlaLeuGluCysLeuLysProLysGlu 2503
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2504 IleLeuAsnGlyLysPheSerThrAspLeuHisTyrGlyGlnThrValThrTyrSer 2523
7577 ATTTTGAATGGCAAAATTTCTTACACGGACCTACACTATGGACAGACCGTTACTCTCT 7636
2524 CysAsnAlaGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAsp 2543
7637 TGCNACCGAGGCTTTCCGCTCGAGGTCCAGTCCCTGACCTGTTTACAGACAGTGTAT 7696
2544 TrpAspValAspAlaProSerCysAsnAlaLeuHisCysAspSerProGlnProLysGlu 2563
7697 TGGATGTAGATGCCCATCTTGCATATGCTATCCACTGTGATTTCCCAACCAATTTGAA 7756
2564 AsnGlyPheValGluGlyAlaAspTyrSerTyrGlyValAlaLeuLysTyrSerCysPhe 2583
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7817 CTGGGTTTTTCAGTGGCTGGTCTATGCCATGCAGACCTGTGTGAGAGTCAGGTCACT 7876
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7877 TCCATCCCAACATGTATGCCAATAGACTGTGGCTCTCCCTCATATATAGATTTTGGAGAC 7936

2624 CysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspMetMetGluVal 2643
7937 TGTACTAAACTCAAGATGACCAGGATATTTTGACCAAGACACGATCATGTGGAAGTT 7996
2644 ProTyrValThrProHisProTyrHisLeuGlyValAlaLysThrTrpGluAsn 2663
7997 CCATATGTGACTCTCTCACCTCTTATCAATTTGGGAGCAGTGGCTAAAACCTGGGAAAT 8056
2664 ThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyr 2683
8057 ACAAGAGAGTCTCTCTGCTACATTCATCAAACTTTCTGTATGTATACCATGGTTTCATAC 8116
2684 ThrCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuLysCysGlnGluAspGly 2703
8117 ACTGTAAATCCAGGATATGAATCTCTGGGAAACCTCTGTCTGATCTGCCAGGAGATGGA 8176
2704 ThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuProThrAlaPro 2723
8177 ACTTGGATGGCAGTGCACCATCTGCAATTTCAATTTGAATGTGACTTGCCTACTGCTCCT 8236
2724 GluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGlnTyrSerCys 2743
8237 GAAAATGGCTTTTTCGGTTTTTACAGAGACTAGCATGGGAAGTCTGTGCCAGTATAGCTGT 8296
2744 LysProGlyHisIleLeuAlaGlySerAspLeuValGlyLeuGluAsnArgLysTrp 2763
8297 AAACCTGGACACATTTCTACAGGCTCTGACTTAAAGCTTTGTCTAGAGATAGAAAGTGG 8356
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8357 AGTGTGTGCTCCCAAGCTGTGAAGCCATTTTCATGCAAAAAGCAAAATCCAGTCATGAAT 8416
2784 GlySerIleLysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGluCysAspPro 2803
8417 GGATCCATCAAAAGGAGCAACTACATCTCTGAGCAGCTGTGTATGATGTGAGTGTGACCCC 8476
2804 GlyTyrValLeuAsnGlyThrGluArgArgThrCysGlnAspAspLysAsnTrpAspGlu 2823
8477 GGATATGTCTGTATGGCACTGAGAGGAGACATGTCAGGATGACAAAACTGGGATGAG 8536
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8537 GATGAGCCCATTTGCAATCTCTGTGACTGCAGTTCACCCCTCAGCTCAGCAATGGCCAG 8596
2844 ValArgGlyAspGluTyrThrPheGlnLysGluIleGluTyrThrCysAsnGluGlyPhe 2863
8597 GTGAGAGGAGACGAGTACACATTTCCAAAAGAGATTGAATACACTTGCATTAAGGGGTTTC 8656
2864 LeuLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTrpSerGlyAlaThr 2883
8657 TTGCTTGAGGGAGCCAGAGTGGGTTTGTCTTGCCCAATGGAAGTTGGAGTGGAGCACT 8716
2884 ProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGlyValThrGlu 2903
8717 CCGACTGTGTGCTCTCTGAGATGTGCCACCCGCCCACTGGCCCAATGGGGTGACCGAA 8776
2904 GlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGluGlyTyrIleLeu 2923
8777 GGCCTTGACTATGGCTTTCATGAGGAGTAACATTTCCACTGTCCAGGGGCTACATCTTG 8836
2924 HisGlyValaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAlaGluIleProLeu 2943
8837 CACGGTCTCCAAAACCTCACTGTCTGAGTGGCACTGGGATGCGAGATTCCTCTCTC 8896
2944 CysLysProValAsnCysGlyProGluAspLeuAlaHisGlyPheProAsnGlyPhe 2963
8897 TGTAAACCACTCAACTGTGGACCTCTGAAGATCTTGCCCAATGGTTTCTCTAATGGTTTT 8956
2964 SerPheIleHisGlyHisIleGlnTyrGlnCysPheProGlyTyrLysLeuHisGly 2983
8957 TCTTTTATTCATGGGGGCCATATACAGTATCAGTGTCTTCTCGTATATAGCTCCATGGA 9016
2984 AsnSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySerProSerCysLeu 3003

Db 9017 AATTCATCAAGAGTGCCTCTCCAAATGGCTCTGGAGTGGCAGCTCACCTTCTGCTG 9076
Qy 3004 ProCysArgCysSerThrProValIleGluTyrGlyThrValAsnGlyThrAspPheAsp 3023
Db 9077 CCTTGCAGATGTTCCACACCAAGTAATTAATGAAATATGGAATCTGTAATGGGACAGATTTTGAC 9136
Qy 3024 CysGlyValAlaAaGlyIleGluCysPheLysGlyPheLysLeuLeuGlyLeuSerGlu 3043
Db 9137 TGTGAAAGGAGCCCGGATTCAGTGCCTTCAAGGCTTCAAGCTCTTAGGACTTTCGAA 9196
Qy 3044 IleThrCysGluAlaAspGlyGlnTrpSerSerGlyPheProHisCysGluHisThrSer 3063
Db 9197 ATCACTGTGAAGCGATGGCAGTGGAGCTCTGGTTCCTCCCACTGTGAACACACTTCT 9256
Qy 3064 CysGlySerLeuProMetIleProAsnAlaPheIleSerGluThrSerSerTrpLysGlu 3083
Db 9257 TGTGTTCTCTTCCAAATGATACCAATGCGTTCATCAGTGAGACAGCTCTTGGAAAGGA 9316
Qy 3084 AsnValIleThrThrSerCysArgSerGlyTyrValIleGlnGlySerSerAspLeuIle 3103
Db 9317 AATGTGATAACTTACAGCTGCAGGCTTGGATATGTCATACAGGCGAGTTCAGATCTGATT 9376
Qy 3104 CysThrGluLysGlyValTrpSerGlnProTyrProValCysGluProLeuSerCysGly 3123
Db 9377 TGTACAGAAAGGGGTATGAGCCAGCTTATCCAGTCTGTGAGCCCTTGTCTGTGG 9436
Qy 3124 SerProSerValAlaAsnAlaValAlaThrGlyGluAlaHisThrTyrGluSerGlu 3143
Db 9437 TCCCAACCGTCTGTGCCAATGCAAGTGCAGTGCAGTGCAGAGGACACACCTATGAAAGTGA 9496
Qy 3144 ValLysLeuArgCysLeuGluGlyTyrThrMetAspThrAspThrAspThrPheThrCys 3163
Db 9497 GTGAAACTCAGATGTCTGGAAGGTATACGATGATACGATGATACAGATACATTCACCTGT 9556
Qy 3164 GlnLysAspGlyArgTrpPheProGluArgIleSerCysSerProLysLysCysProLeu 3183
Db 9557 CAGAAAGATGTCGTGCTGCTTCCCTGAGAGATCTCTGCAGCTCTTAAAAATGCTCTC 9616
Qy 3184 ProGluAsnIleThrHisIleLeuValHisGlyAspAspPheSerValAsnArgGlnVal 3203
Db 9617 CCGAAACATACATACATATCTGTACATGGGAGCATTTTCAAGTGTGAATAGCAAGTT 9676
Qy 3204 SerValSerCysAlaGluGlyTyrThrPheGluGlyValAsnIleSerValCysGlnLeu 3223
Db 9677 TCTGTGTCATGTGCAGAGGGTATACCTTTGAGGGAGTTAAATATCATATCATGTATGT 9736
Qy 3224 AspGlyThrTrpGluProPheSerAspGluSerCysSerProValSerCysGlyLys 3243
Db 9737 GATGAACTGGAGCCACCATCTCCAGTGAATCTTGCACTCCAGTTTCTTGTGGAAA 9796
Qy 3244 ProGluSerProGluHisGlyPheValValGlySerLysTyrThrPheGluSerThrIle 3263
Db 9797 CCTGAAAGTCCAGACATGGATTTGTGGTGGCAGTAAATAACCTTTGAAAGACAAAT 9856
Qy 3264 IleTyrGlnCysGluProGlyTyrGluLeuGluGlyAsnArgGluArgValCysGlnGlu 3283
Db 9857 ATTTATCATGTGTGACCTGGCTGTATGAACTAGAGGGGACAGGAAACGTGTCTGCCAGAG 9916
Qy 3284 AsnArgGlnTrpSerGlyGlyValAlaIleCysLysGluThrArgCysGluThrProLeu 3303
Db 9917 AACACAGTGTGAGGGGTGGCAATATGCAAGAGACAGAGTGTGAATCCACTT 9976
Qy 3304 GluPheLeuAsnGlyLysAlaAspIleGluAsnArgfThrThrGlyProAsnValValTyr 3323
Db 9977 GAATTTCTCAATGGGAAAGCTGACATTTGAAACAGACGACGTGGACCCCAACGCTGGTATAT 10036
Qy 3324 SerCysAsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysfThrGluAsnGly 3343
Db 10037 TCCTGCACAGAGGCTTACAGTCTTGAAGGGGCCATCTGAGGGACACTGCACAGAAATGA 10096
Qy 3344 ThrTrpSerHisProValProLeuCysLysProAsnProCysProValProPheValIle 3363

Db 10097 ACCTGGAGCCACCAGCTCCCTCTCTGCAAAACCAATCCATGCCCTGTTCTTTTGAT 10156
Qy 3364 ProGluAsnAlaLeuLeuSerGluLysGluPheTyrValAspGlnAsnValSerIleLys 3383
Db 10157 CCGGAATGCTCTGCTCTGAAAGAGGTTTATGTATGTATCAGATGTGTCATCAAA 10216
Qy 3384 CysArgGluGlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAsnProAspGluThr 3403
Db 10217 TGTAGGAAGGTTTCTGCTGAGGGCCAGCGCATCATTTACCTGCAACCCCGACGAGAG 10276
Qy 3404 TrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProProAlaHisValGlu 3423
Db 10277 TGGACACAGACAGCGCAAAATGTGAAAAATCTCATGTGGTCCACAGCTCAGCTAGAA 10336
Qy 3424 AsnAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyrSerCysTyr 3443
Db 10337 AATGCAATGTCTGAGGGCGTCAATATCAATATGAGACATCATCACCTACTCATGTTAC 10396
Qy 3444 SerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGlyThrTrpThr 3463
Db 10397 AGTGATACATGTTGGAGGTTTCTTGAGGAGTGTGTTTGTAGAAAATGGAACATGGACA 10456
Qy 3464 SerProProfileCysArgAlaValCysArgPheProCysGlnAsnGlyGlyIleCysGln 3483
Db 10457 TCACCTCTATTTGGCAGAGCTGTCTGTGCAATTTCCATGTGAGATGGGGGCATCTGCCAA 10516
Qy 3484 ArgProAsnAlaCysSerCysProGluGlyTyrMetGlyArgLeuCysGluProIle 3503
Db 10517 CGCCCAATGTGTGTTCTGTCCAGAGGGCTGAGTGGGGCGCTCTGTGAAGAACCAATC 10576
Qy 3504 CysIleLeuProCysLeuAsnGlyGlyArgCysValAlaProTyrGlnCysAspCysPro 3523
Db 10577 TGCATCTCTCTGCTGTCTGACGAGGTGCTGTGTGGCCCTTACCAGTGTGATGCCCG 10636
Qy 3524 ProGlyThrThrGlySerArgCysHisThrAlaValCysGlnSerProCysLeuAsnGly 3543
Db 10637 CCTGCTGGACGGGCTCTCGCTGTATACAGCTGTGTGTCAGTCTCCCTGCTTAAATGGT 10696
Qy 3544 GlyLysCysValArgProAsnArgCysHisCysLeuSerSerTrpThrGlyHisAsnCys 3563
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Qy 3564 SerArgLysArgArgThrGlyPhe 3571
Db 10757 TCCAGAAAAGGAGGACTGGGTTT 10780

RESULT 7

US-10-028-248A-5

; Sequence 5, Application US/10028248A

; Publication No. US20030235882A1

; GENERAL INFORMATION:

; APPLICANT: Shimkete, Richard

; APPLICANT: Patturajan, Meera

; APPLICANT: Vernet, Corine

; APPLICANT: Casman, Stacie

; APPLICANT: Malyankar, Uriel

; APPLICANT: Shenoy, Suresh

; APPLICANT: Spytek, Kimberly

; APPLICANT: Gangolli, Esha

; APPLICANT: Miller, Charles

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Smithson, Glennnda

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Liu, Xiaohong

; APPLICANT: Colman, Steven

; APPLICANT: Tchernev, Velizar

; APPLICANT: Si, Jingsheng

; APPLICANT: Edinger, Shlomit

; APPLICANT: Stone, David

; APPLICANT: Sciore, Paul

1697 CTGAGATGACCACTCTCGAATAATGGAATGTGGAGTTCCAGCACTGTGTGAAGAC 1756
562 ValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGlnGln 581
1757 GTGGAGGCTCCTCAAACTCAACTGTCTTAAGCAATAGAGGCTAAGACTCTGGAAACAGCA 1816
582 AspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysVal 601
1817 GATTCTGCCAATGTATACCTGGCAGATTCACACAGCTAAAGACAACTCTGGTGAAGAGTG 1876
602 SerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspValAla 621
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622 IleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisLys 641
1937 ATCGTATACAGGCAACTGACCTATCCGCAACAGCCAGCTGCATTTTCCATATCAAG 1996
642 ValIleAspAlaGluProProValIleAspTrpCysArgSerProProValGlnVal 661
1997 GTTATTGATGCAGAACCACTGTCTAGACTGGTGAGATCTCCACCTCCCGTCCAGGTC 2056
662 SerGluLysValHisAlaLysSerTrpAspGluProGlnPheSerAspAsnSerGlyAla 681
2057 TCGGAGAGGTATATGCCGCACTGGATGAGCCTCAGTTCTCAGAACAACTCAGGTGCT 2116
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2177 GTACAGATATACAGCCACTGACCTCCCTCAGGCAATACAGAGGACATGTGATATCCATATGTC 2236
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2237 ATAAAGAGTTCTCCCTGTGAAATTCATTCACACCTGTAAATGGGATTTATATGCACT 2296
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2297 CCAGATAATACAGGAGTCACTGACATTAATTAATTCCTGGAGGCTATGATTTTCACAGAA 2356
762 GlySerThrAspLysThrCysAlaLysArgPheAlaAsnHisGlyPheLysSerPheGlu 781
2357 GGGTCTACTGACAAAGTATTATGTGCTTATGAGATGGCGTCTGGAAACCAATATACC 2416
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2477 ATGTTCTACAAAGCAGCTCGTTGCTGATGACACAGATCTGATGAAGAAGTTTCTGAAGCA 2536
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2597 TGCAGACTGGAGGAGAACCTGCACCAAAAATATTTGCTAGATATTAATATGACTATGAA 2656
862 AsnGlyPheAlaIleGlyProGlyGlyTrpGlyAlaAlaAsnArgLeuAspTyrSerTyr 881
2657 AATGGCTTTGCAATTTGGTCCAGGTGGCTGGGCTGCAGCTAATAGCTGGATTACTCTTAC 2716
882 AspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 901
2717 GATGATCTTCGGACACTGTGCAAGAAACAGCCACCAAGCATCGCAATGCGCAATGCTTCA 2776
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2837 GCTAGTGTGCATTTACCCGATGAAGAAATGATACCTTGAATGGGAAAATTCAGCAACGA 2896
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2957 ATGTATTCTCTTTCAGCTTGCATCAGAAATATCTATAGCCGACAGCAATTTCAATTAGAAACA 3016
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3017 AAAAAGGCTTTCCCTTCTGCAGACCCAGCTCAGTGTGAGAGGCGGTATGTGTGTCAAT 3076
1002 CysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGly 1021
3077 TGCCCTTTGGAACTTATATATCTGGAACATTTTACCTGTGAAGCTGCCGGATCGGA 3136
1022 SerTyrGlnAspGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThr 1041
3137 TCCTATCAGATCAAGAGGCAACTTTGAGTGCAGCTTTGCCCTCTGGGATGTACAG 3196
1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
3197 GAATATATCCATTCAGAAACATCTCTGATTTGTAAGCTCAGTGTAAACAGGACCTTAC 3256
1062 SerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPhe 1081
3257 TCATACAGTGGACTTGAGACTTGTGATCTGTGTCCACTGGGCACTTATCAGCCAAATTT 3316
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1122 ProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeu 1141
3437 CCTGTGACCACTGCTCTGTGACTATTACCACTTAATGACAGGAGGACCTTCTGCTGTG 3496
1142 AlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSer 1161
3497 GCCTGTCCCTTTTATGGAACCTACCCCATTCGCTGTTCCAGATCCATCAGAGATGTTCA 3556
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3557 AGTTTTAGTTTCAACTTTCTCAGCGCAGAGAAAGTGTGGTGGCCCTTCTGCTCTTGA 3616
1182 HisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnPro 1201
3617 CATATTAAAGAGGCAATGAAATCAGCACTCAGCAAGTCAATGAATGCTTCTTTAACCT 3676
1202 CysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeu 1221
3677 TGCCACAATAGTGGAACTGCGCAGCAACTTGGGCGTGGTTATGTTGCTCTGTCCACTT 3736
1222 GlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeu 1241
3737 GGATATACAGGTTTAAAGTGTGAACAGACATCGATGAGTGCAGCCCACTGCTTGGCTC 3796
1242 AsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyr 1261
3797 AACAAATGGAGTTTGTAAAGACCTAGTTGGGGAATTCATTTGTGAGTGCCTCATAGTTAC 3856
1262 ThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLys 1281
3857 ACAGGTAAGCACTGTGAATTTGAACATCAATGAATGTCACTTAATCCATGTAGAATACAG 3916

Qy	1282	GlyIleCysValaspGlyIvalAlaGlyTyrArgCysThrCysValIysGlyPheValGly	1301
Db	3917	GCACCTGTGTGGATGAATTAATTCATACAGTTGTAAATGTCAGCCAGGATTTTCAGGC	3976
Qy	1302	LeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaVal	1321
Db	3977	AAAAGGTGTGAACAGGTATGTATCAACTCAGTGTATTATAATACCTTTAATAATGCACTG	4036
Qy	1322	CysGluAspGlnValGlyGlyPheLeuCysIysCysProProGlyPheLeuGlyThrArg	1341
Db	4037	TGTGAGACACGAGTTTGGGGATTTCTTTGTGCANAATGCCCACTGGATTTTGGGTACCGA	4096
Qy	1342	CysGlyIysAsnValAspGluCysLeuSerGlnProCysIysAsnGlyAlaThrCysLys	1361
Db	4097	TGTGGAAGAACGTCGATGAGTGTCTCAGTCAGCCATGCAAAAATGAGCTACTCTGTAAA	4156
Qy	1362	AspGlyAlaAsnSerPheArgCysLeuCysAlaIalGlyPheThrGlySerHisCysGlu	1381
Db	4157	GACGGTGCCAAATAGCTTCAGGTGCTGTGTGCAGCTGGCTTCACAGATCACACTGTGAA	4216
Qy	1382	LeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu	1401
Db	4217	TTGACATCAATGAATGTCACTTAATCCATGTAGANAATCAGGCCACTGTGTGATGAA	4276
Qy	1402	LeuAsnSerTyrSerCysLysCysGlnProProGlyPheSerGlyGlnArgCysGluThrGlu	1421
Db	4277	TTAAATTCATACAGTTGTAAATGTCCAGCAGGATTTTCAGSCAAAAGGTGTGAAACAGAA	4336
Qy	1422	GlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeu	1441
Db	4337	CAGTCTACAGGCTTTAACTGGATTTTGAAGTTTCTGGCATCTATGATATGATCATGCTA	4396
Qy	1442	AspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAsp	1461
Db	4397	GATGGCATGCTCCCATCTCTCCATGCTCTAACCTGTACCTTCTGGATGAATCTCTGAC	4456
Qy	1462	AspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeu	1481
Db	4457	GACATGAACATATGGAACACCAATCTCTATGACGTTCATACGCGACGCAATACCTTG	4516
Qy	1482	LeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsn	1501
Db	4517	CTCTGACTGATTAATACGGGTGGGTCTTTATGTGAATGGCAGGAAAAGATAACAAAC	4576
Qy	1502	CysProSerValAsnAspGlyArgTrpPheHisIleAlaIleThrTrpThrSerAlaAsn	1521
Db	4577	TGTCCTCGGTGAATGATGGCAGATGGCATCATATTGCAATCACTTGGACAAGTACTGGT	4636
Qy	1522	GlyIleTrpIysValTyrIleAspGlyLysLeuSerAspGlyAlaGlyLeuSerVal	1541
Db	4637	GGAGCCTGGAGGGGTATATATAAATGGGGAATATATCTGACCGTGGTACTGGCCCTCTCCAT	4696
Qy	1542	GlyLeuProIleProGlyGlyIValAlaLeuValLeuGlyGlnGluAsnAspLysGly	1561
Db	4697	GGCAAAACCATACTGTGTGGCGGTGCATTAGTCTTGGCAGAGCAGACAAAAGGA	4756
Qy	1562	GluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrpAsp	1581
Db	4757	GAGGGGTTCACCCGGCTGAGTCTTTTGTGGGCTCCCAATAGACCAGCTCAACCTCTGGGAC	4816
Qy	1582	TyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeuSer	1601
Db	4817	TATGTCTGTCTCCACAGCAGGTGAGTCACTGGCTACCTCTCTGCCACAGAGAACTCAGT	4876
Qy	1602	LysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValIysIle	1621
Db	4877	AAAGAAACGTTGTAGCATGCCCTGATTTCTTGTGAGGAATTTGGGGGAAGTGAAGATC	4936
Qy	1622	AspSerIysSerIlePheCysSerAspCysProArgLeuGlyIysSerValProHisLeu	1641
Db	4937	GATTTCAAGAGCATATTTTGTTCGATGGCCACGCTTGGAGGGTCAGTGCCTCATCTG	4996

Qy	1642	ArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGly	1661
Db	4997	AGAACTGCATCTGAAGATTTAAACCACGAGTTCCAAAGTCAAATCTGTTCTGTGACACCGGC	5056
Qy	1662	PheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGlnPro	1681
Db	5057	TTCCAGCTGTGTGGGAACCCCTGTGCGAGTACTGTCTGAATCAGAGACAGTGGACACAAACCA	5116
Qy	1682	LeuProHisCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPheHis	1701
Db	5117	CTCCCCACTGTGACGCAATTCGCTGTGGGGTCCACCTCTTTTGGAGAATGCTTCCAT	5176
Qy	1702	SerAlaAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyr	1721
Db	5177	TCAGCCGATCACTTCTATGCTGGCAGCACAGTAACCTTACCAGTGCACCAATATGGCTACTAT	5236
Qy	1722	LeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSerPro	1741
Db	5237	CTATTGGGTCACTCAAGAGATTTCTGTACAGATAATGGGAGCTGGAAACGCGTTTTCACCA	5296
Qy	1742	SerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCys	1761
Db	5297	TCTGCTTAGATGTGATGAGTGTGCAGTTGGATCAGATTGATGAGCATGCTTCTTGC	5356
Qy	1762	LeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyLys	1781
Db	5357	CTGAACGTAGATGCATCTACATATGTTCAATGTGCCACCGTACACAGAGATGGGAAA	5416
Qy	1782	AsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSerSer	1801
Db	5417	AACGTGCGAAGACCTATAAANAATGAAGGCTCCAGGAAATCCGGAAATGGCCACTCTCTCA	5476
Qy	1802	GlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeu	1821
Db	5477	GGTGAGATTTATACAGTAGGTGCGAAGTCCACATTTTCTGTCTCAGGAGAGATACCACTTG	5536
Qy	1822	MetGlyValThrLysIleThrCysLeuGluSerGlyGluTyrPheHisLeuIleProTyr	1841
Db	5537	ATGGGAGTAACCAAAATCACAATGTTGGAGTCTGGAGAAATGGAAATCATCTAAATACCATAT	5596
Qy	1842	CysLysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGluLeu	1861
Db	5597	TGTAAAGCTGTGTTTCATGTGGTAAACCGCTTATTTCCAGAAATGGTTGCAATTGAGGAGTTA	5656
Qy	1862	AlaPheThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAlaGly	1881
Db	5657	GCAATTTACTTTTGGCAGCAAGTGACATATAGTGTGTAAATAGGATATATCTCTGGCCGGT	5716
Qy	1882	AspLysGluSerSerCysLeuAlaAsnSerSerTrpSerHisSerProProValCysGlu	1901
Db	5717	GATAAAGATCATCTCTGTCTGTCTAACAGTTCTTGAGTCAATTCCTCCCTCTCTGTGTGGAA	5776
Qy	1902	ProValLysCysSerSerProGluAsnIleAsnAsnGlyLysTyrIleLeuSerGlyLeu	1921
Db	5777	CCAGTAGAAGTGTTCTTAGTCCGGAATAATAAAATATGGAAATATATATTTTGAGTGGGCTT	5836
Qy	1922	ThrTyrLeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuGlnGlyProSer	1941
Db	5837	ACCTACCTTCTACTGCATCATATTCATGCCATACAGGATACAGCTTACAGGSCCTCTCC	5896
Qy	1942	IleIleGluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeuVal	1961
Db	5897	ATTATTGAATGCACGGCTTCTGGCATCTGGGACAGAGCGCACCTGCTGCTACCTCTGCT	5956
Qy	1962	PheCysGlyGluProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThrPhe	1981
Db	5957	TTCTGTGGAGAACCACTGCATCAACAAAGATGCTGTCTATTACGGGGAAATAACTTCACTTTC	6016
Qy	1982	ArgAsnThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThrIle	2001
Db	6017	AGGAACACCGTCACTTACACTTGCRAAGAGGCTATATCTTCTGCTGCTTGCACACCAT	6076
Qy	2002	GluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnGlnCysLeuAlaValSerCys	2021

6077 GAATGCTGGCCGACGGCAGTGGAGTAGAGTACCAGCAGTGCCTGGCTGCTCTCTGT 6136
2022 AspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGlyAsp 2041
6137 GATGAGCCACCAATGTCGACCAACGCTCTCCAGAGACTGCCCATCGGCTCTTTGGAGAC 6196
2042 IleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeuCys 2061
6197 AITGCAATCTTACTACTGCTCTGATGGTTAAGCTTAGCAGACAAATTCGCCAGCTTCCTGC 6256
2062 AsnAlaGlnGlyLysTrpValProProGluGlnAspMetProArgCysIleAlaHis 2081
6257 AATGCCACGGCAGTGGGTACCCCCAGAAAGGTCAAGACATGCCCCCGTTGTATAGCTCAT 6316
2082 PheCysGluLysProProSerValSerTyrSerIleLeuGlnSerValSerLysAlaLys 2101
6317 TTTCTGTAAGAAACCTCATCGGTTTCTATAGCATCTTGGAAATCTGTGAGCAAGCAAAA 6376
2102 PheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThrSer 2121
6377 TTTGAGCTGGCTCAGTTGTAGCTTTTAAATGATGGAAGGCTTTGTACTGAAACACTCA 6436
2122 AlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGlnCys 2141
6437 GCAGAGATTGAATGATGAGAGGTGGCAGTGGAAACCTTCCCCCATGTCCATCCAGTGC 6496
2142 IleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySerAsn 2161
6497 ATCCCTGTGCGGTGTCGAGAGCCACCAAGCATCATGAATGGCTATGCAAGTGGATCAAAC 6556
2162 TyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGlyGlu 2181
6557 TACAGTTTTGGAGCCATGGTGGCTTACAGCTGCACAAAGGGGTTCATCATCAAGGGGAA 6616
2182 LysLysSerThrCysGluAlaThrGlyGlnTrpSerSerProIleProThrCysHisPro 2201
6617 AAGAGAGCACCTGCGAGGCCACAGGCGAGTGGAGTAGTCTCTATACCGAGTGCACCCG 6676
2202 ValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrGlyArg 2221
6677 GTATCTTGTGGTGAACCACTAAGGTTGAGATGGCTTTCTGGAGCATCAACTGGCAGG 6736
2222 IlePheGluSerGluValArgTyrGlnCysAsnProGlyTyrLysSerValGlySerPro 2241
6737 ATCTTTGAGAGTGAAGTGGATTCAGTGTAAACCCGGCTTAAAGTCAGTGGGAAGTCTT 6796
2242 ValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysValPro 2261
6797 GTATTTGTCTGCCAGCCATCGCCACTGGCAGTGGATGCCCTCTGTATGTGTCTCT 6856
2262 LeuAspCysGlyLysProProProIleGlnAsnGlyPheMetLysGlyGluAsnPheGlu 2281
6857 CTCGACTGTGGAAACCTCCCGCATCCAGATGGCTTCATGAAGAGAGAAAACTTTGAA 6916
2282 ValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSerSer 2301
6917 GTAGGTCACAGGTTTCAAGTTTCTGTATAGGGTTATGAGCTTGTGTGACAGTTCT 6976
2302 TrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAla 2321
6977 TGGACATGTCAGAAATCTGGCAATGGAATAGAACTCAATCCAAAGTGATGCCCTGCC 7036
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7217 ACCCCACCTCCCTAAATTCCTTTGGTGTCCCAATTCCTTCTCTGCTCTTCATTTTGA 7276
2402 SerThrValLysTyrSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrThrLeu 2421
7277 AGTACTGTCAAGTATCTTGTGTAGGTGGGTTCCTTAGAGGAAATCTTACCACCCCTC 7336
2422 CysGlnProAspGlyThrTrpSerSerProLeuProGluCysValProValGluCysPro 2441
7337 TGCACACCTGATGGCACCTGAGCTTCCACTGCCAGATGTGTTCAGAGTAGAATGTCCC 7396
2442 GlnProGluLysProAsnGlyIleIleAspValGlnGlyLeuAlaTyrLeuSerThr 2461
7397 CAACCTGAGGAAATCCCAATGGAATCAATGATGTGACAGCCCTTGCTATCTCAGACAA 7456
2462 AlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCysGly 2481
7457 GCTCTCTATACCTGCAAGCCAGGCTTTGAATTTGGTGGAAATACTACCACCTTTTGTGA 7516
2482 GluAsnGlyHisTrpLeuGlyLysProThrCysLysAlaIleGluCysLeuLysPro 2501
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2522 TyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThr 2541
7637 TACTCTTGCACCGAGGCTTTGGCTCGAAGTCCCAAGTGCCTTGACCTGTGTAGAGACA 7696
2542 GlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGlnPro 2561
7697 GGTGATGGGATGATAGATGCCCATCTTGCATGCCATGCCAGCTGTGATTCGCCCAACC 7756
2562 IleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIleIleTyrSer 2581
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2582 CysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrp 2601
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2602 SerSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAspPhe 2621
7877 TCAAGTTCCATCCCAACATGATGTCCAATAGACTGTGGCCTCCCTCCTCATATAGATTTT 7936
2622 GlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspAspMetMet 2641
7937 GGAGACTGTACTAAACTCAAAAGATGACCGGGATATTTTGAGCAAGAGAGACATGATG 7996
2642 GluValProTyrValThrProHisProTyrHisLeuGlyAlaValAlaLysThrTrp 2661
7997 GAAGTTCCATATGTGACTCTCCACCTCTCTATCAITTTGGAGCAGTGGCTTAAACCTCG 8056
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8117 TCATACACCTGTGAATCAGGATATGAATCTCTGGGAACCTCTGTGCTGATCTGCAGAA 8176
2702 AspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuProThr 2721
8177 GATGGAACTTGGAAATGGCAGTGCACCATCTCTGCATTTCAATTTGAATGTGACTTGCCTACT 8236
2722 AlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGlnTyr 2741
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QY 2742 SerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArg 2761
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QY 2762 LysTrpSerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProVal 2781
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QY 2782 MetAsnGlySerIleLysGlySerAsnTrpThrLeuSerThrLeuTrpGluCys 2801
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QY 2802 AspProGlyTrpValLeuAsnGlyThrGluArgArgThrCysGlnAspLysAsnTrp 2821
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QY 2822 AspGluAsnGluProIleCysIleProValAspCysSerProProValSerAlaAsn 2841
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QY 2842 GlyGlnValArgGlyAspGluTrpThrPheGlnLysGluIleGluTrpThrCysAsnGlu 2861
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DB 9377 CTGATTTGTACAGAGAAAGGGGTATGAGCCAGCCTTATCCAGTCTGTGAGCCCTTGTTC 9436
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Db 10577 CCAATCTGCATTTCTCCCTGTCTGAACGGAGGTGCTGTGTGGCCCTTACCAAGTGTGAC 10636
QY 3522 CysProGlyTyrTrpThrGlySerArgCysHisThrAlaValCysGlnSerProCysLeu 3541
Db 10637 TGGCCGCTGCTGGAGGGGTCTGCTGTGTATACAGCTGTGTGGCAGTCTCCCTGCTTA 10696
QY 3542 AsnGlyGlyCysValArgProAsnArgCysHisCysLeuSerSerTrpThrGlyHis 3561
Db 10697 AATGGTGGAAATGTGTAAAGCAACCAACCGATGTCACCTGTCTTTCTTTGGACGGGACAT 10756
QY 3562 AsnCysSerArgCysArgArgThrGlyPhe 3571
Db 10757 AACTGTTCAGGAAAGGAGGACTGGGT 10786

RESULT 8

US-10-107-782-5
; Sequence 5: Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie,
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Baha,
; APPLICANT: Rekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zernusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215

; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 5
; LENGTH: 11158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: {77}..(10786)
US-10-107-782-5
Alignment Scores:
Pred. No.: 0 Length: 11158
Score: 19566.00 Matches: 3503
Percent Similarity: 98.57% Conservative: 16
Best Local Similarity: 98.12% Mismatches: 47
Query Match: 97.96% Indels: 4
DB: 16 Gaps: 2
US-09-977-053-4 (1-3571) x US-10-107-782-5 (1-11158)
QY 4 ArgLeuAlaPheCysCysTyrGlyLeuAlaLeuValSerGlyTyrAlaThrPheGlnGln 23
Db 83 AGAATTTGGCGGGCTTGTGGGGTCTGGCGTCTGTTTGGGCTGGCGACCTTTTCAGCAG 142
QY 24 MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro 43
Db 143 ATGTCCCGTTCGGCAATTTCAAGCTTCGGCTCTTCCCGAGACCGCGCGGGGCCCC 202
QY 44 GlySerIleProAlaProAlaProGlyAspGluAlaGlySerArgValGluArg 63
Db 203 GGGAGTATCCCGCGCGCGCTCTCTGGCGACGAGCGGGGAGCAGAGTGGAGGG 262
QY 64 LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgGlu 83
Db 263 CTGGCGCGGGCTTC-----CGGTGCGGCTGCTGCGGGAGCTCAGCGAGCGCTGGAG 316
QY 84 LeuValPheLeuValAspSerSerSerValGlyGluValAsnPheArgSerGluLeu 103
Db 317 CTGTCTCTCTGGTGGATGATTCGTCCAGCGTGGCGCAAGTCAACTTCCCGCAGCGAGCTC 376
QY 104 MetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThrArgValAla 123
Db 377 ATGTTCGTCCGCAAGCTGTCTGCGACTTCCCGTGGTGGCCACGCGCACCGCGGTGGCC 436
QY 124 IleValThrPheSerSerLysAsnTyrValProArgValAspTyrIleSerThrArg 143
Db 437 ATCTGACCTTCTGTCCAAGAACTAGTGTGGCGCGGTGCGATTCATCTCCACCCGC 496
QY 144 ArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluIleProAlaIleSerTyrArg 163
Db 497 CGCGCGCGCCAGCACAAAGTGGCGCTGCTCTCCAGAGATCCCTGCCATCTCTTACCGA 556
QY 164 GlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAla 183
Db 557 GGTGGCGGCACCTACACCAAGGGCGCTTCCAGCAGCGCGCAAAATTTCTTTCATGCT 616
QY 184 ArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAsp 203
Db 617 AGAGAAACCTCAACAAAAGTTGTATTCTCATCTAGTGATATTCATATGGGGAGAC 676
QY 204 ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle 223
Db 677 CCTAGACCAATTCAGCGTCACTGCGAGATTCAGGAGTGGAGATCTTTCACCTTTGGCATA 736
QY 224 TrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCys 243
Db 737 TGGCAAGGGGAACATTCGAGAGCTGAATGACATGGCTTCCACCCCAAGAGGAGCAGCTGT 796
QY 244 TyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArg-----ArgAlaLeuHis 261
Db 797 TACCTGTACACAGTTTTTGAGAAATTTGAGGCTTTAGTGGCCCTCTGTGCATATGTTATTT 856
QY 262 GluAspLeuProSerGlySerPheIleGlnAspMetValHisCysSerTyrLeuCys 281

1002 CysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGly 1021
Db TGCCCTTTGGGAACCTATTATAATCTGGAACTTTTCACTGTGAAAGCTGCGGATCGGA 3136
1022 SerTyrGlnAspGluGluGlnLeuGluCysValLeuCysProSerGlyMetTyrThr 1041
Db TCCATATCAGATGAAGAGGCACTTGAGTGCAGCTTTGCCCTCTCGGAGTACACG 3196
1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
Db GAATATATTCATTCAGAAACATCTCTGATTGTAAGCTCAGTGTAAACAGACCTAC 3256
1062 SerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPhe 1081
Db TCATACAGTGGGACTTCAGACTTGTGAATCTGTCCACTGGGCACTTATCAGCCAAATTT 3316
1082 GlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaVal 1101
Db GGTTCGCGAGCTGCCCTCTCGTGTCCGAAACACCTCAACTGTGAAAGAGAGCCGTG 3376
1102 AsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMet 1121
Db AACATTTCTGCATGTGGAGTCTCTGTCTCCAGAGGAATTTCTCGGTTTAATG 3436
1122 ProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeu 1141
Db CCTGTCAACCATGTCTCGTCACTATTACCAACCTAATGCAGGAGGCGCTTCTGCCTG 3496
1142 AlaCysProPheTyrGlyThrProPheAlaGlySerArgSerIleThrGluCysSer 1161
Db GCTGTGCCCTTTTATGGAACTACCCCATTCGCTGGTTCAGATCCATCAAGAAATGTTCA 3556
1162 SerPheSerThrPheSerAlaAlaGluGluSerValProProAlaSerLeuGly 1181
Db AGTTTATAGTTCAACTTTCTCAGCGGCAGAGGAAGTGTGTGCCCTCTCTCTGGA 3616
1182 HisIleLysLysArgHisGluLeuSerSerGlnValPheHisGluCysPhePheAsnPro 1201
Db CATATTAAGAAGGCGATGAATATCAGCAGTCAGGCAAGTCATGAATGCTTCTTAAACCT 3676
1202 CysHisAsnSerGlyThrCysGlnGlnLeuGluValGlyTyrValCysLeuCysProLeu 1221
Db TGCCCAATAGTGAACCTGCGCAGCAACTTGGCGGTGTTATGTTGTCTGTCCACTT 3736
1222 GlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeu 1241
Db GGTATATACAGTTTAAAGTGTGAACAGACATCGATGAGTGCAGCCCACTGCCCTTGCCTC 3796
1242 AsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyr 1261
Db AACAATGGAGTTTGAAGACCTTAGTGGGGAAATTCATTTGAGTGGCCCATCAGGTTAC 3856
1262 ThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLys 1281
Db TTTTTCCTGAGTGGTGAATTAATTCATACAGTTGTAATGTCCAGCAGGATTTTCAGGC 3916
1282 GlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGly 1301
Db GCCACCTGTGTGGAATTAATTCATACAGTTGTAATGTCCAGCAGGATTTTCAGGC 3976
1302 LeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaVal 1321
Db AAAAGGTGTGAACAGGTATGATCAACTCAGTGTATTATTAATAACCTTAATATGCGATC 4036
1322 CysGluAspGlnValGlyPheLeuCysLysCysProGlyPheLeuGlyThrArg 1341
Db TGTGAAGACAGGTGTGGGGATTTCTGTGCAATGCCACCTGGATTTTGGGTACCCGA 4096
1342 CysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLys 1361
Db TGTGGAAGAACCTCGATGAGTGTCTCAGTCAGCCATGCAGCAAAATGAGCTACCTGTAAA 4156

1362 AspGlyValAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGlu 1381
Db GACGGTGCCTAATAGCTTTCAGGTGCTGTGTGAGCTGGCTTCACAGATCACACTGTGAA 4216
1382 LeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu 1401
Db TTGAACATCAATGAATGTCTGATCTAATCCATGTAGAAATCAGGCCACTGTGTGATGAA 4276
1402 LeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyLysArgCysGluThrGlu 1421
Db TTAATTTATACAGTTGTAAATGTTCAGCCAGGATTTTTCAGGCCAAAGGTGTGAAACAGA 4336
1422 GlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeu 1441
Db CAGTCTACAGGCTTTAAACCTGGATTTTGAAGTTTCTGCGCATCTATGATATGTCATGCTA 4396
1442 AspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetLysSerSerAsp 1461
Db GATGGCATGCTCCCATCTCTCCATGCTTAACCTGTACCTTCTGGATGAATTCCTCTGAC 4456
1462 AspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeu 1481
Db GACATGAACCTATGCAACACCAATCTCTATGCAAGTTGATAACGCGCAGCAATATACCTTG 4516
1482 LeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyValGlyLysIleThrAsn 1501
Db CTCCTCACTGATTATTAACCGGGTGGTCTTTATGTGAATGGCAGGGAAGATAACAAAC 4576
1502 CysProSerValAsnAspGlyArgTyrHisHisIleAlaIleThrTyrThrSerAlaAsn 1521
Db TGTCCCTCGGTGAATGATGGCAGATGGCATCATATATGTCATCACTTGGACAGTACTGGT 4636
1522 GlyIleTyrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerVal 1541
Db GGAAGCTCGAGGCTCATATAAATGGGAATTAATCTGACGGTGTGATCTGCGCTCTCCAT 4696
1542 GlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGluGlnAspLysLysGly 1561
Db GGAAGACCATACCTCGTGGCGGTGATGTTCTTGGGCAAGCAGCAAGCAAAAGGA 4756
1562 GluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTyrAsp 1581
Db GAGGGTTCACCCCGCTGAGTCTTTTGTGGGCTCCATAAGCCAGCTCAACCTCTGGAC 4816
1582 TyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeuSer 1601
Db TATGTCCTGTCTCCACAGCAGGTGAAGTCACTGCTACCTCTGCCCGCAGGAACTCAGT 4876
1602 LysGlyAsnValLeuAlaTyrProAspPheLeuSerGlyIleValGlyLysValLysIle 1621
Db AAGGAAACGTGTAGCATGCGCTGATTTCTGTGAGAAATGTGGGAAATGAGTGAATC 4936
1622 AspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHisLeu 1641
Db GATTTCTAAGAGCATATTTGTTCTGATGCGCCAGCTTGGAGGGTCACTGCTCATCTG 4996
1642 ArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGly 1661
Db AGAACTGCATCTGAAGATTTAAACCCAGGTTCCAAAGTCAATCTGTTCTGTGAACCCAGC 5056
1662 PheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGlnPro 1681
Db TTCACGCTGTGGGAACCCCTGTGCGAGTACTGTCTGAATCAAGACAGTGGACACAACCA 5116
1682 LeuProHisCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPheHis 1701
Db CTCCCCCATCTGTGAACGATTCCTGTGGGGTGGCCACTCTCTTTGGAGATGGCTTCAT 5176
1702 SerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyr 1721
Db TCAGCCGATGACTTCTATGCTGGCAGCACAGTAACCTTACCAGTGCACAAATGGCTACTAT 5236
1722 LeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTyrAsnGlyValSerPro 1741

Qy	2462	AlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCysGly	2481
Db	7457	GCTCTCATACCTGCAGCCAGGCTTGGATTGGTGGGAATACTACCAACCCCTTGTGGA	7516
Qy	2482	GluAsnGlyHisThrLeuGlyGlyPheProThrCysLysAlaLeuGluCysLeuLysPro	2501
Db	7517	GAAATGGTCACTGGCTTGGAGGAAACCAACATGTAAGCCATTGAGTGCCCTGGAACCC	7576
Qy	2502	LysGluLeuLeuAsnGlyLysPheSerTyrThrAspLeuHisTyrGlyGlnThrValThr	2521
Db	7577	AAGAGATTTTGAATGGCAAAATCTCTTACAGGACCTACACTATGACACAGACGCTTACC	7636
Qy	2522	TyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThr	2541
Db	7637	TACTCTTGCACACGAGGCTTGGCTCGAAGGTCCCAAGTCCCAAGTCCCTTGCACCTGTTTAGAGACA	7696
Qy	2542	GlyAspTrpAspValAspAlaProSerCysAsnAlaLeuHisCysAspSerProGlnPro	2561
Db	7697	GGTGATTGGGATGTAGATGCCCCCATCTTGCAAATGCCATTCACACTGTGTANTCCCCACAAACC	7756
Qy	2562	IleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaLeuIleIleIleTyrSer	2581
Db	7757	ATTGAAAAATGGTTTTGTAGAAGGTGCAGATTACAGCTATGGTGCCATAATCANTACAGT	7816
Qy	2582	CysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrp	2601
Db	7817	TGCTTCCCTGGGTTTCAGGTGGCTGGTCATGCCCATGTCAGACCTGTGAAGAGTCCAGGATGG	7876
Qy	2602	SerSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAspPhe	2621
Db	7877	TCAAGTTCCATCCCAACATGTATGCCAATAGACTGTGGCTCTCCCTCTCTCATATAGATTTT	7936
Qy	2622	GlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspAspMetMet	2641
Db	7937	GGAGACTGTACTAAACTCAAAGATGACCCAGGATATTTTCAGCAAGAAGACGACATGATG	7996
Qy	2642	GluValProTyrValThrProHisProProTyrHisLeuGlyAlaValAlaLysThrTrp	2661
Db	7997	GAAGTTCCATATGTGACTCTCTCAACCTCTTATCATTTGGGAGCAGTGGCTTAAACCTCG	8056
Qy	2662	GluAsnThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetVal	2681
Db	8057	GAATAACAAGAGTCTCTCTGTACACATTCATCAAACTTCTGTATATGATGATCAATGGTT	8116
Qy	2682	SerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCysGlnGlu	2701
Db	8117	TCATACACCTGTAATCCAGGATATGAACCTTCGGGGAAACCTGTGTGCTGATCTGCCAGAA	8176
Qy	2702	AspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuProThr	2721
Db	8177	GATGGAACTTGGAAATGGCAGTGACCAATCTGTCAATTTCAATTAAGATGTGACTTGGCCTACT	8236
Qy	2722	AlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGlnTyr	2741
Db	8237	GCTCCTGAAAAATGGCTTTTTCGTTTTTACAGAGACTAGCATGGGAAGTGTGTGTCAGTAT	8296
Qy	2742	SerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArg	2761
Db	8297	AGCTGTAAACCTGGACACATTTCTAGCAGGCTCTGACCTTAAGGCTTTTGTCTAGAGAAATAGA	8356
Qy	2762	LysTrpSerGlyAlaSerProArgCysGluAlaIleSerCysIleValLysProAsnProVal	2781
Db	8357	AAGTGGAGTGGTGCTTCCCAACGCTGTGAAGCCATTTTCATGCAAAAGCCAAATCCAGTC	8416
Qy	2782	MetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGluCys	2801
Db	8417	ATGAAATGGATCCATCAAGGAGGACCACTACACATACCTGAGCAGCTGTACTATGAGTGT	8476
Qy	2802	AspProGlyTyrValLeuAsnGlyThrGluArgArgThrCysGlnAspAspLysAsnTrp	2821
Db	8477	GACCCCGGATATGTGCTGAATGGCACTGAGAGAGAGACATGCCAGATGCAAAAACTGG	8536

Qy	2822	AspGluAspGluProIleCysIleProValAspCysSerSerProProValSerAlaAsn	2841
Db	8537	GATGAGGATGAGCCCATTTGCAATCTCTGTGGCACTGCAGTTTCACCCCGAGTCTCAGCCAA	8596
Qy	2842	GlyGlnValArgGlyAspGluTyrThrPheGlnIysGluIleGluTyrThrCysAsnGlu	2861
Db	8597	GGCCAGGTGAGAGAGACAGTAGTACACATTCAAAGAGAGATTGAATACACTTGTGCATGAA	8656
Qy	2862	GlyPheLeuLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTrpSerGly	2881
Db	8657	GGGTTCCTGCTTGAGGGAGCCAGGAGTGGGTTCCTCCCAATGGAAGTGGAGTGA	8716
Qy	2882	AlaThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGlyVal	2901
Db	8717	GCCACTCCCGACTGTGTGCCCTGTGCAGATGTGCCACCCCGCACAACTGGGCCAATGGGGTG	8776
Qy	2902	ThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGluGlyTyr	2921
Db	8777	ACGAGAGCCCTGGACTATGCGCTTCATGAGAGAGTAGTACATTTCACATGTCACGAGGGCTAC	8836
Qy	2922	IleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAlaGluIle	2941
Db	8837	ATCTTGACCGGTCTCCAAAACCTCACCTGTCACTCAGATGGCAACTGGGATGCAGAGATT	8896
Qy	2942	ProLeuCysLysProValAsnCysGlyProProGluAspLeuAlaHisGlyPheProAsn	2961
Db	8897	CCTCTCTGTAACCCAGTCAACTGTGGACCTCTCGAAGATCTTGCCCATGTGTTCCCTAA	8956
Qy	2962	GlyPheSerPheIleHisGlyGlyHisIleGlnTyrGlnCysPheProGlyTyrLysLeu	2981
Db	8957	GGTTTTTCTTTATTCATGGGGGCCATATACAGTATCAGTGCCTTCCTGTGTATAAGCTC	9016
Qy	2982	HisGlyAsnSerSerArgCysLeuSerAsnGlySerTrpSerGlySerSerProSer	3001
Db	9017	CATGGAAATTCATCAAGAAAGGTGCCTCTCCATATGGCTCTGGAGTGGCAGCTCACCTTCC	9076
Qy	3002	CysLeuProCysArgCysSerThrProValIleGluTyrGlyThrValAsnGlyThrAsp	3021
Db	9077	TGCTGCTCTTGCGATGTTCCACACCACTAGTAATATGAAATATGCAATGGACACAGAT	9136
Qy	3022	PheAspCysGlyLysAlaAlaArgIleGlnCysPheIysGlyPheLysLeuLeuGlyLeu	3041
Db	9137	TTTGACTGTGGAAAGGCAGCCCGGATTCAGTGTCTCAAAGGCTTCAAGCTCCCTAGGACTT	9196
Qy	3042	SerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGlyPheProHisCysGluHis	3061
Db	9197	TCTGAAATACCTGTGAGGCCGATGGCCAGTGGAGCTCTGGTTCCTCCCACTGTGAACAC	9256
Qy	3062	ThrSerCysGlySerLeuProMetIleProAsnAlaPheIleSerGluThrSerSerTrp	3081
Db	9257	ACTTCTTGTTGGTCTCTTCCAAATGATACCAATATGGTTCATCATGTGAGACAGCTCTTGG	9316
Qy	3082	LysGluAsnValIleThrTyrSerCysArgSerGlyTyrValIleGlnGlySerSerAsp	3101
Db	9317	ARGGAAATATGTAATCATTCACGCTCGAGTCTGGGATATGTATCATCAAGGCGAGTTCAGAT	9376
Qy	3102	LeuIleCysThrGluLysGlyValTrpSerGlnProTyrProValCysGluProLeuSer	3121
Db	9377	CTGATTTGTACAGAAAGGGGTATGGAGCCAGCCTTATCCAGTCTGTGAGCCCTTGTCC	9436
Qy	3122	CysGlySerProProSerValAlaAsnAlaValAlaThrGlyGluAlaHisThrTyrGlu	3141
Db	9437	TGTGGGTCCCCACCGTCTGTGGCCATGCAGTGGCAACTGGAGAGGGCACACACTATGAA	9496
Qy	3142	SerGluValLysLeuArgCysLeuGluGlyTyrThrMetAspThrAspThrAspThrPhe	3161
Db	9497	AGTGAAGTGAACCTCAGATGCTCTGGAAAGGTTATACGATGGATACAGATACAGATCATTC	9556
Qy	3162	ThrCysGlnLysAspGlyArgTrpPheProGluArgIleSerCysSerProLysLysCys	3181
Db	9557	ACCTGTCAAGAAAGATGTCTGCTGTTCCCTGAGAGAAATCTCTTCGAGTCTCTAAATAATGT	9616
Qy	3182	ProLeuProGluAsnIleThrHisIleLeuValHisGlyAspAspPheSerValAsnArg	3201

180 LeuLeuHisAlaArgGluAsnSerThrIysValValPheLeuLeuThrAspGlyTyrSer 199
 716 CTTGGTCACTTAGAGAAATCTCCAAAGTCATATTTCTCAACACCGACGGCTATTCC 775
 200 AsnGlyGlyAspProArgProIleAlaIleAspLeuArgAspSerGlyValGluIlePhe 219
 776 AATGGCGGAGACCCAGACCTATTGACGATCCCTTCGGGATTCGGAGTGGAGATCTTC 835
 220 ThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLys 239
 836 ACCTTCGGGATTGGCAGGGGAATATCCGGAACTGAATGACATGGCTTCCACCCGGAAG 895
 240 GluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAla 259
 896 GAAGAACATTTGTTACCTGCTCCACAGTTTGAAGAATTTGAGGCTTTAGCTCGCAGGGCG 955
 260 LeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyr 279
 956 TTGCATGAAGATCTACTTCTGGAGTTTATCCAGAGATATGGCCCACTGCTCTAT 1015
 280 LeuCysAspGluGlyLysAspCysAspArgMetGlySerCysLysCysGlyThrHis 299
 1016 CTTCTGAGGCTGGGAAAGACTCTGTGACAGAAATGGCCAGCTGCAAAATGTGGACACAC 1075
 300 ThrGlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGlu 319
 1076 ACGGGTCAATTTGAATGTCATCTGTGAGAGGGGTATTACGGGAAGGTCTGACAGCATGAG 1135
 320 CysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSer 339
 1136 TGACAGCTTGGCCATCAGGACATATAGCCGAGCTTCTCAGGAGGATCAGCACC 1195
 340 CysIleProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAsp 359
 1196 TGCATCCATGCTCTGAGTAAAGCACCACCTCCCACTGGAAGACTTCCCTGGAAGAC 1255
 360 CysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysPro 379
 1256 TGGGTGGCGAGAGGATACAGAGATCTGGCCAGACCTGTGAGGTGTGCCACTGTCT 1315
 380 AlaLeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsn 399
 1316 GCCTGAGACCTCTGAAATATGTTTTTTATACAAACACTTGCAAAACTACTTCAAT 1375
 400 AlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeu 419
 1376 GCCGCTGTGGGTCCGATGTCGCCCGGGCTTTGACCTTGTGGGAGCAGCATCCATTG 1435
 420 CysLeuProAsnGlyLeuTrpSerGlySerGlySerTyrCysArgValArgThrCysPro 439
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Db 8564 GAGTGTGATCTCGGCTATATTCTCAATGGCTCTAAGAGAGGACATGCCCAAGAAATAGA 8623
Qy 2820 AsnTrpAspGluAspGluProIleCysIleProValAspCysSerSerProProValSer 2839
Db 8624 GATTGGGATGGCATGAGCCCATGTGTATCTCTGTAGACTGTGGCTCACCCCGAGTCCCC 8683
Qy 2840 AlaAsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluLeuGluTyrThrCys 2859
Db 8684 ACCAATGCGGAGTGAAGGAGAGATACATTCCAAAGAGAGATTACATACTCTTGC 8743
Qy 2860 AsnGluGlyPheLeuLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTrp 2879
Db 8744 CGTGAAGGTTTCATACTCGAAGGAGCCAGAGTCTGTATCTGTCTTACCATGGAAGTTGG 8803
Qy 2880 SerGlyAlaThrProAspCysValProValArgCysAlaThrProGlnLeuAlaAsn 2899
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Qy 2900 GlyValThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGlu 2919
Db 8864 GGGGTGGCAGTGGCTAGACTATGGGTTCAAGAGAGAGTAGCGTTCACATGCTCTAGAG 8923
Qy 2920 GlyTyrIleLeuHisGlyValaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAla 2939
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Qy 2960 ProAsnGlyPheSerPheHisGlyHisIleGlnTyrGlnCysPheProGlyTyr 2979
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Qy 2980 LysLeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySerSer 2999
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Qy 3000 ProSerCysLeuProCysArgCysSerThrProValIleGluTyrGlyThrValAsnGly 3019
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Qy 3020 ThrAspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGlyPheLysLeuLeu 3039
Db 9224 ACTGATTTGGGATGGGAAAGACGGTCCAGATTGATGTCTTCAAAGGCTTCAAGCTGCTT 9283
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QY 3240 SerCysGlyLysProGluSerProGluHisGlyPheValValGlySerTyrThrPhe 3259
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RESULT 10
US-10-150-821-3
: Sequence 3, Application US/10150821
: Publication No. US20020192758A1
: GENERAL INFORMATION:
: APPLICANT: Welcher, Andrew A.
: APPLICANT: Elliott, Gary S.
: TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES
: TITLE OF INVENTION: THEREOF
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: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 11230
: TYPE: DNA
: ORGANISM: Mus musculus
US-10-150-821-3
Alignment Scores:
Pred. No.: 0 Length: 11230
Score: 16707.00 Matches: 2915
Percent Similarity: 89.72% Conservative: 289
Best Local Similarity: 81.63% Mismatches: 361
Query Match: 83.65% Indels: 6
DB: 14 Gaps: 5
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QY 21 PheGlnGlnMetSerSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro 40
DB 236 TTTCAGCCCGTGGCCCTCTTCTGCTCACTTCCAGCTTCCGCTGTCCCGAGGCTCTCCG 295
QY 41 GlyValaProGlySerIleProAlaProAlaProGly---AspGluAlaAlaGlySer 59
DB 296 GGCGCTCTGGGACACTGGCGGTACCTCCCGGTCCAGTCCAGTGGAGGAGGAGGAGGAGG 355
QY 60 ArgValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSer 79
DB 356 AAAGTGGAGCGCTGGCGCGCGGCTTCGAGCGCGGCTTCGAGGAGCTGCGGAGCTCAGC 415

QY 80 GluArgLeuGluLeuValPheLeuValAspSerSerValGlyGluValAsnPhe 99
 DB 416 GGCACCTGGAGCTGGTCTCTGGTGGACGAGTGTCCAGGTGGGCGCAACCACTTC 475
 QY 100 ArgSerGluLeuMetPheValArgLysLeuLeuSerAspPheProValProThrAla 119
 DB 476 CTCACGAGCTCAAGTTCGTGGCGAAGCTGTGTCCGACTTCCCGTGGTCCAGGCC 535
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 QY 140 IleSerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIleProAla 159
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 QY 160 IleSerTyrArgGlyGlyGlyThrTyrThrLysGlyValAlaPheGlnGlnAlaGlnIle 179
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 DB 2033 GTGGCCATCACCTACACGCAACCGACTCATCGGTAAACCAAGCAGCTGCACCTTCTAC 2092
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RESULT 11

US-09-898-570-21

; Sequence 21, Application US/09898570

; Patent No. US20020123612A1

; GENERAL INFORMATION:

; APPLICANT: GERLACH, VALERIE L.

; APPLICANT: ELLERMAN, KAREN

; APPLICANT: MACDOUGALL, JOHN R.

; APPLICANT: SMITHSON, GLENDA

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; TITLE OF INVENTION: METHODS OF USING THE SAME

; FILE REFERENCE: 15966-776CIP

; CURRENT APPLICATION NUMBER: US/09/898,570

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; PRIOR APPLICATION NUMBER: 60/198,293

; PRIOR FILING DATE: 2000-04-19

; PRIOR APPLICATION NUMBER: 60/198,645

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: 60/210,809

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/199,476

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/200,025

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/224,610

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/200,024

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/199,880

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/218,591
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 60/271,814
 ; PRIOR FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 60/215,855
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 09/839,446
 ; PRIOR FILING DATE: 2001-04-19
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 6153
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; NAME/KEY: modified_base
 ; LOCATION: (1010)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ; DESCRIPTION: Description of Unknown Organism: POLYX
 ; OTHER INFORMATION: 10327789_1
 ; US-09-898-570-21

Alignment Scores:

Pred. No.: 0 Length: 6153
 Score: 8427.00 Matches: 1535
 Percent Similarity: 78.65% Conservative: 1
 Best Local Similarity: 78.60% Mismatches: 5
 Query Match: 42.13% Indels: 412
 Ds: 9 Gaps: 3

US-09-977-053-4 (1-3571) x US-09-898-570-21 (1-6153)

QY 1993 TyrThrLeuAlaGlyLeuAspThrIleGluCysLeuAlaAspGlyLysTrpSerArgSer 2012
 DB 193 TATATCTTCCTGGCTTGGACACCAATGTAATGCCCTGGCCGACGCGCAAGTGGAGTAGAGT 252
 QY 2013 AspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAspHisAlaSerPro 2032
 DB 253 GACCAGCAGTGGCTGGCTCTCTCTGTGATGAGCCACCCATTTGTGGACCCAGCCCTCTCCA 312
 QY 2033 GluThrAlaHisArgLeuPheGlyAspIleAlaPheTyrTyrCysSerAspGlyTyrSer 2052
 DB 313 GAGACTGCCCATCGGCTCTTTGGAGACATTTGCAATTTACTACTGCTCTGTAGTGGTTACAGC 372
 QY 2053 LeuAlaAspAsnSerGlnLeuLeuCysAsnAlaGlnGlyLysTrpValProProGluGly 2072
 DB 373 CTAGCAGACAAATTCACGCTCTCTGCAATGCCAGGGCAGTGGGTACCCCGCAGAGGT 432
 QY 2073 GlnAspMetProArgCysIleAlaHisPheCysGluLysProProSerValSerTyrSer 2092
 DB 433 CAAGACATGCCCGTGTATAGCTCATTTCTGTGAAACCACTCCATCGGTTTCTCTATAGC 492
 QY 2093 IleLeuGluSerValSerLysAlaLysPheAlaAlaGlySerValValSerPheLysCys 2112
 DB 493 ATCTTGGAAATCTGTGAGCAAGCAAAATTTGCAGCTGGCTCAGTTGTGTAGGCTTTAAATGC 552
 QY 2113 MetGluGlyPheValLeuAsnThrSerAlaLysIleGluCysMetArgGlyGlnTrp 2132
 DB 553 ATGGAGGCTTTGTACTGAACACCTCAGCAAGAAATGAAATGATGAGAGGTGGCAGTGG 612
 QY 2133 AsnProSerProMetSerIleGlnCysIleProValArgCysGlyGluProProSerIle 2152
 DB 613 AACCTTCCCCATGTCCATCCAGTGCATCCCTGTGGGTGGTGGAGAGCCACCAAGCATC 672
 QY 2153 MetAsnGlyTyrAlaSerGlySerAsnTyrSerPheGlyAlaMetValAlaTyrSerCys 2172
 DB 673 ATGAATGGCTATGCAAGTGGATCAATACAGTTTTCGAGCCATGCTGGCTTACAGCTGC 732
 QY 2173 AsnLysGlyPheTyrIleLysGlyGlnLysLysSerThrCysGluAlaThrGlyGlnTrp 2192
 DB 733 AACAGGGGGTTCTACATCAAGGGGAAAGAGAGACCTCGGAAGCCACAGGGCAGTGG 792
 QY 2193 SerSerProIleProThrCysHisProValSerCysGlyGluProProLysValGluAsn 2212

DB 793 AGTAGTCTTATACCCGACGTCGCCACCCGGTATCTTGTGGTGAACCCACTAAGTTGAGAT 852
 QY 2213 GlyPheLeuGluHisThrThrGlyArgIlePheGluSerGluValArgTyrGlnCysAsn 2232
 DB 853 GGCCTTTCTGGAGCATACAACTGGCAGGATCTTTGGAGAGTGAAGTGAAGTATCAGTGTAAAC 912
 QY 2233 ProGlyTyrLysSerValGlySerProValPheValCysGlnAlaAsnArgHisTrpHis 2252
 DB 913 CCGGGCTATAGTCAGTCGGAGTCCCTGTATTTGTCTGCCAAGCCAATCGCCACTGGCAC 972
 QY 2253 SerGluSerProLeuMetCysValProLeuAspCysGlyLysProProIleGlnAsn 2272
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 QY 2273 GlyPheMetLysGlyGluAsnPheGluValGlySerLysValGlnPhePheCysAsnGlu 2292
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5293	DB	ACAGAGCTCCAGAGGAAGAGCAGGCAGCATCTTTTGTCTTCTGACGGCTCGCTGGA	5352
3413	QY	-----	3413
5353	DB	AAAGCAGCAANTGGCGCAGAGGCTAGGATTGATGCAATTGAAAGATAGGCTTCAGAAAG	5412
3413	QY	-----	3413
5413	DB	TGGGTAAATAAGATTGGCTGAGCTAAAGGAACATGTTCTAAACCAATGCAAAAGACGCC	5472
3413	QY	-----	3413
5473	DB	AAGAACAGGATAAACAATTACAGGATCCGTTAACAGATATACCAGTTTAGAAAGGAAT	5532
3413	QY	-----	3413
5533	DB	GTAATGACCTGATGGAGCTGMAAAACACAAACAGAGAACTTCACAAATGCAACACAAA	5592
3413	QY	-----	3413
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3414	QY	-----IleSerCysGlyProProAla	3420
5653	DB	ATCAACCCCAAGACACATATCTCTCAGGTTCTCCAGAAATCTCAATGTGTCACCAAGCT	5712
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5713	DB	CACGTAGAAAATGCAATTGCTCGAGGCGTACATTATCAATATGAGACATGATCACCTAC	5772
3441	QY	SerCysTyrSerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGly	3460
5773	DB	TCATGTTACAGTGGATACATGTTGGAGGGTTTCTCGAGGAGTGTCTGTGCAATTTCCATGTCAAGATGGGGC	5832
3461	QY	ThrTrpThrSerProProlIleCysArgAlaValCysArgPheProCysGlnAsnGlyGly	3480
5833	DB	ACATGGACATCACCTCTATTTCAGAGCTGTCTGTGCAATTTCCATGTCAAGATGGGGC	5892
3481	QY	IleCysGlnArgProAsnAlaCysSerCysProGluGlyTrpMetGlyArgLeuCysGlu	3500
5893	DB	ATCTGCCAACGCCCAATGTGTTGCTGTGCCAGAGGGCTGGATGGGGGCCCTCTGTGAA	5952
3501	QY	GluProIleCysIleLeuProCysLeuAsnGlyGlyArgCysValAlaProTyrGlnCys	3520
5953	DB	GNACCAATCTGCATCTTCCCTCTGTGACGGAGGTCGCTGTGTGGGCCCTTACCAAGTGT	6012
3521	QY	AspCysProProGlyTrpThrGlySerArgCysHisThr	3533
6013	DB	GACTGCCCGCTGGCTGCGAGCGGGTCTCGCTGTCTACATA	6051

RESULT 12

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US-091 12
RES-01 12
US-09-839-446-21
; Sequence 21, Application US/09839446
; Publication No. US20030050232A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS,
; TITLE OF INVENTION: METHODS OF USING THE
; FILE REFERENCE: 15966-776
; CURRENT APPLICATION NUMBER: US/09/839,446
; CURRENT FILING DATE: 2001-04-19

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; PRIOR APPLICATION NUMBER: 60/198,293
 ; PRIOR FILING DATE: 2000-04-19
 ; PRIOR APPLICATION NUMBER: 60/198,645
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: 60/210,809
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/199,476
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/200,025
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/224,610
 ; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: 60/200,024
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/199,880
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/218,591
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 60/271,814
 ; PRIOR FILING DATE: 2001-02-27
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 6153
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (1010)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ; OTHER INFORMATION: Description of Unknown Organism: POLYX
 ; OTHER INFORMATION: 1032789_1
 US-09-839-446-21

Alignment Scores:

Pred. No.: 0 Length: 6153
 Score: 8427.00 Matches: 1535
 Percent Similarity: 78.65% Conservative: 1
 Best Local Similarity: 78.60% Mismatches: 5
 Query Match: 42.19% Indels: 412
 DB: 10 Gaps: 3

US-09-977-053-4 (1-3571) x US-09-839-446-21 (1-6153)

QY 1993 TyrThrLeuAlaGlyLeuAspThrIleGluCysLeuAlaAspGlyLysTrpSerArgSer 2012
 DB 193 TATACTCTTGGTCTTGACACCATTAATGCTGGCCGACGCGCAAGTGGAGTAGAAGT 252
 QY 2013 AspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAspHisAlaSerPro 2032
 DB 253 GACCCAGCAGTGGCTGCTGCTGCTGATGAGCCACCCATGTGGACCAACGCTCTCCA 312
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 DB 313 GAGACTGCCATCGGCTCTTGGAGACATTCGCACTTCTACTGCTCTGATGGTTACAGC 372
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 QY 2073 GlnAspMetProArgCysIleAlaHisPheCysGluLysProProSerValSerTyrSer 2092
 DB 433 CAAGACATGCCCGTGTATAGCTCATTTCTGTGAATAAACCTCCATCGGTTTCCTATAGC 492
 QY 2093 IleLeuGluSerValSerLysAlaLysPheAlaAlaGlySerValValSerPheLysCys 2112
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 QY 2113 MetGluGlyPheValLeuLeuThrSerAlaLysIleGluCysMetArgGlyGlnTrp 2132
 DB 553 ATGGAGGCTTTGTACTGAACACCTCAGCAAGATTAATGATGATGAGGTGGGCAGTGG 612
 QY 2133 AsnProSerProMetSerIleGlnCysIleProValArgCysGlyGluProProSerIle 2152

DB 613 AACCCCTTCCCATGTCATCCAGTCATCCCTCTGCGGTGTGGAGACCACCAAGCATC 672
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RESULT 13
US-10-311


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; Sequence 24, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Valda
; APPLICANT: LU, Dyrong Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAPALIA, April J. A.; BAUGHN, Mariah R.
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; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 3991
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 3998749CB1
US-10-311-623-24

Alignment Scores:
Pred. No.: 0 Length: 3991
Score: 7471.00 Matches: 1327
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 3
Query Match: 37.41% Indels: 2
DB: 17 Gaps: 0

US-09-977-053-4 (1-3571) x US-10-311-623-24 (1-3991)
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DB 1 GGTGAACCACTAAGGTGTGAAGATGGCTTTCTGGAGCATCAACTGGCAGATCTTTTGAG 60
QY 2225 SerGluValArgTyrGlnCysAsnProGlyTyrIleSerValGlySerProValPheVal 2244
DB 61 AGTGAAGTGAAGTATCAGTGTAAACCGGGCTATAAGTCAGTGGAGTCTCTGATTGTC 120
QY 2245 CysGln-AlaAsnArgHisTrpHisSerGluSerProLeuMetCysValProLeuAspCys 2264
DB 121 TGCCAAAGGCCAATGCGCCACTGGCACAGTGAATCCCTCTGATGTGTCTCTCCGACTG 180
QY 2264 sGlyLysProProProGlnAsnGlyPheMetLysGlyGluAsnPheGluValGlySe 2284
DB 181 TGAAACCTCCCGGATCCAGATGGCTTCATGAAGAGGAGAAACTTTGAGTAGGGTC 240
QY 2284 rLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSerSerTrpThrC 2304
DB 241 CAAGGTTCAAGTTTCTGTAATGAGGGTATGAGCTTGTTGGTGGACAGTCTTTGGACATG 300
QY 2304 sGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAlaLysCysPr 2324
DB 301 TCAGAAATCTGGCAATGGAATGAAGATCAAAATCCAAAGTGCATGCTCCCAAGTGCC 360
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QY 2324 oGluProProLeuLeuGluAsnGlnLeuValLeuLysGluLeuThrThrGluValGlyVa 2344
DB AGAGCCGCCCTCTCTGGAAAACCCAGCTAGTATTAAAGGAGTTGACCCAGGAGTAGGAGT 420
QY 2344 lValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerValLeuLysCysLe 2364
DB TGTGACATTTTCTGTAAAGAGGCGATGCTGCAAGGCCCTCTGTCTCTGGAATGCTT 480
QY 2364 uProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeuCysThrProPr 2384
DB GCCATCCAGCAATGGAGTACTCTTTCCCTGTTTGAAGATTGTTCTTTGTACCCACC 540
QY 2384 oProLeuIleSerPheGlyValProIleProSerSerAlaLeuHisPheGlySerThrVa 2404
DB TCCCTTAATTTCTTGTGTTGCCCATTCCTTCTCTGCTCTTCATTTTGGAGTACTGT 600
QY 2404 lLysTyrSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrThrLeuCysGlnPr 2424
DB CAAGTATTCTTGTAGTGGTGTTCCTTAAGAGGAATTTCTACCACTCTGCAACC 660
QY 2424 oAspGlyThrTrpSerSerProLeuProGluCysValProValGluCysProGlnProGl 2444
DB TGTGGCACCCTGGAGCTCTCCACTGCCAGAAATGTTCCAGTAGAATGTTCCCAACCTGA 720
QY 2444 uGluIleProAsnGlyIleIleAspValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTy 2464
DB GERAAATCCCAATGGAAATCAATGATGTGCAAGGCTTGGCTATCTCAGCACAGCTCTCTA 780
QY 2464 rThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsnGl 2484
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QY 2484 yHisTrpLeuGlyGlyLysProThrCysLysAlaIleGluCysLeuLysProLysGluI 2504
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QY 2544 pAspValAspAlaProSerCysAsnAlaIleHisCysAsnSerProGlnProIleGluAs 2564
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QY 2564 nGlyPheValGluGlyAlaAspTyrSerTyrGlyValaIleIleIleTyrSerCysPhePr 2584
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QY 2584 oGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrpSerSerSe 2604
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QY 2624 sThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspMetMetGluValPr 2644
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QY 2664 rLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyrTh 2684
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QY 2684 rCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCysGlnGluAspGlyTh 2704
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1441 CTGTAATCAGGATATGAACCTTCTGGGAACCTGTGCTGATCTGCCGAAGATGGAAAC 1500
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2724 uAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGlnTyrSerCysIy 2744
1561 AAATGGCTTTTTCGCGTTTACAGAGACTAGCATGGGAAGTGTGTGCAGTATAGCTGTAA 1620
2744 sProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArgLysTrpSe 2764
1621 ACCTGGACACATCTAGCAGGCTCTGACTTAGAGCTTTGTCTAGAGATAGAAATGGAG 1680
2764 rGlyAlaSerProArgCysGluAlaIleSerCysLysIleSerProAsnProValMetAsnG1 2784
1681 TGGTGCTCCCTCCCACTGTGAAGCAATTCATGTCAAAAGCAATCCAGTCATGAATGG 1740
2784 ySerIleLysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGluCysAspProG1 2804
1741 ATCCATCAAGGAAGCAACTACACATACCTGAGCACTGTGTACTATGAGTGTGACCCCGG 1800
2804 yTyrValLeuAsnGlyThrGluArgArgThrCysGlnAspAspLysAsnTrpAspGluAs 2824
1801 ATATGTGCTGAATGGCACTGAGAGGAACAATGCCAGGATGACAAATACTGGGATGAGA 1860
2824 pGluProIleCysIleProValAspCysSerSerProProValSerAlaAsnGlyGlnVa 2844
1861 TGAGGCCAATTCGATTCCTGTGAGCTGCAGTTCACCCCGAGTCTCAGCCAAATGGCCAGT 1920
2844 lArgGlyAspGluTyrThrPheGlnLysGluIleGluTyrThrCysAsnGluGlyPheLe 2864
1921 GAGAGGAGCAGTACACATTCCTCAAAAGAGATTTGAATACACTTGCATTAAGAGGTTCTT 1980
2864 uLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTrpSerGlyAlaThrPr 2884
1981 GCTTGAGGAGCAGGAGTGGGTTTGTCTTCCCAATGAGAGTTGAGGTGGAGCCACTCC 2040
2884 oAspCysValProValArgCysAlaThrProGlnLeuAlaAsnGlyValThrGluG1 2904
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2761 CCCACGCTGTGCGCAATGSCAGTGGCAACTGGAGAGGCCACCCACCTATGAAAGTGAAGT 2820
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RESULT 14
US-09-764-853-214
; Sequence 214, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 3804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-214
Alignment Scores:
Pred. No.: 0 Length: 3804
Score: 6452.00 Matches: 1135
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.91% Mismatches: 0
Query Match: 32.30% Indels: 0
DB: 9 Gaps: 0
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QY 2536 LeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAenAlaIleHis 2555
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QY 2556 CysAspSerProGlnProIleGluAenGlyPheValGluGlyAlaAspTyrSerTyrGly 2575
DB 371 TGTGATTTCCCAACACCATTCGAAATGTTTTGTAGAAAGTGCAGATTACAGTATGGT 430
QY 2576 AlaIleIleIleTyrSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThr 2595
DB 431 GCCATAATCATCTACAGTTGCTTCCTCGGTTTTCAGGTGGCTGGTCATCCATGCGAGAC 490
QY 2596 CysGluGluSerGlyTyrSerSerIleProThrCysMetProIleAspCysGlyLeu 2615
DB 491 TGTGAAGAGTCAGGATGTCAAGTTCCATCCCAACATGTATGCCAATAGACTGTGGCCTC 550
QY 2616 ProProHisIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGlu 2635
DB 551 CCTCTCATATAGATTTTGGAGACTGTACTAACTCAAGATGACCAGGGATATATTTGAG 610
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QY 2656 AlaValAlaLysThrTrpGluAenThrLysGluSerProAlaThrHisSerSerAenPhe 2675
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QY 2696 ValLeuIleCysGlnGluAspGlyThrTrpAenGlySerAlaProSerCysIleSerIle 2715
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2936 AsnTrpAspAlaGluIleProLeuCysLysProValAsnCysGlyProProGluAspLeu 2955
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2976 PheProGlyTyrLysLeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrp 2995
1631 TTTCTCTGGTTAATAGCTCCATGGAAATTCATCAAGAGGTGCCTCTCCATGGCTCTCTGG 1690
2996 SerGlySerSerProSerCysLeuProCysArgCysSerThrProValIleGluTyrGly 3015
1691 AGTGGCAGCTCACCTTCCTGCTTGCCTTGCAGATGTTCCACACCAAGTAATGAATATGGA 1750
3016 ThrValAsnGlyThrAspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGly 3035
1751 ACTGTCAATGGACAGATTTTGACTGTGGAAAGGCAGCCCGGATTCAGTGTCTTCAAGGC 1810
3036 PheLysLeuLeuGlyLeuSerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGly 3055
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3056 PheProHisCysGluHisThrSerCysGlySerLeuProMetIleProAsnAlaPheIle 3075
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1931 AGTCAGACCACTCTTGGAGAGAAATGTGATTAACCTACAGCTGCGAGTCTGGATATGTC 1990
3096 IleGlnGlySerSerAspLeuIleCysThrGluLysGlyValTrpSerGlnProTyrPro 3115
1991 ATACAAGGCAGTTCAGATCTGATTGTACAGAGAAAGGGTATGGAGCCAGCCCTTATCCA 2050
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2051 GTCTGTGAGCCCTTGTCTGTGGTCCACCGTCTGTGCCAATGCAAGTGGCAACTGGA 2110
3136 GluAlaHisThrTyrGluSerGluValLysLeuArgCysLeuGluGlyTyrThrMetAsp 3155
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3156 ThrAspThrAspThrPheThrCysGlnLysAspGlyArgTrpPheProGluArgIleSer 3175
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3196 AspPheSerValAsnArgGlnValSerValSerCysAlaGluGlyTyrThrPheGluGly 3215
2291 GATTTCAAGTGTGAATAGCAGATTTCTGTGTCAATGTGCAAGAGGTATACCTTTGAGGGA 2350
3216 ValAsnIleSerValCysGlnLeuAspGlyThrTrpGluProProPheSerAspGluSer 3235
2351 GTTAACATATCAGTATGTGAGCTTGTGATGAACTTGGAGCCACCAATCTCCGATGAATCT 2410
3236 CysSerProValSerCysGlyLysProGluSerProGluHisGlyPheValValGlySer 3255
2411 TGCAGTCCAGTGTCTTGTGGGAAACCTGAAAGTCCAGAAACATGGAATTTGTGGTGGCAGT 2470
3256 LysTyrThrPheGluSerThrIleIleTyrGlnCysGluProGlyTyrGluLeuGluGly 3275

2471 AAATACACCTTTGAAAGCACAAATTTATTTATCAGTGTGAGCCTGGCTATGAACCTAGAGGGG 2530
3276 AsnArgGluArgValCysGlnGluAsnArgGlnTrpSerGlyGlyValAlaIleCysLys 3295
2531 AACAGGGAACCGTGTCTGCCAGGAGACACAGACTGTGGAGTGGAGGGGTGGCAATATGCAAA 2590
3296 GluThrArgCysGluThrProLeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArg 3315
2591 GAGACAGGTGTGAAATCTCCTGAAATTTCTCAATGGGAAAGCTGACATTTGAAACAGG 2650
3316 ThrThrGlyProAsnValValTyrSerCysAsnArgGlyTyrSerLeuGluGlyProSer 3335
2651 ACGACTGGACCAACGCTGTATATTCCTGCAACAGAGCTACAGTCTTGAAGGCCCATCT 2710
3336 GluAlaHisCysThrGluAsnGlyThrTrpSerHisProValProLeuCysLysProAsn 3355
2711 GAGGCACACTGCACAGAAATGGAACTGGAGGCCACCCAGTCCCTCTCTGCAAAACCAAT 2770
3356 ProCysProValProPheValIleProGluAsnAlaLeuLeuSerGluLysGluPheTyr 3375
2771 CCATGCCCTGTCTCTTGTGATTCCTGAGATGCTCTGCTGCTGAAAAAGAGTTTAT 2830
3376 ValAspGlnAsnValSerIleLysCysArgGluGlyPheLeuLeuGlnGlyHisGlyIle 3395
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3396 IleThrCysAsnProAspGluThrTrpThrGlnThrSerAlaLysCysGluLysIleSer 3415
2891 ATTACCTGCAACCCCGACGACGCTGGACACAGACGCGCAATGTGAAAAATCTCA 2950
3416 CysGlyProProAlaHisValGluAsnAlaIleAlaArgGlyValHisTyrGlnTyrGly 3435
2951 TGTGTTCACCAAGCTCAGTAGAAAAATCAATTTGTCGAGGGGTACATTTATCAATATGA 3010
3436 AspMetIleThrTyrSerCysTyrSerGlyTyrMetLeuGluGlyPheLeuArgSerVal 3455
3011 GACATGATCACCTACTCATGTTTACAGTGCATACATGTTGGAGGGTTCCTGAGGAGTGT 3070
3456 CysLeuGluAsnGlyThrTrpThrSerProPheCysArgAlaValCysArgPhePro 3475
3071 TGTTTAGAAATATGAAACATGACATCACCTCTCTATTTCAGAGAGCTGTCTGATTTCCA 3130
3476 CysGlnAsnGlyGlyIleCysGlnArgProAsnAlaCysSerCysProGluGlyTrpMet 3495
3131 TGTCAAGATGGGGCATCTGCCAGCCCAATGCTGTCTCTGTCAGAGGGCTGGATG 3190
3496 GlyArgLeuCysGluGluProIleCysIleLeuProCysLeuAsnGlyGlyArgCysVal 3515
3191 GGGCGCTCTGTGAAGAACCAATCTGCATTTCTCTCTGTCGAGAGGGTCTGCTGTGTG 3250
3516 AlaProTyrGlnCysAspCysProGlyTyrThrThrGlySerArgCysHisThrAlaVal 3535
3251 GCCCTTACCAAGTGTGACTGCCCGCTGGTGGACGGGGTCTCGCTGTCTATACAGCTGT 3310
3536 CysGlnSerProCysLeuAsnGlyGlyLysCysValArgProAsnArgCysHisCysLeu 3555
3311 TGCCAGTCTCTCTCTCTTAAATGGTGAATGTGTGAAGCAACCAACCGATGTCTGTCTT 3370
3556 SerSerTrpThrGlyHisAsnCysSerArgLysArgArgThrGlyPhe 3571
3371 TCTTCTGAGGGGACATACTGTTCCAGGAAAAAGAGGAGGAGTGGGTTT 3418

RESULT 15

US-09-764-898-60

; Sequence 60, Application US/09764898

; Patent No. US2002090673A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PU201

; CURRENT APPLICATION NUMBER: US/09/764,898

; CURRENT FILING DATE: 2001-01-17


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QY 3076 SerGluThrSerSerSerTrpIysGluAsnValIleThrTyrSerCysArgSerGlyTyrVal 3095
DB 1931 AGTGAGACGAGCTCTTGTGAAGGAAAATGTGATAACTTACAGCTGCAGGCTCTGGATATGTC 1990
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DB 1991 ATACAGGAGGTTCAATCTGATTTGTACAGAGAAAGGGGTATGGAGCAGGCTTATCCA 2050
QY 3116 ValCysGluProLeuSerCysGlySerProProSerValAlaAsnAlaValAlaThrGly 3135
DB 2051 GTCTGTGAGCCCTTGTCTCTGTGGTCCCCACCGTCTGTGCGCAATGTCAGTGGCAACTGGA 2110
QY 3136 GluAlaHisThrTyrGluSerGluValLysLeuArgCysLeuGluGlyTyrThrMetAsp 3155
DB 2111 GAGGCACACACCTATGAAAGTGAAGTGAACCTCAGATGCTCGAAGGTTTATACGATGGAT 2170
QY 3156 ThrAspThrAspThrPheThrCysGlnLysAspGlyArgTrpPheProGluArgIleSer 3175
DB 2171 ACAGATACAGATACATTCACCTGTGAGAAGATGCTGCTGCTTCCCTGAGAGATCTCC 2230
QY 3176 CysSerProLysLysCysProLeuProGluAsnIleThrHisIleLeuValHisGlyAsp 3195
DB 2231 TGCAGTCTCTAAAAATGCTCTCTCCGGAAAAACATAACACATATATCTTGTATCATGGGAC 2290
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QY 3216 ValAsnIleSerValCysGlnLeuAspGlyThrTrpGluProPheSerAspGluSer 3235
DB 2351 GTTAAACATATCATGATGATCAGCTTGAATGAACTCGGAGCCACCAATTTCTCCATGATCT 2410
QY 3236 CysSerProValSerCysGlyLysProGluSerProGluHisGlyPheValValGlySer 3255
DB 2411 TGCAGTCCAGTTTCTGTGGGAACTCGAAGTCCAGAACATGATTTGTGGTGGCAGT 2470
QY 3256 LysTyrThrPheGluSerThrIleLysGlnCysGluProGlyTyrGluLeuGluGly 3275
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QY 3276 AsnArgGluArgValCysGlnGluAsnArgGlnTrpSerGlyValAlaIleCysLys 3295
DB 2531 AACAGGAAAGTGTCTGCAGAGAAACAGACAGTGGAGTGGAGGGGTGGCATATGCAAA 2590
QY 3296 GluThrArgCysGluThrProLeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArg 3315
DB 2591 GAGACCAAGTGTGAAACTCCACTTGAATTTCTCAATGGGAAAGCTGACATTCGAAACACAG 2650
QY 3316 ThrThrGlyProAsnValLysSerCysAsnArgGlyTyrSerLeuGluGlyProSer 3335
DB 2651 ACGACTGGACCCCAACGTGGTATATTCCTGCAACAGAGGCTACAGTCTTGAAGGGGCACT 2710
QY 3336 GluAlaHisCysThrGluAsnGlyThrTrpSerHisProValProLeuCysLysProAsn 3355
DB 2711 GAGGCACACTGCAGAGAAATGGAACCTGGAGCCACCCAGTCCCTCTCTGCAAAACCAAT 2770
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DB 2771 CCATGCCCTGTCTCTTTTGTGATTCGAGAAATGCTGCTGCTCTGCAAAAGGAGTTTAT 2830
QY 3376 ValAspGlnAsnValSerIleLysCysArgGluGlyPheLeuLeuGluGlyHisGlyIle 3395
DB 2831 GTTGTATCAGATGTGTGCATCAAAATGTAGGGAAGGTTTCTGCTGAGGGCCACCGGCATC 2890
QY 3396 IleThrCysAsnProAspGluThrTrpThrGlnThrSerAlaLysCysGluLysIleSer 3415
DB 2891 ATTACTGCACCCCGAGAGAGCTGGACAGACAGACAGAGCCCAATGTGAAAAATCTCA 2950
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DB 3071 TGTTTAGAAAATGGAACATGGACATCACCTCTCTATTTGAGAGCTGTCTGTGATTTCCA 3130
QY 3476 CysGlnAsnGlyGlyIleCysGlnArgProAsnAlaCysSerCysProGluGlyTrpMet 3495
DB 3131 TGTCAAGATGGGGCATCTGCCACAGCCCAAAATGCTTGTCTCTGTCAGAGGGCTGGAG 3190
QY 3496 GlyArgLeuCysGluGluProIleCysIleLeuProCysLeuAsnGlyGlyArgCysVal 3515
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QY 3516 AlaProTyrGlnCysAspCysProProGlyTyrThrGlySerArgCysHisThrAlaVal 3535
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QY 3536 CysGlnSerProCysLeuAsnGlyGlyLysCysValArgProAsnArgCysHisCysLeu 3555
DB 3311 TGCCAGTCTCCCTGCTTAAATGTTGGAATAATGTGTAAAGACCAACCGATGTCTGCT 3370
QY 3556 SerSerTrpThrGlyHisAsnCysSerArgLysArgArgThrGlyPhe 3571
DB 3371 TCTTCTTGACGGGACATAACTGTTCCAGGAAAGAGGAGACTGGGTTT 3418

RESULT 16
US-09-764-881-21
; Sequence 21, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 3804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-881-21

Alignment Scores:
Pred. No.: 0 Length: 3804
Score: 6452.00 Matches: 1135
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.91% Mismatches: 0
Query Match: 32.30% Indels: 0
DB: 10 Gaps: 0

US-09-977-053-4 (1-3571) x US-09-764-881-21 (1-3804)
QY 2436 ValProValGluCysProGlnProGluGluIleProAsnGlyIleIleAspValGlnGly 2455
DB 11 GTTCCAGTAGAATGTCCCACTGAGAAAATCCCCAATGGAAATCAATGATGTGCAAGGC 70
QY 2456 LeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsn 2475
DB 71 CTGTCTATCTCAGCACAGCTCTCTATACCTGCAGCCAGGCTTGAATTTGGTGGGAAT 130
QY 2476 ThrThrThrLeuCysGlyGluAsnGlyHisIleTrpLeuGlyLysProThrCysLysAla 2495
DB 131 ACTACCACTCTTGTGGAGAAAATGGTCACTGGCTTGGAGGAAACCAACATGTAAAGCC 190
QY 2496 IleGluCysLeuLysProLysGluIleLeuAsnGlyLysPheSerTyrThrAspLeuHis 2515
DB 191 ATTGAGTGCCTGAAACCCCAAGGAGATTTTGAATGGCAATTTCTTTACACGGGACCTACAC 250
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QY 2516 TyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAla 2535
DB 251 TATGGACAGACCGTTACCTACTCTTGACACCGAGGCTTTTGGCTCGAAGGTCCCGAGTGC 310
QY 2536 LeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHis 2555
DB 311 TTGACCTGTTTACAGACAGGTGATGGGATGTAGATGCCCACTCTTGCAATGCCATCCAC 370
QY 2556 CysAspSerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGly 2575
DB 371 TGTGATTTCCCAACAACCACTTGAATGGTGTGTGTAGAGGTGCAGATTACAGATTGGT 430
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DB 431 GCCATATCATCATCAGTTCCTCCCTGGGTTCAGGTGGCTGATCCATGCAGAC 490
QY 2596 CysGluGluSerGlyTrpSerSerIleProThrCysMetProIleAspCysGlyLeu 2615
DB 491 TGTGAGAGTCAGATGCTCAGTTCCATCCCAACATGTATGCCATAGACTGTGGCTC 550
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DB 551 CCTCCTCATATAGATTTGGAGACTGTACTAACTCAAGATGACCAAGGATATTTTGG 610
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DB 1031 AAAAGCCAAATCCAGTCATGATGATGATCCATCAAGAGAGCAACTACATACCTGAGC 1090
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QY 2816 GlnAspAspLysAsnTrpAspGluAspGluProIleCysIleProValAspCysSerSer 2835
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QY 2836 ProProValSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIle 2855
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QY 2856 GluTyrThrCysAsnGluGlyPheLeuLeuGluGlyAlaAlaArgSerArgValCysLeuAla 2875
DB 1271 GAATACACTTGAATGAAGGTTCTTGCTTGAGGGAGCCAGGAGTCGGTGTGTCTTGCC 1330
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QY 2936 AsnTrpAspAlaGluIleProLeuCysLysProValAsnCysGlyProProGluAspLeu 2955
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QY 2956 AlaHisGlyPheProAsnGlyPheSerPheIleHisGlyGlyHisIleGlnTyrGlnCys 2975
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QY 2976 PheProGlyTyrLysLeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrp 2995
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QY 2996 SerGlySerSerProSerCysLeuProCysArgCysSerThrProValIleGluTyrGly 3015
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QY 3016 ThrValAsnGlyThrAspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGly 3035
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QY 3056 PheProHisCysGlnHisThrSerCysGlySerLeuProMetIleProAsnAlaPheIle 3075
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DB 2111 GAGGCAACACCTATGAAGTGAAGTGAATCTCAGATGTCTGGAAGGTGTATACGATGGAT 2170
QY 3156 ThrAspThrAspThrPheThrCysGlnLysAspGlyArgTrpPheProGluArgLysSer 3175
DB 2171 ACAGATACAGATACATTCACCTGTGCAGAAAGTGGTGGTCTGCTGCTGAGAGAAATCTCC 2230
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DB 2231 TGCAGTCTTAATAAATGTCTCTCCCGGAAAAACATACATATATCTTGTATACATGGGAC 2290
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QY 3216 ValAsnIleSerValCysGlnLeuAspGlyThrTrpGluProProPheSerAspGluSer 3235
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QY 3236 CysSerProValSerCysGlyLysProGluSerProGluHisGlyPheValValGlySer 3255


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Db 2411 TGCACTCCAGTTCTTGTGGGAAACCTGAAAGCTCAGAAACATGGATTTTGTGTTGGCAGT 2470
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Qy 3276 AenArgGluArgValCysGlnGluAenArgGlnTrpSerGlyValAlaIleCysLys 3295
Db 2531 AACAGGAACTGTCTGCCAGGAGAACACAGTGTGAGTGGAGGGGTGGCAATATGCAAA 2590
Qy 3296 GluThrArgCysGluThrProLeuGluPheLeuAenGlyLysAlaAspIleGluAenArg 3315
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Qy 3516 AlaProYrGlnCysAspCysProProGlyTrpThrGlySerArgCysHisThrAlaVal 3535
Db 3251 GCCCCTTACCAGTGTGACTGCCCGCTGCTGGACCGGGGTCTCGCTGTACATACAGCTGT 3310
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Db 3311 TGCAGTCTCCCTGCTTAAATGGTGGAAATGTGTAGACCAACCGATGTCTGTCTT 3370
Qy 3556 SerSerTrpThrGlyHisAenCysSerArgLysArgThrGlyPhe 3571
Db 3371 TCTTCTTGGACGGACATACATCTGTCCAGGAAAGGAGGAGTCTGGGTTT 3418
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RESULT 17

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US-09-764-875-275
; Sequence 275, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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; FILE REFERENCE: PJ202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 275
; LENGTH: 3804
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-875-275

Alignment Scores:
Score: 0 Length: 3804
Pred. No.: 6452.00 Matches: 1135
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.91% Mismatches: 0
Query Match: 32.30% Indels: 0
DB: 11 Gaps: 0
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US-09-977-053-4 (1-3571) x US-09-764-875-275 (1-3804)

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Db 71 CTTCCTATCTCAGCACAGCTCTCTATACCTGCAAGCCAGGCTTTGAAATTTGGTGGGAAAT 130
Qy 2476 ThrThrThrLeuCysGlyGluAenGlyHisTrpLeuGlyGlyLysProThrCysValAla 2495
Db 131 ACTACCACCCTTTGTGGAGAAATGTGCTACTGTGCTTTGGAGGAAACCAACATGTAAAGCC 190
Qy 2496 IleGluCysLeuLysProLysGluIleLeuAenGlyLysPheSerYrThrAspLeuHis 2515
Db 191 ATTGAGTGCTGAAACCCCAAGGAGATTTTGAATGGCAAAATCTCTTACACGGACCTACAC 250
Qy 2516 TyrGlyGlnThrValThrYrSerCysAenArgGlyPheArgLeuGluGlyProSerAla 2535
Db 251 TATGGACAGACCCCTTACCTACTCTTGCACCCGAGGCTTTCCGGCTCGAAGGTCCAGTGCC 310
Qy 2536 LeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAenAlaIleHis 2555
Db 311 TTGACCTGTTTAGAGACAGTGATTTGGGATGTAGATGCCCATCTTGCATATGCATCCAC 370
Qy 2556 CysAspSerProGlnProIleGluAenGlyPheValGluGlyAlaAspYrSerYrGly 2575
Db 371 TGTGATTTCCCAACCAACCCATTGAAATGGTTTGTAGAGGTGCAGATTACAGCTATGTT 430
Qy 2576 AlaIleIleIleYrSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThr 2595
Db 431 GCCATAATCATCTACAGTTGCTTCCCTGGGTTTTCCAGTGTGCTGTGATGCCAATAGACTGGGCTC 490
Qy 2596 CysGluGluSerGlyTrpSerSerSerIleProThrCysMetProIleAspCysGlyLeu 2615
Db 491 TGTGAAGATCAGATGGTCAAGTTCCATCCCAACATGATGCAATAGACTGGGCTC 550
Qy 2616 ProProHisIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyYrPheGlu 2635
Db 551 CCTCTCATATAGATTTGGAGACTGTACTAAACTCAAGATGACCCAGGATATTTTGAG 610
Qy 2636 GlnGluAspAspMetMetGluValProYrValThrProHisProProYrHisLeuGly 2655
Db 611 CAAGAAGACGACATGATGGAAATTTCCATATGTGACTCTCTCACCCTCTTATCATTTGGGA 670
Qy 2656 AlaValAlaLysThrTrpGluAenThrLysGluSerProAlaThrHisSerSerAsnPhe 2675
Db 671 GCAGTGGCTTAAACCTGGGAATAACAAAGAGGCTCTCTGCTACACATTCATCAAACTTT 730
Qy 2676 LeuYrGlyThrMetValSerYrThrCysAenProGlyYrGluLeuLeuGlyAenPro 2695
Db 731 CTGTATGGTACCATGGTTTTCATACACCTGTAATCCAGGATATGAATCTTCTGGGAAACCT 790
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Db 2951 TGTGTCCACCAAGCTCAGCTAGAAAATGCAATGTCTCGAGGCGTACATTTATCAATATGGA 3010
Qy AspMetIleThrTyrSerCysTyrSerGlyTyrMetLeuGluGlyPheLeuArgSerVal 3455
Db 3011 GACATGATCACCCTACTCATGTACAGTGGATACATGTTGGAGGGTTTCTCGAGGAGTGT 3070
Qy CysLeuGluAsnGlyThrTrpThrSerProProlleCysArgAlaValCysArgPhePro 3475
Db 3071 TGTTTAGAAAATGGAACATGAGACATCACCTCCTATTATGACAGAGCTGTCTGTGCGATTTCCA 3130
Qy CysGlnAsnGlyGlyIleCysGlnArgProAsnAlaCysSerCysProGluGlyTrpMet 3495
Db 3131 TGTTCAGAAATGGGGGCATCTGCCAAGCCCAAAATGCTTGTCTCTCCAGAGGCGTGGATG 3190
Qy GlyArgLeuCysGluGluProlleCysIleLeuProCysLeuAsnGlyGlyArgCysVal 3515
Db 3191 GGGCGCCTCTGTGAGAACCAATCTGCATTTCTCCCTGTCTGCAAGGAGTCTGCTGTGTG 3250
Qy AlaProTyrGlnCysAspCysProProGlyTyrTrpThrGlySerArgCysHisThrAlaVal 3535
Db 3251 GCCCTTACCACTGCTGCTGCCCGCTGGCTGGACGGGTCTCTGCTGTCTATACAGCTGT 3310
Qy CysGlnSerProCysLeuAsnGlyGlyIleCysValArgProAsnArgCysHisCysLeu 3555
Db 3311 TGCCAGTCTCCCTGCTTAATGGTGAATAATGTGAAGACCAACCGATGTCACTGTCTT 3370
Qy SerSerTrpThrGlyHisAsnCysSerArgGlySerArgTrpThrGlyPhe 3571
Db 3371 TCTTCTTGACGGGACATAACTGTTCCAGAAAAGGAGGACTGGGT 3418

RESULT 18

US-09-764-881-21
; Sequence 21, Application US/09764881
; Publication No. US20020086821A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 3804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-881-21

Alignment Scores:
Pred. No.: 0 Length: 3804
Score: 6452.00 Matches: 1135
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.91% Mismatches: 0
Query Match: 32.30% Indels: 0
DB: 13 Gaps: 0

US-09-977-053-4 (1-3571) x US-09-764-881-21 (1-3804)

Qy 2436 ValProValGluCysProGlnProGluGluIleProAspGlyIleIleAspValGlnGly 2455
Db 11 GTTCAGTAGAATGCCCCACCTGAGAAAATCCCCAATGGAAATCATTTGATGTGCAGGC 70
Qy 2456 LeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsn 2475
Db 71 CTGTGCTATCTCAGCACAGCTCTATACCTGCAAGCCAGGCTTTGAAATGGTGGCAAT 130
Qy 2476 ThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyIleProThrCysLysAla 2495
Db 131 ACTACACCCCTTGTGGAGAAAATGCTACTGCTTGGAGGAGAAACCAACATGTAAAGCC 190
Qy 2496 IleGluCysLeuLysProLysGluIleLeuAsnGlyLysPheSerTyrThrAspLeuHis 2515

Db 191 ATTGAGTGCCTGAACCCAGAGGATTTTGAATGGCAATTTCTTTACAGGACCTACAC 250
Qy TyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAla 2535
Db 251 FATGACAGACGGTTACTTACTCTTGCAACCGAGGCTTTGGCTCGAAGGCTCCAGTGCC 310
Qy LeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHis 2555
Db 311 TTGACTGCTTTTAGAGACAGGTGATTTGGGATGTAGATGGCCCCATCTTTGCAATGCAATCCAC 370
Qy CysAspSerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGly 2575
Db 371 TGTGATTTCCCAACCAACCATTCGAAATGGTTTGTAGAAAGGTGCAGATTACAGCTATGGT 430
Qy AlaIleIleIleTyrSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThr 2595
Db 431 GCCATAATCATCTACAGTTGCTTCCCTGGGTTCAGGTGGCTCATGTGCATGCGAGACC 490
Qy CysGluGluSerGlyTrpSerSerSerIleProThrCysMetProIleAspCysGlyLeu 2615
Db 491 TGTGAAGAGTCAAGGATGGTCAAGTTCCATCCCAACATGTATGCCAATAGACTGTGGCCTC 550
Qy ProProHisIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGlu 2635
Db 551 CTTCTCTCATATAGATTTTGGAGACTGTACTAACTCAAGATGACCCAGGGATATTTTGAG 610
Qy GlnGluAspAspMetMetGluValProTyrValThrProHisProProTyrHisLeuGly 2655
Db 611 CAAGAAGACGACATGATGGAAGTTCCATATGTGACTCTCCACCCTCTTATCATTTTGGGA 670
Qy AlaValAlaLysThrTrpGluAsnThrLysGluSerProAlaThrHisSerSerAsnPhe 2675
Db 671 GCAGTGGCTTAAACCTTGGGAAAATACAAAGGAGTCTCTGCTACACATTCATCAAACTTT 730
Qy LeuTyrGlyThrMetValSerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnPro 2695
Db 731 CTGTATGTTACCATGTTTCATACACTGTATTCAGGATATGAACCTCTGGGGAACCT 790
Qy ValLeuIleCysGlnGluAspGlyThrTrpAsnGlySerAlaProSerCysIleSerIle 2715
Db 791 GTGCTGATCTGCCAGAGATGGAACCTTGGAAATGGCAGTGCACCATCTGTCATTTCAT 850
Qy GluCysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMet 2735
Db 851 GAATGTGACTTGGCTTACTCTCTCTGAAAATGGCTTTTTCGCTTTTACAGAGACTAGCATG 910
Qy GlySerAlaValGlnTyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArg 2755
Db 911 GGAAGTGTCTGTCAGTATAGCTGTAAACCTGGACACATTCCTAGCAGGCTCTGACTTAAGG 970
Qy LeuCysLeuGluAsnArgLysTrpSerGlyAlaSerProArgCysGluAlaIleSerCys 2775
Db 971 CTTTGTCTAGAGATAGAAAGTGGAGTGGTGGCTTCCCGCTGCTGAAGCCATTTCATGC 1030
Qy LysLysProAsnProValMetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSer 2795
Db 1031 AAAAGCCCAATCCAGTCTATGAATGGATCCATCAAGGAGCACTACACATACCTGAGC 1090
Qy ThrLeuTyrTyrGluCysAspProGlyTyrValLeuAsnGlyThrGluArgArgThrCys 2815
Db 1091 ACGTTGTACTATGAGTGTGACCCCGGATATGTGCTGAATGGCACTGAGAGGAGACATGC 1150
Qy GlnAspAspLysAsnTrpAspGluAspGluProIleCysIleProValAspCysSerSer 2835
Db 1151 CAGGATGACAAAACCTGGGATGAGGATGAGCCATTTCATTCCTGTGGACTCGAGTTCA 1210
Qy ProProValSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIle 2855
Db 1211 CCCCCAGTCTCAGCCATGCCCCAGGTGAGAGGAGCAGGTACACATTCAAAAAGAGATT 1270
Qy GluTyrThrCysAsnGluGlyPheLeuLeuGluGlyAlaArgSerArgValCysLeuAla 2875

GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0209
; CURRENT APPLICATION NUMBER: US/09/764,893
; CURRENT FILING DATE: 2001-01-19
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 43
; LENGTH: 3804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-893-43

Alignment Scores:

Pred. No.: 0 Length: 3804
Score: 6452.00 Matches: 1135
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.91% Mismatches: 0
Query Match: 32.30% Indels: 0
DB: 13 Gaps: 0

US-09-977-053-4 (1-3571) x US-09-764-893-43 (1-3804)

QY	2436	ValProValGluCysProGlnProGluGluLeuProAsnGlyIleLeuAspValGlnGly	2455
DB	11	GTTCAGTAGAATGTCCTCCCAACCTGAGAAATCCCAATGGAATCATTTGATGTGCAAGGC	70
QY	2456	LeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsn	2475
DB	71	CTTGCTTACTCTGACGACAGCTCTCTATACCTGTCAGCCAGGCTTTGAAATGTTGGGGAAT	130
QY	2476	ThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyLysProThrCysLysAla	2495
DB	131	ACTACCACCTTTGTGGAGAAATGGTCTACCTGGCTTGAGGAAACCAACATGTAAAGCC	190
QY	2496	IleGluCysLeuLysProLysGluLeuAsnGlyLysPheSerTyrThrAspLeuHis	2515
DB	191	ATTGAGTGCTCCGAAACCCCAAGAGATTTTGAATGGCAAAATCTCTTACAGGACCTACAC	250
QY	2516	TyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAla	2535
DB	251	TATGGACAGACGGTTACTACTCTTGCAACCCGAGGCTTCGGCTCGAAGGTCCTCCAGTGCC	310
QY	2536	LeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHis	2555
DB	311	TTGACCTGTTTAGACAGCAGGTGATGGGATGTAGATGCCCATCTTGCATATGCCATCCAC	370
QY	2556	CysAspSerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGly	2575
DB	371	TGTGANTCCCCAACACCCCAATTTGAAATGGTTTTGTAGAAGGTGCAGATTTACAGCTATGTT	430
QY	2576	AlaIleIleTyrSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThr	2595
DB	431	GCCATAATCACTACAGTTGCTTCCCTGGTTTCAGGTGGCTGGTTCATGCCATGCAGACC	490
QY	2596	CysGluGluSerGlyTyrSerSerSerIleProThrCysMetProIleAspCysGlyLeu	2615
DB	491	TGTGAAGAGTCAGGATGGTCAAGTTCATCCCAACATGTATGCCAATAGACTGTGGCCCTC	550
QY	2616	ProProHisIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGlu	2635
DB	551	CCTCTCATATAGATTTTGGAGACGTGTACTAACTCAAGATGACAGGAGATTTTGTAG	610
QY	2636	GlnGluAspAspMetGluValProTyrValThrProHisProProTyrHisLeuGly	2655
DB	611	CAAGAGACGACATGATGGAAGTTCATATGTGACTCTCTCCCTCTTATCAATTTGGGA	670
QY	2656	AlaValAlaLysThrTrpGluAsnThrLysGluSerProAlaThrHisSerSerAsnPhe	2675
DB	671	GCAGTGGCTAAACCTGGGAAATCAAAAGGAGTCTCTGCTTACACATTTCAATCAAACTTT	730

QY	2676	LeuTyrGlyThrMetValSerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnPro	2695
DB	731	CTGTATGGTACATGGTTTTCATACCTGTATTCAGGATATGAACCTCTGGGGAACCT	790
QY	2696	ValLeuIleCysGlnGluAspGlyThrTrpAsnGlySerAlaProSerCysIleSerIle	2715
DB	791	GTGCTGATCTGCCAGGAAGATGGAACTTGGAAATGGCAGTGCCACCATCTCTGCAATTC	850
QY	2716	GluCysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMet	2735
DB	851	GAATGTGACTTGTGCTTACTGCTCTCTGAAATGGCTTTTTCGCTTTTACAGAGACTAG	910
QY	2736	GlySerAlaValGlnTyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArg	2755
DB	911	GGAGTGTCTGTCAGTATAGCTGTAAACCTGGACACACTTAGCAGGCTCTGACTTAAGG	970
QY	2756	LeuCysLeuGluAsnArgLysTrpSerGlyAlaSerProArgCysGluAlaIleSerCys	2775
DB	971	CTTTGCTCTAGAGATAGAAAGTGGAGTGGTCTCTCCCAACGCTGTGAAGCCATTTTCATGC	1030
QY	2776	LysLysProAsnProValMetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSer	2795
DB	1031	AAAAAGCCAAATCCAGTCTCATGATGATCCATCAAAAGGAAGCACTACACATACCTGAGC	1090
QY	2796	ThrLeuTyrTyrGluCysAspProGlyTyrValLeuAsnGlyThrGluArgArgThrCys	2815
DB	1091	ACGTTGTTACTATGATGTGACCCCGGATATGTCTGTAATGGCACTGAGAGGAGACATGC	1150
QY	2816	GlnAspAspLysAsnTrpAspGluAspGluProIleCysIleProValAspCysSerSer	2835
DB	1151	CAGGATGACAAAACTGGGATGAGGATGAGGCCATTTGCAATTTCTGTGACTGCAATTC	1210
QY	2836	ProProValSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIle	2855
DB	1211	CCCCAGCTCTCAGCCAAATGGCCAGGTGAGAGACGAGTACACATTCCTCAAAAGAGATT	1270
QY	2856	GluTyrThrCysAsnGluGlyPheLeuLeuGluAlaArgSerArgValCysLeuAla	2875
DB	1271	GAATACACTTGCATGATGAGGTTCTTGTCTTGAGGAGGCCAGGAGTCGGGTTGTCTTGC	1330
QY	2876	AsnGlySerTrpSerGlyAlaThrProAspCysValProValArgCysAlaThrProPro	2895
DB	1331	AAATGAGTTGGAGTGGAGCCACTCCGACTGTGTGCTGTGATGATGTGCCACCCGCCA	1390
QY	2896	GlnLeuAlaAsnGlyValThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPhe	2915
DB	1391	CAACTGGCCAAATGGGGTGCACGGAAGCCTTGCACTATGGCTTCATGAGGAGTAACATTC	1450
QY	2916	HisCysHisGluGlyTyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGly	2935
DB	1451	CACTGTCTCAGAGGGCTACATCTTGCACGGTGTCTCCAAAACTCACCTGTCTCAGTCAG	1510
QY	2936	AsnTrpAspAlaGluIleProLeuCysLysProValAsnCysGlyProProGluAspLeu	2955
DB	1511	AACTGGGATGACAGATTTCTCTCTGTAAACAGTCAACTGTGGAGCTCTCTCAAGATCTT	1570
QY	2956	AlaHisGlyPheProAsnGlyPheSerPheIleHisGlyGlyHisIleGlnTyrGlnCys	2975
DB	1571	GCCCATGTTTCCCTTATGGTTTTTCTTATTCATGGGGCCATATACAGTATCAATGTC	1630
QY	2976	PheProGlyTyrLysLeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrp	2995
DB	1631	TTTCTGCTTATAAGCTCCATGGAATTCATCAAGAGGTGCTCTCTCAATGGCTCTCTGG	1690
QY	2996	SerGlySerSerProSerCysLeuProCysArgCysSerThrProValIleGluTyrGly	3015
DB	1691	AGTGGCAGCTCACCTTCTCTGCTGCTTGCAGATGTTCACACCACTAGTAATTAATGGA	1750
QY	3016	ThrValAsnGlyThrAspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGly	3035
DB	1751	ACTGTCAATGGGACAGATTTTGTACTGTGGAAGGAGCCCGGATTCAGTCTTCAAGGC	1810
QY	3036	PheLysLeuLeuGlyLeuSerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGly	3055


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Db 1811 TTCAAGCTCTAGGACTTTCTGAAATCACCTGTGAGCCGATGCGAGTCTCTGG 1870
Qy PheProHisCysGluHisThrSerCysGlySerLeuProMetIleProAsnAlaPheIle 3075
Db 1871 TTCCCCCAGCTGTGAACACACTTCTGTGGTCTCTTCCAAATGATACCAATGGCTTCATC 1930
Qy SerGluThrSerSerTrpIleThrGluAsnValIleThrTrpSerCysArgSerGlyVal 3095
Db 1931 AGTGAGACCCAGCTCTTGGAGGAAATGATGTAACCTTACAGCTGCAGGCTCTGATATGTC 1990
Qy IleGlnGlySerSerAspLeuIleCysThrGluysGlyValTrpSerGlnProTrpPro 3115
Db 1991 ATACAAGGCAGTTCCAGATCTGATTTGTACAGAGAAAGGGGTATGGAGCCAGCCCTTATCCA 2050
Qy ValCysGluProLeuSerCysGlySerProSerValAlaAsnAlaValAlaThrGly 3135
Db 2051 GTCTGTGAGCCCTGTCTCTGTGGGTCCCCACCCCTCTGTGCGCAATGCAATGGCACTGGA 2110
Qy GluAlaHisThrTrpGluSerGluValIleLeuArgCysLeuGluGlyTrpMetAsp 3155
Db 2111 GAGGCAACACACCTATGAAGTGAAGTGAACCTCAGATGTCTGGAAGGTTATACGATGGAT 2170
Qy ThrAspThrAspThrPheThrCysGlnLysAspGlyArgTrpPheProGluArgIleSer 3175
Db 2171 ACAGATACAGATACATTCACCTGTCCAGAAAGATGGTCTGCTGCTCCCTGAGAGATCTCC 2230
Qy CysSerProLysCysProLeuProGluAsnIleThrHisIleLeuValHisGlyAsp 3195
Db 2231 TGCAGTCTTAAAAATGTCTCTCCCGGAAAAATACATACATATCTTGTACATGGGGAC 2290
Qy AppPheSerValAsnArgGlnValSerValSerCysAlaGluGlyTrpThrPheGluGly 3215
Db 2291 GATTTTCAGTGTGAATAGGCAAGTTCTGTGTCTATGTGCAAGGGTATACCTTTGAGGGA 2350
Qy ValAsnIleSerValCysGlnLeuAspGlyThrTrpGluProProPheSerAspGluSer 3235
Db 2351 GTTAACATATCAGTATGTAGCTGTGTAACCTGGAGGACCCACCTTCTCCGATGATCT 2410
Qy CysSerProValSerCysGlyLysProGluSerProGluHisGlyPheValValGlySer 3255
Db 2411 TGCAGTCCAGTGTCTTGTGGGAAACCTGAAAGTCCAGAAATGGAATTTGTGGTTGGCAGT 2470
Qy LysThrThrPheGluSerThrIleThrCysGlnCysGluProGlyTrpGluLeuGluGly 3275
Db 2471 AAATACACCTTTGAAAGCACATATTTATTCAGTGTGAGCTGGCTGATGAACATAGAGGG 2530
Qy AsnArgGluArgValCysGlnGluAsnArgGlnTrpSerGlyGlyValAlaIleCysLys 3295
Db 2531 AACAGGGAACCTGTCTCCAGGAGACACAGACAGTGGAGTGGAGGGTGGCAATATGCANA 2590
Qy GluThrArgCysGluThrProLeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArg 3315
Db 2591 GAGACCGAGTGTGAAACTCCACTTGAATTTCTCAATGGGAAAGCTGACATTTGAAACAGG 2650
Qy ThrThrGlyProAsnValValTrpSerCysAsnArgGlyTrpSerLeuGluGlyProSer 3335
Db 2651 ACAGCTGGACCCCAACCTGGTATATCTCTGCAACAGAGGCTACAGTCTTGAAGGGCCATCT 2710
Qy GluAlaHisCysThrGluAsnGlyThrTrpSerHisProValProLeuCysLysProAsn 3355
Db 2711 GAGGCACTGTCACAGAAATGGAACCTGGAGCCACCCAGTCCCTCTCTGCANACCCAAAT 2770
Qy ProCysProValProPheValIleProGluAsnAlaLeuLeuSerGluLysGluPheTrp 3375
Db 2771 CCATGCCCTGTCTCTTTGTGATTTCCCGAGAAATGCTCTGCTGTCTCAAAAGGAGTTTAT 2830
Qy ValAspGlnAsnValSerIleLysCysArgGluGlyPheLeuGluGlnGlyHisGlyIle 3395
Db 2831 GTTGATCAGAAATGTGTCCATCAATGTAGGGAAGGTTTCTGTCTGAGGCGCCAGGCATC 2890
Qy IleThrCysAsnProAspGluThrTrpThrGlnThrSerAlaLysCysGluLysIleSer 3415
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Db 2891 ATTACCTGCAACCCCGACGAGACGCTGACACACAGACGCGCAAAATGTGAAAAATCTCA 2950
Qy CysGlyProProAlaHisValGluAsnAlaIleAlaArgGlyValHisTrpGlnTrpGly 3435
Db 2951 TGTGGTCCACAGCTCACGTAGAAAAATGCAATTCCTCAGGCGGTACATTTATCAATATGGA 3010
Qy AspMetIleThrTrpSerCysTrpSerGlyTrpMetLeuGluGlyPheLeuArgSerVal 3455
Db 3011 GACATGATACCTACTCATGTTCAGTGGATACATGTTGGAGGGTTTCTCTGAGGAGTGT 3070
Qy CysLeuGluAsnGlyThrTrpThrSerProProIleCysArgAlaValCysArgPhePro 3475
Db 3071 TGTTTAGAAAAATGGAACATGGACATCACCTCTATTTTCAGAGCTGTCTGTGCAATTTCCA 3130
Qy CysGlnAsnGlyGlyIleCysGlnArgProAsnAlaCysSerCysProGluGlyTrpMet 3495
Db 3131 TGTGAGAAATGGGGCATCTGCCAACGCCCAAAATGCTTCTGTCTCAGAGGGCTGGAGT 3190
Qy GlyArgLeuCysGluGluProIleCysIleLeuProCysLeuAsnGlyGlyArgCysVal 3515
Db 3191 GGGCGCTCTGTGAGAGAACCAATCTGCATCTTCCCTGTCTGACGGAGGTGCTGTGTG 3250
Qy AlaProTrpGlnCysAspCysProProGlyTrpThrGlySerArgCysHisThrAlaVal 3535
Db 3251 GCCCTTACAGTGTGACTGCCGCTGGCTGGAGCGGGTCTCGCTGTCTACAGCTGT 3310
Qy CysGlnSerProCysLeuAsnGlyGlyLysCysValArgProAsnArgCysHisCysLeu 3555
Db 3311 TGCAGCTCTCCCTGCTTAAATGGTGGAAATGTGTAAAGCCAAACCGATGTCTGTCTT 3370
Qy SerSerTrpThrGlyHisAsnCysSerArgLysArgArgThrGlyPhe 3571
Db 3371 TCTCTTGGACGGGACATAACTGTTCAGGAAAGGAGGACTGGGTTT 3418
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RESULT 20

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US-10-073-865-43
; Sequence 43, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FUZ09C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 3804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-073-865-43
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Alignment Scores:
Pred. No.: 0 Length: 3804
Score: 6452.00 Matches: 1135
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.91% Mismatches: 0
Query Match: 32.30% Indels: 0
DB: 15 Gaps: 0
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US-09-977-053-4 (1-3571) x US-10-073-865-43 (1-3804)

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Qy 2436 ValProValGluCysProGlnProGluGluIleProAsnGlyIleIleAspValGlnGly 2455
Db 11 GTTCCAGTAGAATGTCCCAACCTCGAAGAAATCCCAATGGAATCATTTGATGTGCAAGGC 70
Qy 2456 LeuAlaTrpLeuSerThrAlaLeuThrCysLysProGlyPheGluLeuValGlyAsn 2475
Db 71 CTTGCTTATCTCAGCACAGCTCTCTATCTTACCTGCAAGCAGGCTTTGAATGGTGGAAAT 130
Qy 2476 ThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyLysProThrCysLysAla 2495
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131 ACTACCAACCTTTGTGGAGAAATGCTCACTGGCTTTGGAGGAAAAACCAACATGTAAAGCC 190
2496 IleGluCysLeuIysProLysGluIleLeuAsnGlyLysPheSerThrThrAspLeuHis 2515
191 ATTGAGTGCCTGAACCCCAAGGAGATTTTGAATGGCAAAATTTCTTTACACGGACCTTACAC 250
2516 TyrGlyGlnThrValThrThrSerCysAsnArgGlyPheArgLeuGluGlyProSerAla 2535
251 TATGGACAGACGTTTACCTACTCTTCCAAACCGAGGCTTTCGGCTCGAAGGTCCAGTGGCC 310
2536 LeuThrCysLeuGluThrGlyAspThrAspValAspAlaProSerCysAsnAlaIleHis 2555
311 TTGACCTGTTTAGACAGACGTTGATGGATGTAGATGCCCTTCTTGCATGCAATGCCATCCAC 370
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RESULT 21

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US-10-242-747-21
; Sequence 21, Application US/10242747
; Publication No. US20040005577A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ07C1
; CURRENT APPLICATION NUMBER: US/10/242,747
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,881
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 3804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-747-21

Alignment Scores:
Pred. No.: 0 Length: 3804
Score: 6452.00 Matches: 1135
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.91% Mismatches: 0
Query Match: 32.30% Indels: 0
DB: 16 Gaps: 0

US-09-977-053-4 (1-3571) x US-10-242-747-21 (1-3804)

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QY 2476 ThrThrThrLeuCysGlyGluAsnGlyHisThrLeuGlyGlyLysProThrCysValAla 2495
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 QY 3556 SerSerTrpThrGlyHisAsnCysSerArgLysArgArgThrGlyPhe 3571
 DB 3371 TCTTCTTGGACGGACATACACTGTTCCAGAAAGAGGAGTGGT 3418

RESULT 22

US-09-984-429-525/c
 ; Sequence 525, Application US/09984429
 ; Publication No. US20040010132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 53 Human Secreted Proteins
 ; FILE REFERENCE: P2018P2
 ; CURRENT APPLICATION NUMBER: US/09/984,429
 ; CURRENT FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/244,591
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 09/288,143
 ; PRIOR FILING DATE: 1999-04-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/21142
 ; PRIOR FILING DATE: 1998-10-08

; PRIOR APPLICATION NUMBER: 60/061,463
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/061,529
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/071,498
 ; PRIOR FILING DATE: 1997-10-09
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 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/061,536
 ; PRIOR FILING DATE: 1997-10-09
 ; PRIOR APPLICATION NUMBER: 60/061,532
 ; PRIOR FILING DATE: 1997-10-09
 ; NUMBER OF SEQ ID NOS: 727
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 525
 ; LENGTH: 7286
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-984-429-525
 Alignment Scores:
 Pred. No.: 0 Length: 7286
 Score: 5848.00 Matches: 1160
 Percent Similarity: 48.31% Conservative: 1
 Best Local Similarity: 48.27% Mismatches: 2
 Query Match: 29.28% Indels: 1242
 DB: 11 Gaps: 2
 US-09-977-053-4 (1-3571) x US-09-984-429-525 (1-7286)
 QY 2061 CysAsnAlaGlnGlySerTrpValProGluGlyGlnAspMetProArgCysIleAla 2080
 DB 7285 TGCATGCCAGGGCAAGTGGGTACCCCCAGAGGTCCAGACATGCCCTTTGTATAGCT 7226
 QY 2081 HisPheCysGluLysProProSerValSerTyrSerIleLeuGluSerValSerLysAla 2100
 DB 7225 CATTTCTGTGAAACCTCCATCGTTTCTATAGCATCTTGGAACTCTGTGAGCAAGCA 7166
 QY 2101 LysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThr 2120
 DB 7165 AAATTTGCACTGTGCTCAGTTGTGAGCTTTAAATGCAATGGAAGCTTTGTACTGAACACC 7106
 QY 2121 SerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGln 2140
 DB 7105 TCAGCAAGATTCATGATGAGAGGTGGGCACTGGAGACCTTCCCCCATGTCTCATCCAG 7046
 QY 2141 CysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySer 2160
 DB 7045 TGCATCCCTGTGCGTGTGGAGAGCCACCAGCATCATGAATGGCTATGCAAGTGGATCA 6996
 QY 2161 AsnTyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGly 2180
 DB 6985 AACTACAGTTTGTGAGCCATGTTGGCTTACAGCTGCAACAAAGGGGTTCTACATCAAAGGG 6926
 QY 2181 GluLysLysSerThrCysGluAlaThrGlyGlnTrpSerProIleProThrCysHis 2200
 DB 6925 GAAAGAAGAGCACCTGCGAAGCACAGGGCAGTGGAGTAGTCTTATACCGACGTGCGAC 6866
 QY 2201 ProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGlu----- 2216
 DB 6865 CCGGTATCTTGTGTGAACCAACCACTAAGTTGAGAAATGGCTTTCTGGA-GGTAAGAGAGCA 6807
 QY 2216 ----- 2216
 DB 6806 ATTAGCAATGGTCTGTGGCTTTTGTACAGGGGCCCATATAATAATAAATAAACAACAA 6747
 QY 2216 ----- 2216
 DB 6746 ATAATTGAGTCCAAACACATGCCCAAGTTCATAAGGCATGGAACTGGAAATTACTATTAT 6687
 QY 2216 ----- 2216
 DB 6686 CACTAACAAAGATCATGATAATCTTTTAAACATTTTTCATAATAATTAATTCATCTCTTGATG 6627

QY	2216	-----	2216
Db	6626	AAITAAITCATCTGCTAAGGTTGTGAATCACTTTCTGGAGGTAAGAGACTAAATTAGCAA	6567
QY	2216	-----	2216
Db	6566	ATGCTCTGTGGCTTTTCATCACTTACAGGGCCAGCCACTGTGTGAAGCCACTATTTCAGA	6507
QY	2216	-----	2216
Db	6506	AGCGGGCAATGAACAAATTAATTATTCGAAAAACAGAAATGCTAAATCTACAGGTAGT	6447
QY	2216	-----	2216
Db	6446	GAAGACTGGAAAAAATAATGAAGATGATTATGAATCTTTTGTATATATACTTTCTGCA	6387
QY	2216	-----	2216
Db	6386	TTTTACTAGTATAGGCAITTTCAAGTGTCTTTGTGGCAACAGCTTAGCCCTAAATAGGAA	6327
QY	2216	-----	2216
Db	6326	GTTAGAATAAACCAATTTTAATATAATATTTTGTTTTACAGAGGTTTTTTCAGGATGATA	6267
QY	2216	-----	2216
Db	6266	TATGCTTTATTTTATAGAAGCAAGGTCTAAATGGAACTTAGAGAAATATATTATAATTT	6207
QY	2216	-----	2216
Db	6206	TAAATGCTTAGACAAAAAGTAGGGTAAACCAATAATATGTAGTTTTTACAAATCTCTGTTTG	6147
QY	2216	-----	2216
Db	6146	GTAACCTAAAGGTAAITTTCACTGTGTATGGAACAAGAGTTTCAGTCCAACCAATAATGT	6087
QY	2216	-----	2216
Db	6086	CCTGCTTTCAAGCTAAATGTGTCTTTCTCAATAGCCTACCAAGAAATAGGAATGAGAA	6027
QY	2216	-----	2216
Db	6026	TCTATTCGCCAAATCAAGGGCCATTTGAAATGACCATATTTCTAATTAACACATTTTTT	5967
QY	2216	-----	2216
Db	5966	AAAACCCACATATATACACAGTACAACTTTTCTCTTTTACATTCAAATAACAAAAACAG	5907
QY	2216	-----	2216
Db	5906	TAAAAGCCTTTTATTTAAGGCTTTTGTCTAGATTTTAGTACTTTTTCATTGGGAAGGGTA	5847
QY	2216	-----	2216
Db	5846	CAGAGTATAGTAGAGGTGTTCATTTATTAATTGGAAGAGGTATAGAGTATAAGTAG	5787
QY	2216	-----	2216
Db	5786	AGAGGTGTTCAITTTATATAAATTTAATAAATATTTCTAGAGCTCTGCTTGGCACCAGGTAC	5727
QY	2216	-----	2216
Db	5726	AGTTCTGAGAATCAGCGACTAGCATTTTAAACAAACACAGATTAGATGTGTAAATGGCATGGT	5667
QY	2216	-----	2216
Db	5666	GCTTACATGATGGGAGACACAAAGCAATGCATAAACAAATGAGTAATTTTGTGTTATTT	5607
QY	2216	-----	2216
Db	5606	TGTTTATGACCTGTTATATTATACATGTGTTTGAATTTTTCAGATCACGAATATTAAATTTTTT	5547

QY	2216	-----	2216
Db	5546	GTTTTAAAGATAGGATATATTATTTTCTATTGTGTACAGCAGTAATTTTTTAAGAAATATGTT	5487
QY	2216	-----	2216
Db	5486	AATATAAACAAAATTTTGTAGTAGTATTTCTTAAGACATACCATAAAAAACATTTTATTTGAC	5427
QY	2216	-----	2216
Db	5426	TATTTATGATCTAACACAACTTAACAAATACATGTTAAATTGTTTATGTGCTTCTTTACTAG	5367
QY	2216	-----	2216
Db	5366	CAITTTCTTTGGGCAGAAAGTTTTTTTGAACCTGAGTAATTTATCATTTTTAGCGTTGCGCTC	5307
QY	2216	-----	2216
Db	5306	ATCAGTTCACCAATCAATATATATAGATTACTGATCTTTTACTTTGTTATGGGCTCAAAACTG	5247
QY	2216	-----	2216
Db	5246	TAGTAAGGATTTCTGCAGTGGGATTTACTTAATTTGAATTTTCTTTTCTTTTCTTTTCT	5187
QY	2216	-----	2216
Db	5186	TTCTTCCCTTTAGACAGAGTCTTGCTCTGTCTCCAGGCTGGAGTGCAGTGGCACAATCT	5127
QY	2216	-----	2216
Db	5126	CAGCTCACTGCAACCTCTGCTCTCTGGGTTCAAGTGATTTCTCTGCTCAGCTTCCCAA	5067
QY	2216	-----	2216
Db	5066	TGCGCTGAGATTACAGGCACATACCACTGCTAGCTAATTTTGTACAGGTTTCACCAT	5007
QY	2216	-----	2216
Db	5006	GTGGCCAGGCTGTCTCGAACTCTTAACCTCAAGTGTCTCTGCTCTGCTCGGCTGCCAA	4947
QY	2216	-----	2216
Db	4946	AGTGTGGGATTTAGGCATGAATCGTCATCGGAGCCTTAAGTTGACTTTTCTACTATCAT	4887
QY	2216	-----	2216
Db	4886	TTTCACTTATTTAAAAAATAGAAATGGATCTATTGGAAAAACATAAATCATTTATTTGCT	4827
QY	2216	-----	2216
Db	4826	TACTTCTTAATTTGATTCATTTTAAACATAGACCTTTTAGTTTTTTTCTACTATCCAGGATTT	4767
QY	2216	-----	2216
Db	4766	TAGTTAATGCTATCATCTGTTATATACAAATCGCACTCACTTCTCTCTGTGTGCACAG	4707
QY	2217	HisThrThrGlyArgIlePheGluSerGluValAlaGlyTyrGlnCysAsnProGlyTyrLys	2236
Db	4706	CATACACTGGCAGGATCTTTGAGAGTGAAGTGAATATCAGTGTAAACCGGCTATAAG	4647
QY	2237	SerValGlySerProValPheValCysGlnAlaAsnArgHisTyrPheHisSerGluSerPro	2256
Db	4646	TCGTCCGAGTCCCTGTATTTGTCTGCCAAGCCATTCGCCACTGGCAGTGAATCCCT	4587
QY	2257	LeuMetCysValProLeuAspCysGlyLysProProIleGlnAsnGlyPheMetLys	2276
Db	4586	CTGATGTGTGTTCTCTCGACTGTGAAAAACCTCCCGCATCCAGAAATGGCTTCATGAAA	4527
QY	2277	GlyGluAsnPheGluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeu	2296
Db	4526	GGAGAAAACTTTGAAGTAGGGTCCAAGGTTCAAGTTTTCTGTAAATGAGGGTTATGAGCTT	4467
QY	2297	ValGlyAspSerSerTyrThrCysGlnLysSerGlyLysTyrPheAsnLysLysSerAsnPro	2316

Db 4466 GTTGGTGACAGTCTTCTGGGACATGTCAGAAATCTGGCAATGGAATGAAGTCAAATCCA 4407
Qy LysCysMetProAlaLysCysProGluProProLeuLeuGlnLeuValLeuLys 2336
Db 4406 AAGTGCATGCTCCGCAAGTGCAGAGCCGCCCTCTTGGAAACACGCTAGTATTAAG 4347
Qy GluLeuThrThrGluValGlyValValThrPheSerCysLysGluGlyHisValLeuGln 2356
Db 4346 GAGTTGACACCGAGGTAGAGTTGTGACATTTCTGTAAAGAGGCGCATGCTTCGCAA 4287
Qy GlyProSerValLeuLysCysLeuProSerGlnGlnTrpAsnAspSerPheProValCys 2376
Db 4286 GGCCCTCTGCTGCTGAAATGCTTGCCATCCACGAATGAATGCACTCTTTCCTGTTGT 4227
Qy LysIleValLeuCysThrProProProLeuIleSerPheGlyValProIleProSerSer 2396
Db 4226 AAGATTGTTCTTTGTACCCACCTCCCTAAATTTCTTGTGTGCTGCCCATTCCTTCTCT 4167
Qy AlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGlyPhePheLeuAtqGly 2416
Db 4166 GCTCTTCATTTTGGAAAGTACTGTCAAGTATTTCTTGTGTAGGTGGGTTTTTCTTAAGAGGA 4107
Qy AsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerProLeuProGluCysVal 2436
Db 4106 AATTCTACCACTCTTGCACCTGATGGCACTCTGAGCTCTCCACTGCCAGAAATGTGT 4047
Qy ProValGluCysProGlnProGluGluIleProAsnGlyIleIleAspValGlnGlyLeu 2456
Db 4046 CCAGTAGAATGTCCCAACCTGAGGAATCCCAATGGAATCAATTGATGTGCAAGGCCCTT 3987
Qy AlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThr 2476
Db 3986 GCCTATCTCAGCAGCTCTCTATCTGACGACCGAGCTTTGAAATTTGTGGGAATACT 3927
Qy ThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyLysProThrCysLysAlaIle 2496
Db 3926 ACCACCTTTGTGGAGAAATGTCATCTGCTTGGAGGAAACCAACATGTAAGGCCATT 3867
Qy GluCysLeuLysProLysGluIleLeuAsnGlyLysPheSerThrAspLeuHisTyr 2516
Db 3866 GAGTGCCTGAAACCCCAAGGAGATTTTGAATGGCAAAATCTCTTACACGGACCTACACTAT 3807
Qy GlyGlnThrValThrTyrSerCysAsnAlaGlyPheArgLeuGluGlyProSerAlaLeu 2536
Db 3806 GGACACCGCTTACCTACTCTTGCACCGAGGCTTTTCGGCTCGAAGTCCAGTCCAGTCCCTTG 3747
Qy ThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCys 2556
Db 3746 ACCTGTTTAGACAGAGTGATGGATGTAGATGCCCATCTTGCATGCAATGCCACTGT 3687
Qy AspSerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAla 2576
Db 3686 GATTCCCCCAACCCCATTTGAAATGGTTTTTGTAGAAGGTGCAGATTACAGCTATGGTGCC 3627
Qy IleIleIleTyrSerCysPheProGlyPheGluValAlaGlyHisAlaMetGlnThrCys 2596
Db 3626 ATAATCATCTACAGTTGCTTCTCCCTGGGTTTCAGGTGGCTGTGATGCTCATGCTGAGACCTGT 3567
Qy GluGluSerGlyTrpSerSerIleProThrCysMetProIleAspCysGlyLeuPro 2616
Db 3566 GAAGAGTCAGAGTGTCAAGTTCCATCCCAACATGATATGCAATAGACTGTGGCTCCCT 3507
Qy ProHisIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGln 2636
Db 3506 CCTCATATAGATTTTGGAGACTGTACTAAACTCAAGATGACACCGAGGATATTTGAGCAA 3447
Qy GluAsnAspMetMetGluValProTyrValThrProHisProProTyrHisLeuGlyAla 2656
Db 3446 GAAGACACATGATGGAAGTTCCATATGTGACTCTCCACCTCTCTATCATTTTGGAGCA 3387
Qy ValAlaLysThrTrpGluAsnThrLysGluSerProAlaThrHisSerSerAsnPheLeu 2676

Db 3386 GTGGCTAAAAACCTGGGAAAAATACAAAGGAGTCTCTCTGCTACACATTCATCAAACTTTCTG 3327
Qy TyrGlyThrMetValSerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnProVal 2696
Db 3326 TATGGTACCATTGGTTTCTACACTGTATTCAGAGATATGAATCTTCTGGGGAACCTCTGTG 3267
Qy LeuIleCysGlnGluAspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGlu 2716
Db 3266 CTGATCTGCCAGGAGAGTGAATCTTGAATGGCAGTGCACCATCTCTGCAATTTCAATTCGA 3207
Qy CysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGly 2736
Db 3206 TGTGACTGTGCTACTGCTCTCTGAAAATGGCTTTTTTGGCTTTTACAGAGACTAGCATGGGA 3147
Qy SerAlaValGlnTyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeu 2756
Db 3146 AGTGTCTGTGAGATATAGCTGTAAACCTTGGACACATTTCTAGCAGCTCTGACTTAAGGCTT 3087
Qy CysLeuGluAsnArgLysTrpSerGlyValAserProArgCysGluAlaIleSerCysLys 2776
Db 3086 TGTCTAGAGAAATAGAAAGTGGAGTGGTGCCTCCCCACGCTGTGAAGCCATTTTCATGCAA 3027
Qy LysProAsnProValMetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSerThr 2796
Db 3026 AAGCCAAATCCAGTCAATGAATGGATCCATCAAGGAAGCACTACACATACCTGAGCAG 2967
Qy LeuTyrTyrGluCysAspProGlyTyrValLeuAsnGlyThrGluArgAtqThrCysGln 2816
Db 2966 TTGTACTATCAGTGTGACCCCGGATATGTCTGAATGGCACTGAGAGGAGAACATGCCCAG 2907
Qy AspAspLysAsnTrpAspGluAspGluProIleCysIleProValAspCysSerSerPro 2836
Db 2906 GATGACAAATCTGGGATGAGGATGAGCCCATTTTCATCTCTGTGCACTGCGAGTTCACCC 2847
Qy ProValSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIleGlu 2856
Db 2846 CCAGTCTCAGCCCAATGGCCAGGTGAGAGAGACGAGTACACATTTCCAAAAAGAGATTGAA 2787
Qy TyrThrCysAsnGluGlyPheLeuGluValAlaArgSerArgValCysLeuAlaAsn 2876
Db 2786 TACATTTGCATTAAGGGTCTTCTGCTTGGAGGAGCCAGGAGTGGGTTTGTCTTCCCAAT 2727
Qy GlySerTrpSerGlyAlaThrProAspCysValProValArgCysAlaThrProGln 2896
Db 2726 GGAAGTTGGAGTGGAGCCACTCCCGACTGTCTGCTGTGCATGTGCCACCCGCCACAA 2667
Qy LeuAlaAsnGlyValThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHis 2916
Db 2666 CTGGCCAAATGGGGTGACGGAAGGCTTGGACTATGGCTTCATGAAGGAAGTAACATTCCAC 2607
Qy CysHisGluGlyTyrIleLeuHisGlyValAlaProLysLeuThrCysGlnSerAspGlyAsn 2936
Db 2606 TGTACAGAGGCTTACATCTTGCACGGTGTCTCAAAACTCACCCTGTGCTGAGTGAAGTGCAC 2547
Qy TrpAspAlaGluIleProLeuCysLysProValAsnCysGlyProProGluAspLeuAla 2956
Db 2546 TGGGATCAGAGATTTCTCTCTGTAAACCACTCACTGTGAGCCCTCTCTGAAGATCTTGCC 2487
Qy HisGlyPheProAsnGlyPheSerPheIleHisGlyHisIleGlnTyrGlnCysPhe 2976
Db 2486 CATGGTTTCCCTAATGGTTTTTCTCTTTATTCATGGGGGCCATATACAGTATCAGTGTCTT 2427
Qy ProGlyTyrLysLeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrpSer 2996
Db 2426 CCTGGTTATAGCTCCATGGAATTCATCAAGAGGTGCTCTCTCCATGGCTCTCTGGAGT 2367
Qy GlySerSerProSerCysLeuProCysArgCysSerThrProValIleGluTyrGlyThr 3016
Db 2366 GGCAGCTCACCTTCTGCTGCTGCTTGCAGATGTTCCACACAGTAAATTAATGAAATATGGAAT 2307
Qy ValAsnGlyThrAspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGlyPhe 3036
Db 2306 GTCAATGGGACAGATTTTGTGCTGGAAAGGACGCCCGGATTCAGTGTCTTCAAGGCTTC 2247

QY	3037	LysLeuLeuGlyLeuSerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGlyPhe	3056	QY	3146	-----	3146
DB	2246	NAGCTCTAGGACTTTCTGAATCACCCTGTGAAGCCGATGGCAGTGGAGCTCTGGGTC	2187	DB	1167	TGTATTCTACTAGTATCTGAGTCCATGTAGGTATTCATAAATACATATGAATATGCTGT	1108
QY	3057	ProHisCysGluHisThrSerCysGlySerLeuProMetIleProHisAlaPheIleSer	3076	QY	3146	-----	3146
DB	2186	COCCACTGTGAACACACTTCTTGTGGTCTCTTCCAAATGATACCAATCGTTCATCAGT	2127	DB	1107	ATTCTCTACTAGTATCTGAGTCCATGTAGGTATTCATAATACATATGAATATGCTGTATT	1048
QY	3077	GluThrSerSerTrpLysGluAsnValIleThrTrpSerCysArgSerGlyTrpValIle	3096	QY	3146	-----	3146
DB	2126	GAGACAGCTCTTGAAGGAATGATAACTTACGCTGCAGGCTCTGATATGTCTATA	2067	DB	1047	CCTACTAGTATCTGAGTCCATGTAGGTATTCATAATACATATTAATATGCTGTATTCTCT	988
QY	3097	GinglySerSerAspLeuIleCysThrGluLysGlyValTrpSerGlnProTrpProVal	3116	QY	3146	-----	3146
DB	2066	CAAGGCAGTTCAGATCTGATTTGTACAGAGAAGGGGTATGGAGCCAGCTTATCCAGTC	2007	DB	987	ACTAGTATCTGAGTCCATTTTGAGACTGTCTAGAAATTTCTCGAACTGTTAGCTGTATTAG	928
QY	3117	CysGluProLeuSerCysGlySerProProSerValAlaAsnAlaValAlaThrGlyGlu	3136	QY	3146	-----	3146
DB	2006	TGTGAGCCCTTGTCTGTGGGTCCCAACCTCTGTCCCAATGCAGTGGCAACTGGAGAG	1947	DB	927	AATATAAATGAATTCATTAATAATAATATCCACAATAAGGTAAATAACATCAAAAACACT	868
QY	3137	AlaHisThrTrpGluSerGluValLysLeu-----	3146	QY	3146	-----	3146
DB	1946	GCACACACTATGAAGTGAAGTGAACCT- CAGGTAAGATCATGGCTCTAGGGTCTCCAA	1888	DB	867	TAAAGTAATTTAGTCTCTGATTAACCTTTTCATGTGGATAACTGAGAACTGATCTGGTTAT	808
QY	3146	-----	3146	QY	3146	-----	3146
DB	1887	CGGGTGGGGCAGGATTATGAATGAATGAATGTGATCGATCAAAATTTTGTGATGGGAA	1828	DB	807	TACCGGTTTTTGTGTTTTTGTGTTTTTGTGAGAACAGTCTGTCTGTCAACCAGGCTGGA	748
QY	3146	-----	3146	QY	3146	-----	3146
DB	1827	GAAACATCATCTGAACTGCTCCAAACACTGGTGCTTTTAAACATTTGCTTTATTTC	1768	DB	747	GTGAGTGGCATGTTCTGTGCTCACTGCAGCCTCAACCTCTTAGTTTCAAGCAGTCTCTCC	688
QY	3146	-----	3146	QY	3146	-----	3146
DB	1767	TACCTACATTTATGAGAAATCCACTGAGTATATAAATAAATCGATACTTTTTCAGACA	1708	DB	687	CACCTCTGCTCTCCAAAGTAGCTGAGACTACAGGCATGTGCCACGGTCCCAGCTAATTTT	628
QY	3146	-----	3146	QY	3146	-----	3146
DB	1707	TGTTTCTAATAATAATTATCATGACTATCATATTTCTGTGTAGCTTCTGTGAACAAACAGCA	1648	DB	627	GTTTATTTTATAGAGATGAAGTCTCATATGTTTTCCAGCCTAGTACTCAAGCTCTCGG	568
QY	3146	-----	3146	QY	3146	-----	3146
DB	1647	AGATCCTCTAGCTAGCTTGAAGCTCCGGAATCGTGAAGCTGTTTTTAAACATCAGGA	1588	DB	567	ACTCAAGTGGTCTCTGCTCCTCAGCCTTCCAAAGTGCAGGGATTACAGGCATGAGCCACC	508
QY	3146	-----	3146	QY	3146	-----	3146
DB	1587	TAGTAAATTTCTTATGATTATAACTTTGTGATTATATTGACACATGCAAAATATGGGGA	1528	DB	507	GCACCCAGCTCAACTGGTGTGTTATTTGTTATGTTGTTGTTTTCATGCGCAATGCCATCCG	448
QY	3146	-----	3146	QY	3146	-----	3146
DB	1527	CATAAGGCAAAACTGAAGAATTCAGGCCATGATCATGCCAAATATCAGGATTAAGAAG	1468	DB	447	CCTGACATATTGATTGTGCAACAAATCAATATGTTGCACAAAATATCTACTGAGCCTTGTA	388
QY	3146	-----	3146	QY	3146	-----	3146
DB	1467	AAATATCTTATGTAAAGACCTTAGAGCAGCATTGGCACAAGTAGGTATTTCATAATACA	1408	DB	387	ACAGCTTCTTAATCCAAGGATAGATCAGAAACTATATTTCTACTTTTAAGCACTCA	328
QY	3146	-----	3146	QY	3147	-----	3147
DB	1407	TATGAATTATGCTGATTCTCTACTAGTATCTGAGTCCATGTAGTATTTCATAATACATAT	1348	DB	327	TTTTTGCATTTCCATTGCAGATGTCTGGAAGGTTATACGATGATACAGATACAGATACA	268
QY	3146	-----	3146	QY	3161	PheThrCysGlnLysAspGlyArgTrpPheProGluArgIleSerCysSerProLysLys	3180
DB	1347	GAATTATGCTGATTCTCTACTAGTATCTGAGTCCACGCTAGGTATTTCATAATACATATA	1288	DB	267	TTACCTCTCAGAAAGATGGTCCCTGGTTCCTGAGAGATCTCTGCAAGTCTCTTAAAAA	208
QY	3146	-----	3146	QY	3201	ArgGlnValSerValSerCysAlaGluGlyTrpThrPheGluGlyValAlaSerVal	3220
DB	1287	TTATGCTGATTCTCTACTAGTATCTGAGTCCACGCTAGGTATTTCATAATACATATGAATTA	1228	DB	147	AGGCAAGTTTCTGTGTCTCATGTGAGAGGGGTATACCTTTTGGGGGNGTTAATATACGTA	88
QY	3146	-----	3146	QY	3221	CysGlnLeu	3223
DB	1227	TGCTGTATTCTCTACTAGTATCTGAGTCCACGCTAGGTATTTCATAATACAAATGAATATGC	1168				

Db 87 TGTGAGTA 79
|||||:|:
RESULT 23
US-10-302-172-34
; Sequence 34, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 34
; LENGTH: 3448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (415)..(2991)
US-10-302-172-34
Alignment Scores:
Pred. No.: 0 Length: 3448
Score: 5485.00 Matches: 982
Percent Similarity: 99.90% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 27,46% Indels: 0
DB: 13 Gaps: 0
US-09-977-053-4 (1-3571) x US-10-302-172-34 (1-3448)
QY 318 TyrGluCysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyLe 337
Db 1 TATGATGACAGCTTCCCTCGGGGACATCAAACTTGAAGCTTACACAGGAGATC 60
QY 338 SerSerCysIleProCysProAspGluAsnHisThrSerProGlySerThrSerPro 357
Db 61 AGCAGTTGCATTCATGTCCTCCGATGAAATCAACCTCTCCACCTGGAAGCACATCCCT 120
QY 358 GluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHis 377
Db 121 GAAGACTGTGTCTGCAGAGAGGAGATACAGGATCTGGCCAGACCTGTGAACCTTGTCCAC 180
QY 378 CysProAlaLeuLysProGluAsnGlyTyrPheIleGlnAsnThrCysAsnHis 397
Db 181 TGCCCTGACCTGAGCTCCGAAATGTGTTACTTATTCAAAACACTTGCAACACACCAC 240
QY 398 PheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIle 417
Db 241 TTCAATGAGCCCTGTGGGGTCCGATGTCACTCCCTGGATTGATCTTGTGGGAGCAGATC 300
QY 418 IleLeuCysLeuProAsnGlyLeuTyrSerGlySerGluSerTyrCysArgValArgThr 437
Db 301 ATCTATGTCTACCAATGGTTGTGGTTCGGTTTCAGAGAGCTTACTGCAAGTAAGAACCA 360
QY 438 CysProHisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeu 457
Db 361 TGTCTCATCTCCGACGCGGAACATGCGCACATCAGCTGTCTACAGGGAAATGTTA 420
QY 458 TyrLysThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLys 477

Db 421 TATAAGACAACATGTTTGGTCTGTGATGAAGGGTACAGACTAGAAGCGCAGTATAAG 480
QY 478 LeuThrCysGlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGluArgHis 497
Db 481 CTTACTTTGTCAAGAAACAGCCAGTGGGATGGGCGAGAACCCCGGTGTGTGGAGCCGAC 540
QY 498 CysSerThrPheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGln 517
Db 541 TGTTCACCTTTTCAGATGCCCAAGATGTTCATATATATATATATATATATATATAT 600
QY 518 ProAlaLysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGly 537
Db 601 CCAGCCAAATTTGGGACGATCTGTATGTAAAGTTGGCGCAAGGGTTCATATTTATCTGGA 660
QY 538 ValLysGluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAla 557
Db 661 GTCAAGAAATGCTGAGATGTACACTTCTGGAAAAATGGAAATGTCGGAGTTCAGGACGT 720
QY 558 ValCysLysAspValGluAlaProGlnIleAsnProLysAspIleGluAlaLysThr 577
Db 721 GTGTGTAAAGACGTGGAGGCTCTCAATCACTGTCTTAAGGACATAGAGGCTTAAGACT 780
QY 578 LeuGluGlnGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSer 597
Db 781 CTGAAACAGCAGATCTGCAATGTTCCTGGCAGATTCACACAGCTAAAGACAACCTCT 840
QY 598 GlyLysLysValSerValHisValHisProAlaPheThrProTyrLeuPheProIle 617
Db 841 GGTGAAAGGTGTCACTCCACGTTCATCCAGCTTTCACCCACCTTACCTTTTCCCAAT 900
QY 618 GlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIle 637
Db 901 GGAGATGTTGCTATCGTATACACGCAACTGACCTATCCGCAACAGGCGCAGCTGCATT 960
QY 638 PheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArgSerProPro 657
Db 961 TTCATATCAAGGTTATTTGATGCAAGAACCACTGTCTATAGACTGGTGCAGATCTCCACCT 1020
QY 658 ProValGlnValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAsp 677
Db 1021 CCCGTCCAGCTCTCGAGAGAGGTACATGCGCAGCTGGAGTGGAGCTCAGTTCTCAGAC 1080
QY 678 AsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGln 697
Db 1081 AACTCAGGGGCTGAATTTGGTCAATTACAGAGTCAATACACAGGAGACCTTTTCCCTCAA 1140
QY 698 GlyLysThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAsp 717
Db 1141 GGGGAGACTATAGTACAGTATACAGCCACTGACCCCTCAGGCAATACAGGACATGTGAT 1200
QY 718 IleHisIleValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAsp 737
Db 1201 ATCCATTTGTCTATAAAGGTTCTCCCTGTGAATTTCAATTCACCTGTAAATGGGAT 1260
QY 738 PheIleCysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyr 757
Db 1261 TTTATATGACCTCCAGATAATCTGGAGTCACTGATACATTAACCTTGTGGAGGGCTAT 1320
QY 758 AspPheThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLys 777
Db 1321 GATTTTCAGAGAGGGTCTACTGCAAGTATTTATGTGCTTATGAAGATGGCGTCTGAAA 1380
QY 778 ProThrTyrThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPhe 797
Db 1381 CCACATATACCACTGATGGCCAGCTGTGCCAAAAAAGCTTTTGCACCAACCGGTTTC 1440
QY 798 LysSerPheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLys 817
Db 1441 AAGTCTCTTGGAGATGTTCTACAAAGCAGCTCGTTGTGTGATGACACAGATCTGATGAAGA 1500
QY 818 PheSerGluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAla 837
Db 1501 TTTTCTGAAGCATTTGAGACGACCCCTGGGAAAAAATGGTCCCATCATTTTGTAGTATGCA 1560

Pred. No.:	0	Length:	3262
Score:	4930.00	Matches:	947
Percent Similarity:	95.33%	Conservative:	12
Best Local Similarity:	94.14%	Mismatches:	20
Query Match:	24.68%	Indels:	28
DB:	13	Gaps:	4

US-09-977-053-4 (1-3571) x US-10-466-164-29 (1-3262)

QY	1590	LysSerLeuAlaThrSerCysProGluGluLeuSerLysGlyAsnValLeuAlaTrpPro	1609
DB	289	GAGTCACTGGCTACCTCCCTCCAGAGAACTCAGTAAAGAAACGGTTAGCATGGCCT	348
QY	1610	AspPheLeuSerGlyIleValGlyLysValLysIleAspSerLysSerIlePheCysSer	1629
DB	349	GATTCTCTGTCCAGGATTTGGGGGAAGTGAAGATCGATTCTAAGAGCATATTGTGTCT	408
QY	1630	AspCysProArgLeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLys	1649
DB	409	GGTTGCCACGCTTAGGAGGCTCAGTGCCTCATCTGAGAACTGCATCTGAAGATTTAAAG	468
QY	1650	ProGlySerLysValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProVal	1669
DB	469	CCAGGTTCCAAAGTCAATCTGTCTGTGATCCAGGCTTCCAGCTGGTCGGGAACCCCTGTG	528
QY	1670	GlnTyrCysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGluArgIleSer	1689
DB	529	CAGTACTGTCTGANTCAGGACAGTGGACAAACCACTTCTCTCACTGTGAACGATTAGC	588
QY	1690	CysGlyValProProLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAlaGly	1709
DB	589	TGTGGGTTGCCACTCTCTTTGGAGATGGCTTCCATTTCCAGCCGATGACTTCTATGCTGGC	648
QY	1710	SerThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPhe	1729
DB	649	AGCACAGTAACTACCAGTGCACAAATGGCTACTATCTATTGGGTGACTCAGGGATGTTT	708
QY	1730	CysThrAspAsnGlySer-TripAsnGlyValSerProSerCysLeuAspValAspGluC	1749
DB	709	TGTACAGATATATGGAGCTAGGAAACGGCTTCCACCATCTCCCGTGATGTGATGATG	768
QY	1749	AlaValGlySerAspCysSerGluHisAlaSerCysLeu-AsnValAspGlySerTyrI	1769
DB	769	TGCAGTTGGATCAGATTGATGAGCATGCTTCTTGCCTGAAACGTAGATGGATCTCTACA	828
QY	1769	IeCysSerCysValProProTyrThrGlyAspGlyLysAsnCysAlaGluProIleLysC	1789
DB	829	TATGTTTCATGTGTCCACCGGTACACAGGAGATGGGAAACCTGTGCAGAACCTTATAAAT	888
QY	1789	ys-LysAlaProGly--AsnProGluAsnGlyHisSerSerGlyGluIleTyrThr-Va	1807
DB	889	GCTAAGGCTCCAGCGCAGATCCGGAATATGGCCACTCTCTCAGTGAGATTATACAGT	948
QY	1807	lGlyAla---AlaValThrPheSerCysGlnGluGlyTyr-GlnLeuMetGlyValThrL	1826
DB	949	AGGTGCCCGAAGTCACATTATTACGTGTGAGGAAGATACCCAGTTGATGGGAGTAACCA	1008
QY	1826	ylleThrCysLeuGlu-SerGlyGluTyrAsnHisLeuIlePro-TyrCysLysAlaVa	1845
DB	1009	AAATCAATGTTTGGAGTACTCGAGAAATGGAATCATTCTAATACCAATATTGTAAAGCTGT	1068
QY	1845	IeSerCysGlyLysPro-AlaIleProGluAsnGlyCysIleGlu-GluLeuAla---Phe	1863
DB	1069	TTCATGTGTAAACCGGACTATTCAGAAATATGGTTGCATTGAGCGGATAGCACCTTTT	1128
QY	1864	ThrPhe---GlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAlaGlyAsp	1882
DB	1129	ACCTATTGGCGAGCAAGTGCATATAGTGTGTAATAAAGGATATATCTCTGGCCGGTAT	1188
QY	1883	LysGluSerSerCysLeuAlaAsnSerSerTyrHisSerProProValCysGluPro	1902
DB	1189	AAAGAATCATCTCTTCTTGAACAGTCTTGGAGTCAATTCCTCTCTCTCTCTCTCTCTCT	1248

QY	1903	ValLysCysSerSerProGluAsnIleAsnAsnGlyLys-TyrIleLeuSerGlyLeuTh	1922
DB	1249	GTCAAGTGTCTTAGTCCGGCAATATAAATAAATGACAACTATATATAGAGTGGGCTTAC	1308
QY	1922	rTyrLeuSerThrAlaSer-TyrSerCysAspThrGlyTyrSerLeuGlnGlyProSer-	1941
DB	1309	CTACCTTTCTTACTGTCATATAATTCATGCGCATACAGGATACAGCTTACAGGCGCTTCCC	1368
QY	1942	IleIleGluCysThrAlaSerGlyIleTyrAspArgAlaPro-ProAlaCysHisLeuVa	1961
DB	1369	ATTATTGAATGACGGCTTCTGGCATCTGGACAGAGCGGCACCTGCTGTGCACTGT	1428
QY	1961	lPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThrPh	1981
DB	1429	CTTCTGTGGAGAACCACTGCTCCATCAAAAGATGCTGTCTATTACGGGGAATAAATTCAC	1488
QY	1981	eArgAsnThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThrIl	2001
DB	1489	CAGAACACCGCTCATTACACTTTCAAAGAGGCTATATCTCTTCTGTGCTTTCACCAT	1548
QY	2001	eGluCysLeuAlaAspGlyLysTyrSerArgSerAspGlnGlnCysLeuAlaValSerCy	2021
DB	1549	TGAATGCTTGCCGACGCGCAAGTGTAGTAGTGAAGTGAAGTGCCTGGCTGTCTCTG	1608
QY	2021	sAspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGlyAs	2041
DB	1609	TGATGAGCCACCATTTGTGACCAACGCTCTCTCCAGAGACTGCCCATCGCTCTTCGGAGA	1668
QY	2041	lIleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeuCy	2061
DB	1669	CATTGCAATCTTACTACTCTCTGATGGTTACAGCTTAGCAGACAATTTCCAGCTTCTCTG	1728
QY	2061	sAsnAlaGlnGlyLysTyr-ValProGluGlyGlnAspMetProArgCysIleAlaH	2081
DB	1729	CAATGCCAGGCGAAGTGGGGTACCCCCAGAGGTGAAGCATGCCCGCTGTGTATAGCTC	1788
QY	2081	isPheCysGlu-LysProProSerValSerTyrSerIleLeuGluSerValSerLysAla	2100
DB	1789	ATTCTGTGAAAAAACCTCCATCGTTTCTTATAGCATCTTGGAAATCTGTGAGCAAGCA	1848
QY	2101	LysPheAlaAlaGlySerValSerPheLysCysMetGluGlyPheValLeuAsnThr	2120
DB	1849	AAATTTGCACTGGCTCAGTTGTGAGCTTTAAATGCAATGGAAGGCTTTGTACTGAACAC	1908
QY	2121	SerAlaLysIleGluCysMetArgGlyGlyGlnTyrAsnProSerProMetSerIleGln	2140
DB	1909	TCAGCAAGATTTGATATGATGAGGTGGGAGTGGGAAACCTTCCCATGTCCATCCAG	1968
QY	2141	CysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySer	2160
DB	1969	TGCATCTCTGCGGTGTGGAGAGCCACCAAGCATCATGAATGCTATGCAAGTGGATCA	2028
QY	2161	AsnTyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGly	2180
DB	2029	AACTACAGTTTTTGGAGCATGGTGGCTTACAGCTGCAACAGGGGTTCTTACATCAAGGG	2088
QY	2181	GluLysLysSerThrCysGluAlaThrGlyGlnTyrSerSerProIleProThrCysHis	2200
DB	2089	GAAGAAGAGCACCTCTCGAAGCCACAGGCGAGTGGAGTAGTCTCTTACCGAGCTGCCAC	2148
QY	2201	ProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrGly	2220
DB	2149	CCGSTATCTTGTGTGAACCCACCTAAGTTTGAGAAATGGCTTTCTGGAGCATACAACTGC	2208
QY	2221	ArgIlePheGluSerGluVal-ArgTyrGlnCysAsnProGlyTyrLysSerValGlySe	2240
DB	2209	AGGATCTTTTGAGAGTGAAGTTGAGGTATCAGTGTAAACCGGGCTTATAAGTCAGTCGGA	2268
QY	2240	rProValPheValCysGlnAlaAsnArgHisTyrHisSerGluSerProLeuMetCysVa	2260
DB	2269	TCTGTATTGTCTGCCAGCCAAATGCCACTGACAGTGAATCCCTCTGTATGTGTGT	2328
QY	2260	lProLeuAspCysGlyLysProProIleGlnAsnGlyPheMetLysGlyGluAsnPh	2280


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Db 2329 TCCTCTCGACTGTGGAACACCTCCCGCATCAGAAATGGCTTCATGAAGAGGAGAAACTT 2388
Qy eGluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSe 2300
Db 2389 TGAAGTAGGTCGACAGGTTTCAGTTTCTCTGTAAGAGGGTATGAGCTTGTGGTGACAG 2448
Qy rSerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetPr 2320
Db 2449 TCTTGGACATGTCAGAAATCTGGCAATCTGCAATGAAGTCAATTCAGAAATGCAATGCC 2508
Qy oAlaLysCysProGluProProLeuLeuGluAsnGlnLeuValLeuLysGluLeuThrTh 2340
Db 2509 TGCCAAAGTCCAGAGCGCCCTCTGGAACACAGCTAGTATTAAAGAGGTTGACCAC 2568
Qy rGluValGlyValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerVa 2360
Db 2569 CGAGTAGGAGTTGTGACATTTCTCTGTAAGAGGGCATGTCTTGCAGAGGCCCTCTGT 2628
Qy lLeuLysCysLeuProSerGlnGlnTrpAsnAspSerPheProValCysLysLysIleVal 2380
Db 2629 CTTGAATGCTTGCATCCAGCAATGGAATGACTCTTTCCCTGTTTGTAAAGATTGTCT 2688
Qy uCysThrProProProLeuLysPheGlyValProLysPheSerSerAlaLeuHisPh 2400
Db 2689 TTGTACCCACCTCCCTTAAATTTCTTTGTGTGTCCTCCCATTTCTTCTCTCTTCATTT 2748
Qy eGlySerThrValLys-TyrSer-CysValGlyGlyPhePheLeu-ArgGlyAsnSerTh 2419
Db 2749 TGGAGTAGTCTGTGAGGTATTTCTTGATGTAGTGGTGTTCCTTAAGCAGGAAATTTCTAC 2808
Qy rThrLeuCysGlnProAspGlyThrTrp-SerSerProLeuProGluCysValProValG 2439
Db 2809 CACCTCTGCCAACCTGATGCACTTGGAGGCTCTCCACTGACAGAAATGTGTCCAGTAG 2868
Qy lCysProGlnProGluGluLysPheAsnGlyLysLeuValGlnGlyLeuAlaTyrL 2459
Db 2869 AATGTCTCCCACTCAGGAAATCTCCCAATGGAAATCAATGATGTGCAAGGCTTGCCTATC 2928
Qy euSerThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrL 2479
Db 2929 TCAGCAGAGCTCTCTATACCTGCAAGCCAGGCTTGAATTTGGTGGGAATCTACCACT 2988
Qy euCysGlyGluAsnGlyHisTrpLeuGlyGlyLysPheProThrCysLysAlaIleGluCys 2498
Db 2989 TTTGTGAGAAATGCTCACTGCTTGGAGGAAACCAAGATGTAAGCCATTGAGTGCC 3048
Qy LeuLysProLysGluLysLeuAsnGlyLysPheSerTyrThrAspLeuHisTyrGlyGln 2518
Db 3049 GTGAACCCCAAGAGATTTGAATGGCAAAATCTCTTACCGGACCTACACTATGACAG 3108
Qy ThrValThrTyrSerCysAsn-ArgGlyPheArgLeuGluGlyProSerAlaLeuThrCy 2538
Db 3109 ACCGTACTACTCTTGCACACAGAGGCTTTCGGCTGGAAGTCCAGTGCTTGACCTG 3168
Qy sLeuGluThrGlyAspTrpAspValAsp-AlaProSerCysAsnAlaIleHisCysAspS 2558
Db 3169 TTTTAGAGACAGGTGATGGGATGTAGATTGCCCATCTTTGCAATAGCATCCACTGTGATT 3228
Qy eProGlnProLysGluAsnGlyPheValGlu 2568
Db 3229 CCCCAACACCATTTGA--AATGGTTTTGTAAAG 3258

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RESULT 25

US-09-728-952-93

; Sequence 93, Application US/09728952

; Patent No. US20020111302A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

```

; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Yamazaki, Vicki
; APPLICANT: Ujwal, Manusha L.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 799
; CURRENT APPLICATION NUMBER: US/09/728,952
; CURRENT FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 93
; LENGTH: 2437
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (184)..(2172)
US-09-728-952-93

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Alignment Scores:

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Pred. No.: 0 Length: 2437
Score: 4058.00 Matches: 716
Percent Similarity: 99.17% Conservative: 1
Best Local Similarity: 99.03% Mismatches: 6
Query Match: 20.32% Indels: 1
DB: 9 Gaps: 0

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US-09-977-053-4 (1-3571) x US-09-728-952-93 (1-2437)

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Qy 2849 TyrThrPheGlnLysGluIleGluTyrThrCysAsnGluGlyPheLeuLeuGluGlyAla 2868
Db 2 TACACATTTCCAAAAGAGATTGA-TACACTTGCATGAAGAGGGTTCTTGCTTAGAGGAGCC 60
Qy 2869 ArgSerArgValCysLeuAlaAsnGlySerTrpSerGlyAlaThrProAspCysValPro 2888
Db 61 AGGAGTGGGTTTGTCTTGCCTAATGGAACTTGGAGTGGAGGCCACTCCGAGCTGTGTCCT 120
Qy 2889 ValArgCysAlaThrProProGlnLeuAlaAsnGlyValThrGluGlyLeuAspTyrGly 2908
Db 121 GTCAGATGTGCCACCCGCCACAACTGGCCAAATGGGCTGACCGAAGGCCCTGGACTATGGC 180
Qy 2909 PheMetLysGluValThrPheHisCysHisGluGlyTyrIleLeuHisGlyAlaProLys 2928
Db 181 TTCATGAAGAAAGTAACTTCCACTGTCAATAGGGCTACATCTTGACGGTGTCTCCAAA 240
Qy 2929 LeuThrCysGlnSerAspGlyAsnTrpAspAlaGluIleProLeuCysLysProValAsn 2948
Db 241 CTCACCTGTTCAGTCAGATGGCAACTGGGATGCGAGATTCTCTCTGTAAACCAAGTCAAC 300
Qy 2949 CysGlyProProGluAspLeuAlaHisGlyPheProAsnGlyPheSerPheIleHisGly 2968
Db 301 TGTGGACCTCTCGAAGATCTTGCCCATGGTTCCCTAATGGTTTTTCTTTATTCATGGG 360
Qy 2969 GlyHisIleGlnTyrGlnCysPheProGlyTyrLysLeuHisGlyAsnSerSerArgArg 2988
Db 361 GGCCATTAACGATACGATGCTTCTCTGTTATAGCTCATCGAATTCATCAGAGAGG 420
Qy 2989 CysLeuSerAsnGlySerTrpSerGlySerSerProSerCysLeuProCysArgCysSer 3008
Db 421 TGCCTCTCCAAATGGCTCTCGAGTGGCAGCTACCTTCCCTGCTCCCTGTCAGATGTTCC 480
Qy 3009 ThrProValIleGluTyrGlyThrValAsnGlyThrAspPheAspCysGlyLysAlaAla 3028
Db 481 ACACCAAGTAAATGAATATGGAATCTGCAATGGACAGATTTTGACTGTGGAAAGGAGGCC 540
Qy 3029 ArgIleGlnCysPheLysGlyPheLysLeuLeuGlyLeuSerGluIleThrCysGluAla 3048
Db 541 CGGATTCAGTCTTCAGAGCTTCAAGGCTTCAAGCTCTTAGGACTTCTGAAATCACCTGTGAGCC 600
Qy 3049 AspGlyGlnTrpSerSerGlyPheProHisCysGluHisThrSerCysGlySerLeuPro 3068

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Db 601 CATGCCAGTGGAGCTCTGGGTTCACCACTTTGAACACACACTTCTTGTTCTCTTCCA 660
Qy MetIleProAsnAlaPheIleSerGluThrSerSerTrpIysGluAsnValIleThrTyr 3088
Db ATGATACCAAAATCGCTTCATCAGTGGAGACAGCTCTTGGAAAGGAAATGTGTAACCTTAC 720
Qy SerCysArgSerGlyTyrValIleGlnGlySerSerAspLeuIleCysThrGluLysGly 3108
Db AGCTGCAGTCTGGATATGTATACAGGCGAGTTCAGATCTGATTTGTACAGAGAAGGG 780
Qy ValTrpSerGlnProTyrProValCysGluProLeuSerCysGlySerProSerVal 3128
Db GTATGAGGCGAGCTTATCCAGTCTGTGAGCCCTTCTCTGGTGGTCCCGACCGTCTGTC 840
Qy AlaAsnAlaValAlaThrGlyGluAlaHisThrTyrGluSerGlnValIysLeuArgCys 3148
Db GCCAATGCAAGTGGCAATCGAGAGGCGACACCTATGAAGTGAAGTGAACACTCAGATGT 900
Qy LeuGluGlyTyrThrMetAspThrAspThrAspThrPheThrCysGlnLysAspGlyArg 3168
Db CTGGAAGGTTTATCAGATGATACAGTACAGATCAATCACCTGTCCAGAAAGATGTGCGC 960
Qy TrpPheProGluArgIleSerCysSerProLysLysCysProLeuProGluAsnIleThr 3188
Db TGGTTCCTCTGAGAGATCTCTGCACTCTCTAAATAATGCTCTCTCCCGGAAAAACATAACA 1020
Qy HisIleLeuValHisGlyAspAspPheSerValAsnArgGlnValSerValSerCysAla 3208
Db CATATACTTGTATCATCGGAGCGATTTTCAGTGTGAATAGGCAAGTTCCTGTGTCTCATGTGCA 1080
Qy GluGlyTyrThrPheGluGlyValAsnIleSerValCysGlnLeuAspGlyThrTrpGlu 3228
Db GAAGGTATACCTTTGAGGGAGTTAATCATATCAGTATGTGAGCTTGTGGAACCTGGAG 1140
Qy ProProPheSerAspGluSerCysSerProValSerCysGlyLysProGluSerProGlu 3248
Db CCACCAATCTCCGATGAATCTTCCAGTCCAGTTCTTGTGGGAAACCTGAAAGTCCAGAA 1200
Qy HisGlyPheValValGlySerLysTyrThrPheGluSerThrIleIleTyrGlnCysGlu 3268
Db CATGGAATTTGTGGTGGCAGTAAATACCTTTGAAGACACATTTATTTATCATGTGTGAG 1260
Qy ProGlyTyrGluLeuGluGlyAsnArgGluArgValCysGlnGluAsnArgGlnTrpSer 3288
Db CTGTGCTATGAATCAGAGGGAGACAGGAAAGTGTCTGCCAGGAGAACAGACAGTGGAGT 1320
Qy GlyValAlaIleCysLysGluThrArgCysGluThrProLeuGluPheLeuAsnGly 3308
Db CGAGGGGTGGCAATATGCCAAAGAGACAGGTGTGAAACTCCACTTGAATTTCTCAATGGG 1380
Qy LysAlaAspIleGluAsnArgThrThrGlyProAsnValValTyrSerCysAsnArgGly 3328
Db AAAGCTGACATTGAAACACAGGACGATGACACCACTGGTATATTTCTGCAACAGAGGC 1440
Qy TyrSerLeuGluGlyProSerGluAlaHisCysThrGluAsnGlyThrTrpSerHisPro 3348
Db TACAGTCTTGAGGGCCATCTGAGGACACACTGCACAGAAATGGAACTGGAGCCACCCA 1500
Qy ValProLeuCysLysProAsnProCysProValProPheValIleProGluAsnAlaLeu 3368
Db GTCCCTCTCTGCAAAACCAATCCATGCCCTCTTCTCTTTGTGATTCGCGAGAAATGCTCTG 1560
Qy LeuSerGluLysGluPheTyrValAspGlnAsnValSerIleIysCysArgGluGlyPhe 3388
Db CTGTCTGAAAAGGAGTTTATTTGTTGATCAGAAATGTGTCCATCAAAATGTAGGGAAGGTTT 1620
Qy LeuLeuGlnGlyHisGlyIleIleThrCysAsnProAspGluThrTrpThrGlnThrSer 3408
Db CTGCTGCGAGGGCCAGGGCATATTACCTGCAACCCGACGACGACGTGGACACAGACAGC 1680
Qy AlaLysCysGluLysIleSerCysGlyProAlaHisValGluAsnAlaIleAlaArg 3428
Db GCCAAATGTGAAAAAATCTCATGTGTGTCACCGAGCTCAGTAGAAAAATGCAATTTGCTCCA 1740

Qy 3429 GlyValHisTyrGlnTyrGlyAspMetIleThrTyrSerCysTyrSerGlyTyrMetLeu 3448
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Qy GluGlyPheLeuArgSerValCysLeuGluAsnGlyThrTrpThrSerProProIleCys 3468
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Qy ArgAlaValCysArgPheProCysGlnAsnGlyGlyIleCysGlnArgProAsnAlaCys 3488
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 10, 2004, 15:48:01 ; Search time 515.232 Seconds

(without alignments)
3846.286 Million cell updates/sec

Title: US-09-977-053-4

Perfect score: 19973

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	16707	83.6	11230	4	US-09-911-842A-3
3	2282	11.4	1638	1	US-08-253-155A-1
4	2032	10.2	7313	4	US-09-620-312D-259
5	2027	10.1	6951	4	US-09-023-655-1265
6	2016	10.1	6951	6	5256642-1
7	2016	10.1	6951	6	5472939-1
8	1604.5	8.0	5420	6	5256642-3
9	1604.5	8.0	5420	6	5472939-3
10	1184	5.9	3934	4	US-09-023-655-1066
11	1004	5.0	8091	4	US-09-230-652-1
12	987	4.9	8257	4	US-09-484-970B-65

13	978	4.9	9723	1	US-08-083-590A-21	Sequence 21, Appl
14	978	4.9	9723	3	US-08-532-384-21	Sequence 21, Appl
15	838	4.2	763	4	US-09-484-970B-110	Sequence 110, Appl
16	834	4.2	6677	4	US-08-939-366-27	Sequence 27, Appl
17	834	4.2	6677	4	US-09-467-997-6	Sequence 6, Appl
18	763	3.8	4208	3	US-09-214-278-6	Sequence 6, Appl
19	763	3.8	4208	4	US-09-855-722-6	Sequence 6, Appl
20	762.5	3.8	3142	1	US-08-110-158-3	Sequence 3, Appl
21	762.5	3.8	3142	4	US-09-023-655-1090	Sequence 1090, Ap
22	759	3.8	5458	4	US-09-199-865-2	Sequence 2, Appl
23	759	3.8	6454	2	US-08-400-159-5	Sequence 5, Appl
24	759	3.8	6454	3	US-08-611-729A-5	Sequence 5, Appl
25	758.5	3.8	3144	5	PCT-US91-05059-1	Sequence 1, Appl
26	758	3.8	4208	4	US-09-068-740A-10	Sequence 10, Appl
27	758	3.8	5590	3	US-08-882-046-1	Sequence 1, Appl
28	742.5	3.7	4483	2	US-08-611-729A-7	Sequence 7, Appl
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32	710.5	3.6	3582	2	US-08-400-159-9	Sequence 9, Appl
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34	703	3.5	376	4	US-09-833-381-205	Sequence 205, App
35	676.5	3.4	4315	3	US-08-882-046-3	Sequence 3, Appl
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38	631.5	3.2	2663	4	US-09-068-740A-8	Sequence 8, Appl
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54	603	3.0	1878	2	US-08-435-149-17	Sequence 17, Appl
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56	599.5	3.0	3339	4	US-09-423-753-4	Sequence 4, Appl
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61	585	2.9	2055	3	US-08-872-855-3	Sequence 3, Appl
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71	561.5	2.8	3863	4	US-08-482-073-1	Sequence 1, Appl
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73	558.5	2.8	1833	1	US-08-365-470-2	Sequence 2, Appl
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79	499.5	2.5	1981	3	US-08-981-392-26	Sequence 26, Appl
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82	467	2.3	1434	4	US-09-833-381-926	Sequence 926, App
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85	434.5	2.2	14042	3	US-08-652-877-85	Sequence 85, Appl

86 434.5 2.2 14044 3 US-08-652-877-89 Sequence 89, Appl
 87 434.5 2.2 14080 3 US-08-652-877-87 Sequence 87, Appl
 88 434.5 2.2 14083 3 US-08-476-515A-83 Sequence 83, Appl
 89 434.5 2.2 14086 3 US-08-652-877-83 Sequence 83, Appl
 90 429.5 2.2 1556 1 US-08-597-545-3 Sequence 3, Appl
 91 429.5 2.2 1556 1 US-08-457-135-3 Sequence 3, Appl
 92 427.5 2.1 1158 4 US-09-142-027A-11 Sequence 11, Appl
 93 427.5 2.1 1158 4 US-09-142-027A-13 Sequence 13, Appl
 94 427.5 2.1 1573 1 US-08-597-545-4 Sequence 4, Appl
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 98 425 2.1 3448 2 US-08-596-405-3 Sequence 3, Appl
 99 425 2.1 3448 2 US-08-477-620-3 Sequence 3, Appl
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ALIGNMENTS

RESULT 1

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 ; Sequence 1, Application US/09911842A
 ; Patent No. 6656707
 ; GENERAL INFORMATION:
 ; APPLICANT: Amgen Inc.
 ; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
 ; FILE REFERENCE: 01017/37592
 ; CURRENT APPLICATION NUMBER: US/09/911,842A
 ; PRIOR FILING DATE: 2001-07-24
 ; PRIOR APPLICATION NUMBER: US 60/222,438
 ; PRIOR FILING DATE: 2000-08-01
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 10878
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-911-842A-1

Alignment Scores:

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 Best Local Similarity: 99.86% Mismatches: 2
 Query Match: 99.92% Indels: 0
 DB: 4 Gaps: 0

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 QY 41 GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg 60
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1511 TTTTCAGATGCCCAAGATATCATCATATCCCCCACAACTGTGGCAAGCAGCCAGCAAA 1570
521 PheGlyThrIleCysPyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
1571 TTTGGACCATCTGCTATGTAGTTGCCGCAAGGGTTCAATTTTATCTGGAGTCAAGAA 1630
541 MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCysLys 560
1631 ATGCTGAGATGTACCACTTCTGGAATAATGGAATGCGAGTTCAGGCAGCTGTGTGTA 1690
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641 LysValIleAsnAlaGluProProValIleAspTrpCysArgSerProProValGln 660
1931 AAGGTATTATGATGCAACCACTGTGATAGATCTGGTGCAGATCTCCACCTCCGCTCCAG 1990
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1991 GTCTCGGAGAGTACATGCGCAAGCTGGGATGAGCCTCAGTTCACAGCAACTCAGGG 2050
681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyLeuThr 700
2051 GCTGAATTGGTCTATTACCAAGAGTCTATACACAGGAGACCTTTTCCCTCAAGGGGAG 2110
701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
2111 ATAGTACAGTATACAGCCACTGACCCCTCAGGCATTAACAGGACATGTGATATCCATAT 2170
721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
2171 GTCATAAAGGTTCTCCCTGTGAATTCACATTCACACCTGTAAATGGGANTTTATATGC 2230
741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
2231 ACTCCAGATAATATCTGGAGTCAACTGTATTAACCTTGTCTGGAGGCTATGATTTTCA 2290
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781 ThrThrGluTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
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821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
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Qy 3421 HisValGluAenAlaLeuAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyr 3440
Db 10271 CACGTAGAAAATGCAATTTGCTCGAGGCGTACATTTATCAATATGAGACATGATCACCTAC 10330
Qy 3441 SerCysTyrSerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAenGly 3460
Db 10331 TCATGTTACAGTGGATACATGTTGGAGGGTTTCTGAGGAGTGTGTTGTTTGTAGAAAATGGA 10390
Qy 3461 ThrTyrThrSerProPheLeuCysArgAlaValCysArgPheProCysGlnAenGlyGly 3480
Db 10391 ACATGACATCACTCTTATTTGACAGAGTGTCTGTGATTTCCATGTCAGAATGGGGGC 10450
Qy 3481 IleCysGlnArgProAenAlaCysSerCysProGluGlyTyrMetGlyArgLeuCysGlu 3500
Db 10451 ATCTGCCAACGCCCAATGCTTGTCTGTCTCAGAGGGCTGGATGGGGCGCTCTCTGTGAA 10510
Qy 3501 GluProIleCysIleLeuProCysLeuAenGlyGlyArgCysValAlaProTyrGlnCys 3520
Db 10511 GAACCAATCTGCATTTCTTCTGTCTGACAGAGTCTGCTGTGAGGGCTTACAGTGT 10570
Qy 3521 AspCysProGlyTyrThrThrGlySerArgCysHisThrAlaValCysGlnSerProCys 3540
Db 10571 GACTGCCCGCTGGTGGACGGGCTCTGCTGTCTATACAGCTGTTTGCAGTCTCCCTGC 10630
Qy 3541 LeuAenGlyGlyCysValArgProAenArgCysHisCysLeuSerSerTyrThrGly 3560
Db 10631 TTAATAGTGTGAAAATGTTGTAAGACCAACCGATGTCATGCTCTTCTTCTTGGACGGGA 10690
Qy 3561 HisAenCysSerArgGlyValArgThrGlyPhe 3571
Db 10691 CATAACTGTTCCAGGAAAAGAGGACTGGGTTT 10723
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RESULT 2

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US-09-911-842A-3
; Sequence 3, Application US/09911842A
; Patent No. 6658707
; GENERAL INFORMATION:
; APPLICANT: Angen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCES: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911.842A
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11230
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-911-842A-3
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Alignment Scores:

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Pred. No.: 0 Length: 11230
Score: 16707.00 Matches: 2915
Percent Similarity: 89.72% Conservative: 289
Best Local Similarity: 81.63% Mismatch: 361
Query Match: 83.65% Indels: 6
DB: Gaps: 5
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US-09-977-053-4 (1-3571) x US-09-911-842A-3 (1-11230)

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Qy 21 PheGlnClnMetSerProSerArgAenPheSerPheArgLeuPheProGluThrAlaPro 40
Db 236 TTCAGCCCGTGGCCCTTCTGCTCAACTTCAGCTTCCGCTTCCCGCGAGCTCTCTCG 295
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Qy 41 GlyAlaProGlySerIleProAlaProAlaProGly---AspGluAlaAlaGlySer 59
Db 296 GGGGCTCTGGCAGACTGGCGGTACTCTCCGCGTCCAGTGAGGAGGAGGAGGAGGAGGAGC 355
Qy 60 ArgValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSer 79
Db 356 AAAGTGAGGAGCGCTGGCGCGCGTTCGCGAGCGCGTTCGCGCGGAGCTCAGC 415
Qy 80 GluArgLeuGluLeuValPheLeuValAspAspSerSerSerValGlyGluValAenPhe 99
Db 416 GCGAGCTTGGAGCTGCTCTCTGAGCAGCGTCTCCAGCGTGGCCCAACCAACCACTTC 475
Qy 100 ArgSerGluLeuMetPheValArgLeuSerAspPheProValValProThrAla 119
Db 476 CTCACGAGCTCAAGTTGTTGGCAGCTGTGTCCGACTTCCCGTGGTGTCCACGGCC 535
Qy 120 ThrArgValAlaIleValThrPheSerSerIleValValValProArgValAspTyr 139
Db 536 ACGGCTGTGGCCATCTGTCACCTTCTCATCAAGAACCAACGTTGGTGGCGCGCGTGTAT 595
Qy 140 IleSerThrArgArgAlaArgGlnHisCysValAlaLeuLeuGlnGluLeuProAla 159
Db 596 ATCTCCACGAGCGCGCGCACCAACACAGTGGCGCTGCTCAGCGCGAGATCCCGGCC 655
Qy 160 IleSerTyrArgGlyGlyGlyThrTyrThrIleGlyAlaPheGlnGlnAlaGlnIle 179
Db 656 ATCACTTACCGGCTGTGGCCTATATACCAAGGGCGCTTCCAGCAAGCGCGCAATC 715
Qy 180 LeuLeuHisAlaArgGluAenSerThrIleValValPheLeuIleThrAspGlyTyrSer 199
Db 716 CTTCGTCACTCTAGAGAAAACCTCCACCAAGTCAATTTCTCATCACCGCGCTATTTC 775
Qy 200 AsnGlyGlyAspProArgProIleAlaSerLeuArgAspSerGlyValGluIlePhe 219
Db 776 AATGGCGAGACCCAGACCTATTTCAGCATCTGCTTCGGGATTTCCGAGTGGAGATCTTC 835
Qy 220 ThrPheGlyIleTyrGlnGlyAsnIleArgGluLeuAenAspMetAlaSerThrProlys 239
Db 836 ACGTTCCGGATTTGGCAGGGGATATCCGGGAACCTGAATGACATGGCTTCCACCCGAG 895
Qy 240 GluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAla 259
Db 896 GAAGACATTTGTTACCTGCTCCACATTTTGAAGAAATTTAGGCTTTAGTCTCGAGGCG 955
Qy 260 LeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyr 279
Db 956 TTGCATGAAGATCTACCTTCTGGGAGTTTATCAAGAGGATATGGCCACTGCTCTTAT 1015
Qy 280 LeuCysAspGluGlyCysAspCysArgMetGlySerCysIleCysGlyThrHis 299
Db 1016 CTCTGTGAGGCTGGGAAAGACTGCTGTGACAGATGGCCAGCTGCAATGTGGGACACAC 1075
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Qy 320 CysThrAlaCysProSerGlyThrTyrIleProGluGlySerProGlyGlyIleSerSer 339
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Qy 340 CysIleProCysProAspGluAenHisThrSerProGlySerThrSerProGluAsp 359
Db 1196 TGCATCCATGCTCTGACGTAAGGCACACCTCCCGCCAGCTGCACTTCCCTCGAAGAC 1255
Qy 360 CysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysPro 379
Db 1256 TGGCTGTGCGGAGAGGATACAGAGATCTCGCCAGACTCTGAGGTTGTCCACTGTCTCT 1315
Qy 380 AlaLeuIleProProGluAenGlyTyrPheIleGlnAenThrCysAenHisPheAen 399
Db 1316 GCCCTGAAGCTCTGAAATGGTTTTTATACAAACACTTGCAGAACTACTTCAAT 1375
Qy 400 AlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeu 419
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1376 GCGCGCTGTGGGTCGCGATGTCGCGCGGCTTTGACCTTTGTGGAGAGCAGCATCCATTTG 1435
420 CysLeuProAsnGlyLeuTTPSerGlySerGluSerTyrCysArgValArgThrCysPro 439
1436 TGTCAACCCATGGTTGTGTCTGGACAGAAAGCTTCTGACAGTGTGAGACGTGCC 1495
440 HisLeuArgGlnProIlyHisGlyHisLeuSerCysSerThrArgGluMetLeuTyrLys 459
1496 CACCTCCGACAGCCCAACAGCCACATCAGCTGCTCCACTCGCGAATGCTCTACAA 1555
460 ThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThr 479
1556 ACCCTGTGTGTGTACCTGCAATGAAGATACAGATTAGAAGGCGACGACTAGGCTTACC 1615
480 CysGlnGlyAsnSerGlnTTPAspGlyProGluProArgCysValGluArgHisCysSer 499
1616 TGTCAAGGAATGCCGATGGGATGCCCGACAGCCCGGTGTGTAGAACGCCATGTGTGC 1675
500 ThrPheGlnMetProIlyAspValIleSerProHisAsnGlyLysGlnProAla 519
1676 ACCTTCCAGAGCCCAAGCGGTCAATCTTCCACCCAGCTGCGGCAAGCAGCCCGCC 1735
520 LysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLys 539
1736 AGGCTTGGGATGACCTGTGAGTCAAGCTGCGCCAGGATACATTTATTCGCGGGTCAGA 1795
540 GluMetLeuArgCysThrThrSerGlyLysTyrAsnValGlyValGlnAlaValCys 559
1796 GAA---GTGAGATGTGCCACATCTGGAGAGTGGAGTGCCAAAGTTGACAGCGCTGTGTC 1852
560 LysAspValGluAlaProGlnIleAsnGlyProLysAspIleGluAlaLysThrLeuGlu 579
1853 AAAGATGTGGAGCTCCAAATCAGCTGTGCAATGCAATGAGGCAAGACTGGGGAG 1912
580 GlnGlnAspSerAlaAsnValThrTGTGlnIleProThrAlaLysAspAsnSerGlyGlu 599
1913 CAGCAGGATCTGTCTAATGCCCTGGCAAGTCCCAACAGCTTAAAGCAACTCTGTGTGA 1972
600 LysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp 619
1973 AAGGTGTGAGTCCAGCTCCAGCCAGCTTTTACCCACCTTACCTCTCCCAATTTGGAG 2032
620 ValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHis 639
2033 GTGGCCATCACCTACACGGCAACCGACTCATCGGTAAACAGCAGCTGCACTTTCTAC 2092
640 IleLysValIleAspAlaGluProProValIleAspTyrCysArgSerProProVal 659
2093 ATTAAGGTCAATGATGTGAGCCGCTGTGATAGATTGGTGGCGATCTCCACCTCCAAATC 2152
660 GlnValSerGluLysValHisAlaLaserTTPAspGluProGlnPheSerAspAsnSer 679
2153 CAGGTGTAGAGAGGAGCACCCTGACGCTGGGATGAGCTCAGTTCTCAGACAACTCC 2212
680 GlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGlu 699
2213 GGGCTGGAATGTGATCATTACAGCAGCTCACACAAGGGGACATGTTCTCATGGGGAA 2272
700 ThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHis 719
2273 ACGGTGTGTGTGTGACAGCCATGACCTCCCTCAGGCAACAGAGGACCTGTGTGATCCAC 2332
720 IleValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIle 739
2333 ATGTGATTAAGGTTCTCCCTGTGAGTCCCTTCCACCCCTGTAAACGGGAGTTTATC 2392
740 CysThrProAspAsnThrGlyValAsnGlyThrLeuThrCysLeuGluGlyTyrAspPhe 759
2393 TGTGCCAGGATAGTGTGGATTAACTGTAGCTGAGCTGCAAGGAGGCTATGATTC 2452
760 ThrGluGlySerThrAspLysTyrCysAlaTyrGluAspGlyValTyrLysProThr 779

2453 ACAGAGGGTCACTGAGAGTACTACTGTGCTTTTGAAGATGGTATCTGGAGACCA 2512
780 TyrThrThrGluTTPProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSer 799
2513 TACTCTACAGATGGCAGACTGTCTATAAAACGTTTTCGAAACCATGTTTCAAGTCC 2572
800 PheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSer 819
2573 TTGGAATGCTATACAAAACCACTGCTGTGTGATGATGATGATCTGTTTGAAGAATTTCT 2632
820 GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
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2693 ATTGACTGAGACTTGGAGC---CTGACCAAAAATACTGCTGATGATATATTAACA 2749
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900 SerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsn 919
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3470 GCGTGGACATCTCTGCTTGTGAGTGCTTCCCTGCGCAGTAGAGAAATTTCTCCGTTCTGG 3529
1120 LeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPhe 1139
3530 CTAAACACCTTGTACCTTGTGCTTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3589

Qy	1140	CysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGlu	1159
Db	3590	TGCTCGCTGTGTCCTTTATGTAGAACTTACAACCATCATCTGGCGCCACGTCCTCATCAGAC	3649
Qy	1160	CysSerSerPheSerSerThrPheSerAlaAlaGluGluSerValValProProAlaSer	1179
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Qy	1180	LeuGlyHisIleIleIysAlaGlyHisGluIleSerSerGlnValPheHisGluCysPhePhe	1199
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Qy	1200	AsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCys	1219
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Db	4130	GCAGTTGTTAAGAACCAAGTTTGGGGGGTTCCTCGCAANAATGCCACCCCGGATTTTGGGT	4189
Qy	1340	ThrArgCysGlyIysAsnValAspGlyCysLeuSerGlnProCysIysAsnGlyValAlaThr	1359
Db	4190	ACTCGGTGTGAAAAAATGTGGATGATGTCTCAGTCAGCCATGCCAAATGGAGCCACT	4249
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Qy	1400	AspGluLeuAsnSerTyrSerCysIysCysGlnProGlyPheSerGlyGlnArgCysGlu	1419
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Qy	1420	ThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrVal	1439
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Qy	1440	MetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSer	1459
Db	4490	CTGTGATGATGGAGTGTGCCAACCCCTCATGCCGTAACTCTCTATGCATCTTGAGGATGACAAAGCATC	4549
Qy	1460	SerAspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsn	1479
Db	4550	TCTGATGTCACTCAACTACGGAGACCCCAATCTCTATGCATCTTGAGGATGACAAAGCATC	4609
Qy	1480	ThrLeuLeuLeuThrAspTyrAsnGlyTyrPValLeuTyrValAsnGlyArgGluIysIle	1499
Db	4610	ACCTTCCTCTGACTGATTACAACGGCTGGGTTCTTTATGTGAATGAAGAAAGGAATCATC	4669

DB 10121 AGCTCTCTGTTTCTGTCACAGAGGCTACACCTCGGAGGCTCCCGGAGGACACACTGC 10180
QY ThrGluAenGlyThrTrpSerHisProValProLeuCysLeuValProAsnProCysProVal 3359
DB 10181 ACTGCAATGGACCTGGATCCTGACTCCCTCTGCAACCAATCCATGCTGTC 10240
QY PropheValIleProGluAenAlaLeuLeuSerGluLeuGluPheTyrValAspGlnAen 3379
DB 10241 CCTTTTGTGATCTCTGAGAACGCTCTCTTCTGAAAAAGAGTTTTATGTGCACAGAA 10300
QY ValSerIleLeuValCysArgGluCysPheLeuLeuGlnGlyHisGlyIleLeuValCysAen 3399
DB 10301 GTATCTATCAATGTCAGGAGGAGCTCTCTGCTCAAGGCAATGGTGTATCATCGTGCAGC 10360
QY ProAspGluThrTrpThrGlnThrSerAlaLeuValCysGluLeuValIleSerCysGlyProPro 3419
DB 10361 CCTGACGAGCATGACGACACCAATGCCAGATGTGAAAAATCTCTGTGTGCTCTCCA 10420
QY AlaHisValGluAenAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThr 3439
DB 10421 AGTCAGGTAGAAATGCAATGCTGTCAGGAGGTATTTACAGTATGGGACATGATCACC 10480
QY TyrSerCysTyrSerGlyThrMetLeuGluGlyPheLeuArgSerValCysLeuGluAen 3459
DB 10481 TACTCTGTGTTACAGTGGCTACATGCTAGAGGTCTCCCTCCGAGGTGTTTGCCTAGAAAT 10540
QY GlyThrTrpThrSerProProIleCysArgAlaValCysArgPheProCysGlnAenGly 3479
DB 10541 GGAACATGACACCATCTCTGTTTGCAGAGCTGCTGTGCTGCTCCATGTCCAGATGCA 10600
QY GlyIleCysGlnArgProAsnAlaCysSerCysProGluGlyThrMetGlyArgLeuCys 3499
DB 10601 GGTGTCTGTCAAGCTCAATGCTGCTCATGCCAGAGGCTGGATGGAGGCTCTCTGT 10660
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DB 10661 GAAGAGCAATATGATCATCTCCCTGTTTGAATGGTGGGCGCTGTGTGCTTATCAG 10720
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DB 10721 TGTGATGCTCCACAGGCTGGAGTGGTCCGCTGTGTATACAGTACTTGTCTCAGTCC 10780
QY CysLeuAenGlyGlyLysCysValArgProAsnArgCysHisCysLeuSerSerTrpThr 3559
DB 10781 TGCTTAAATGGGGGAAATGCAATGCAAGACCAACCGATGCTTGTCTCTCAGCCTGGACA 10840
QY GlyHisAenCysSerArgIleArgThrGly 3570
DB 10841 GGACATGATGTTTCCAGGAAAGGAGAGCGGG 10873

RESULT 3

US-08-253-155A-1

; Sequence 1, Application US/08253155A

; Patent No. 5691147

; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jeno

; APPLICANT: Draetta, Giulio

; TITLE OF INVENTION: CDK4 Binding Proteins

; NUMBER OF SEQUENCES: 95

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/253,155A
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: M11-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-253-155A-1

Alignment Scores:

Pred. No.: 1.88e-179 Length: 1638
Score: 2282.00 Matches: 413
Percent Similarity: 97.65% Conservative: 3
Best Local Similarity: 96.95% Mismatches: 2
Query Match: 11.43% Indels: 8
DB: 1 Gaps: 0

US-09-977-053-4 (1-3571) x US-08-253-155A-1 (1-1638)

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DB 76 ATCTCTGCGAGCTTAAAAATGTCCTCTCCCGAAATACATACATATATCTGTGAGAGA 135
QY 3194 GlyAspAspPheSerValAsnArgGlnValSerValSerCysAlaGluGlyTyrThrPhe 3213
DB 136 GGGGAGCATTTTCAGTGTGAATAGGCAAGTTTCTGTGTCTATGTGCAAGGGGTATACCTTT 195
QY 3214 GluGlyValAsnIleSerValCysGlnLeuAspGlyThrTrpGluProProPheSerAsp 3233
DB 196 GAGGAGGTAAACATATCAGTATGTGAGTGTGAGACCTGGGAGCCACCATTTCTCCGAT 255
QY 3234 GluSerCysSerProValSerCysGlyLysProGluSerProGluHisGlyPheValVal 3253
DB 256 GAATCTTGCAGTCCAGTTTCTTGTGGGAAACCCAGAAAGTCCAGAACATCGATTGTGGTT 315
QY 3254 GlySerLysTyrThrPhe-GluSerThrIleIleTyrGlnCysGluProGlyTyrGluLe 3273
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QY 3293 leCysLysGluThrArgCysGluThrProLeuGluPheLeuAenGlyLysAlaAspIleG 3313
DB 436 TATGCAAAAGAGAGACAGGCTGTGAAATCTCCACTTGAATTTCTCAATGGGAAAGCTGACATTG 495
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DB 556 GGCCATCTGAGGACACATGTCACAGAAAAATGGAACCTGGAGCCACCCAGTCCCTCTCTGCA 615
QY 3353 yProAenProCysProValProPhe-ValIleProGluAenAlaLeuLeuSer-GluTy 3372
DB 616 AACCAAAATCCATGCTGTTCTTTTGGTGAATTTCCCGAGAAATGCTCTGTCTGTCTTGA 675

3372	Qy	sGluPheTyrValAspGlnAsnValSerIleLysCysArgGluGlyPheLeuLeuGlnG1	3392
676	Db	GGAGTCTTTATGTGATCAGAAATGTGTCCATCAAAATGTAGGAGAGGTTTCTGTCTGCAGGG	735
3392	Qy	yHisGlyIleIleThrCysAsnProAspGluThrTrrPThrGlnThrSerAlaLysCysG1	3412
736	Db	CCACGGCATCTACTTGCACACCCGACGAGACGTGGACACACAGACGCGCCAAATGTGA	795
3412	Qy	uLysIleSerCysGlyProProAlaHisVal - GluAsnAlaIleAlaArgGlyValHisT	3432
796	Db	AAAANTCTCATGTGGTCCACCAGCTCACGTAGCAAAATGCAATTGTCTCGAGGCGTACATT	855
3432	Qy	yrGlnTyrGlyAspMetIleThrTyrSerCysTyrSerGlyTyrMetLeuGluGlyPheL	3452
856	Db	ATCAANTATGGAGACATGATCACCTACTCATGTGTACAGTGGATACATGTTGGAGGGTTTCC	915
3452	Qy	euArgSerValCysLeuGluAsnGlyThrTrrPThrSerProProIleCysArgAlaValC	3472
916	Db	TEAGGAGTGTTGTTTAGMAAATGGACATCGACATCACCTCTCTATTTTGCAGAGCTGTCT	975
3472	Qy	ysArgPheProCysGln - AsnGlyGlyIleCysGlnArgProAsnAlaCysSerCysPro	3491
976	Db	GTCCATTTCCATGTCAAGAAATGGGGGCATCTGCCAAGCCCAAAATGCTGTGTCTGTCCA	1035
3492	Qy	GluGlyTrrPMetGlyArgLeu - CysGluGluProIleCysIleLeuProCysLeuAsnG1	3511
1036	Db	GAGGGCTGGATGGGGGGCCCTCTGTGAAGAAACCAATCTGCATTTCTTCCCTGTCTGAACGG	1095
3511	Qy	yGlyArgCysValAlaProTyrGlnCysAspCysProProGlyTrrPThrGlySerArgCy	3531
1096	Db	AGTGCCTGTGTGGCCCTTACCAGTGTGACTGCGCGCTGGCTGGACGGGGTCTCGCTG	1155
3531	Qy	sHisThr - AlaValCysGlnSerProCysLeuAsnGlyGlyLysCysValArgProAsnA	3551
1156	Db	TCAAACAGAGCTGTTTGCAGCTCCCTGCTTAAATGTGTGAATAATGTGAAGACCAAACC	1215
3551	Qy	rgCysHisCysLeuSerSerTrrPThrGlyHisAsnCysSerArgLysArgThrGlyP	3571
1216	Db	GATGTCACTGTCTTCTTCTTGGACGGGACATACTGTTCAGGAAAGAGGAGACTGGGT	1275
3571	Qy	he	3571
1276	Db	TT	1277

RESULT 4

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US-09-620-312D-259
; Sequence 259, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25

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Db 988 GAAAGTGTCTACAGCTGTGAGCCGCTACGACCTCAGAGGGCGCTCGCTATGCGCTGC 1047
Qy 1888 LeuAlaAsnSerSerTrpSerHisSerProProValCysGluProValLysCysSerSer 1907
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Qy 2171 SerCysAsnLysGlyPheTyIleLysGlyGluLysLysSerThrCysGluAlaThrGly 2190
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Db 1945 GTGGTGACTACCGCTGCAATCCCGGAGCGGAGGAGAGAGTGTTTTCAGCTTTGGGT 2004
Qy 2240 SerProValPheValCysGlnAlaAsnArgHis-----TrpHisSerGluSer 2255
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Qy 2333 LeuValLeu-----LysGluLeuThrThrGluValGlyValValThrPheSerCysLys 2350
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Qy 3250 GlyPheVal-----ValGlySerLysTyrThrPheGluSerThr 3262

Db 5188 GCGCGTGTCTACTTCCACTTAATCTCCAGCTTGGGGCAAGGTGTCTTT----- 5238

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RESULT 5

US-09-023-655-1265
 : Sequence 1265, Application US/09023655
 : Patent No. 6607879
 : GENERAL INFORMATION:
 : APPLICANT: Cocks, Benjamin G.
 : APPLICANT: Susan G. Stuart
 : APPLICANT: Jeffrey J. Seilhamer
 : TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 : TITLE OF INVENTION: EXPRESSION
 : NUMBER OF SEQUENCES: 1508
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 : STREET: 3174 PORTER DRIVE
 : CITY: PALO ALTO
 : STATE: CALIFORNIA
 : COUNTRY: USA
 : ZIP: 94304
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/023,655
 : FILING DATE: HEREWITH
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Zeller, Karen J.
 : REGISTRATION NUMBER: 37,071
 : REFERENCE/DOCKET NUMBER: PA-0001 US
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (650) 855-0555
 : TELEFAX: (650) 845-4166
 : INFORMATION FOR SEQ ID NO: 1265:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 6951 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : IMMEDIATE SOURCE:
 : LIBRARY: GENBANK
 : CLONE: g30185
 : US-09-023-655-1265

Alignment Scores:
 Pred. No.: 3,77e-157 Length: 6951
 Score: 2027.00 Matches: 563
 Percent Similarity: 40.08% Conservative: 265
 Best Local Similarity: 27.25% Mismatches: 832
 Query Match: 10.15% Indels: 406
 DB: 4 Gaps: 85

US-09-977-053-4 (1-3571) x US-09-023-655-1265 (1-6951)

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QY 1793 GlyAsnProGluAsnGly-----HisSerSerGlyGluIleTyrThrValGlyAla 1809
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Db 1408 GACCTCATTTGGAGAGACACCATCCGCTGCACAAAGTGAC----- 1446
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QY 2112 CysMetGluGlyPheValLeuAsnThrSerAlaLysIleGluCysMetArgGlyGlyGln 2131
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Db 2182 GCTTTGTGATGAAGAGACCCCGCGGTGTGAGTGCACAGGCCCTGACAAATATGGAGCGG 2241
QY 2313 LysSerAsnProLysCysMetProAlaLysCysProGluProProLeuLeuGluAsnGln 2332
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QY 2333 LeuValLeu-----LysGluLeuThrThrGluValGlyValThrPheSerCysLys 2350
Db 2299 CGTACCACAAAGGACAAAGGCAACTTTTACCCCGGCGAGGAAGTGTCTTACAGCTGTGAG 2358

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Db	2359	CCCGCTATGACCTCAGAGGGCGTCGTCTATGCGCTGCACACCCAGGAGACTGGAGC	2418
Qy	2371	AspSerPheProValCysLysIleValLeuCysThrPro-----ProProLeuIleSer	2388
Db	2419	CCTCAGCCCCCACAATGTGAATGAATTCCTGTGATGACTTTCATGGGCCAACTTCTTAAAT	2478
Qy	2389	PheGlyValProIleProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCys	2408
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Db	2536	GATGAAGGATTCATTAATAAAGGCAGCTCTGTAGTTATTGTGTCTTGGCTGGAAATGGAA	2595
Qy	2427	---ThrTrpSerSerProLeuProGluCysValProValGluCysProGlnProGluGlu	2445
Db	2596	AGCCTTTGGAAATACAGGTTCCTCAGTGTGTGAACAAATCTTTTGTCCAAGTCTCCAGTT	2655
Qy	2446	IleProAsnGlyIle-----IleAspValGlnGlyLeuAlaTyrLeuSerThrAla	2462
Db	2656	ATTCTTAATGGAGACACACAGGAACCTCTGGAAGTCTTCCCTTGGAAAGCAGTA	2715
Qy	2463	LeuTyrThrCysLysPro-----GlyPheGluLeuValGlyAsnThr	2476
Db	2716	AATTACACATCGCACCCGCCACACAGAGGAGCGAGCTTCGACCTCATTTGGAGAGAGC	2775
Qy	2477	ThrThrLeuCysGlyGlu-----AsnGlyHisIleTrpLeuGlyGlyLysProThr	2492
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Qy	2493	CysLysAlaIle---GluCysLeuLysProLysGluIleLeuAsnGlyLysPhe-----	2509
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Qy	2510	-----SerTyrAspLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGly	2527
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Qy	2528	PheArgLeuGluGlyProSerAlaLeuThrCysLeuGlnThrGlyAspTrpAspValAsp	2547
Db	2956	TAC---TACGGGAGGCCATCTCTATCATCATGTCTAGATACCTGGTCTGTCTCAAGTCCC	3012
Qy	2548	AlaProSerCysAsnAlaIleHisCysAspSerProGlnProIleGluAsnGlyPheVal	2567
Db	3013	AAAGATGCTCTTAACGTAATCATCATGATAAACTCCTCCAGATCCAGTGAATGGCATGGT	3072
Qy	2568	GluGly---AlaAspTyrSerTyrGlyAlaIleIleIleTyrSerCysPheProGlyPhe	2586
Db	3073	CATGTGATCACAGACATCCAGGTGGATCCAGAAATCAACTATTCTTGTACTACAGGGCAC	3132
Qy	2587	GlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGly-----TrpSer	2602
Db	3133	CGACTATTGTCATCTCATCTGCTGGAATGATATCTCTCAGGCAATATCTGCCCATGGAGC	3192
Qy	2603	SerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAspPheGly	2622
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Qy	2623	AspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspAspMetMetGlu	2642
Db	3253	GATTTCATT-----	3261
Qy	2643	ValProTyrValThrProHisProProTyrHisLeuGlyAlaValAlaLysThrTrpGlu	2662
Db	3261	-----	3261
Qy	2663	AsnThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSer	2682
Db	3262	-----AGCACCAACAGACAGAAATTTTCACTATGATCATGTGATGCTGATGCTGAC	3303

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Qy	2697	LeuIleCysGlnGluasp-----GlyThrTrpAsnGlySerAlaProSerCys	2712
Db	3364	ATTATCTGCACCAGCAATACGATTCAGTGGGCATCTGGAGCGGCCCGCCCTTCAGTGC	3423
Qy	2713	IleSerileGluCysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThrGlu	2732
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Qy	2807	LeuAsnGlyThrGluArgAgThrCysGluAspAspIleAsnTrpAspGluAspGluPro	2826
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RESULT 8

5256642-3

; Patent No. 5256642

; APPLICANT: PEARON, DOUGLAS T.; KLUICKSTEIN, LLOYD B.; WONG,

; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN

; H.; MAKIDES, SAVVAS; MARSH, HENRY C. JR.

; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT

; RECEPTOR 1 (CRI) AND A THROMBOLYTIC AGENT, AND THE METHODS OF

; USE THEREOF

; NUMBER OF SEQUENCES: 30

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2223 CGAGGACAGTGGAGCCCTCGAAGCCCGAGATGTGCAGTGAATACTCTGTGAT----- 2273
Db
2838 ValSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGln----- 2852
Qy
2274 ---GACTTCTTGGTCAACTCCCTCATGGCGGTGTGCTATTTCCACTTAATCTCCAGCTT 2330
Db
2853 ---LysGluIleGluTyrThrCysAsnGlyGlyPheLeuLeuGluGlyValaArgSerArg 2871
Qy
2331 GGGCAAGGTGCTCTTGTCTGTGATGAAGGGTTTGTCTTAAGGGCGGTTCCTGTAGT 2390
Db
2872 ValCysLeuAlaAsnGlySer-----TrpSerGlyAlaThrProAspCysValPro 2888
Qy
2391 CATTTGTCTTGTGGTGAATGAGAAGCCTTTTGAATAACAGTGTCTCTGTGTGAACAT 2450
Db
2889 ValArgCysAlaThrProProGlnLeuAlaAsnGlyValThrGluGlyLeu----- 2905
Qy
2451 ATCTTTTGTCCAAATCTCTCCAGCTATCTTAAATGGGACACACAGAGAACTCCCTCTCGA 2510
Db
2906 AspTyrGlyPheMetLysGluValThrPheHisCysHisGlu----- 2919
Qy
2511 GATATTCCTTGGAAAGAAATATCTTACATGTGTGACCCCAACCCACAGAGGGGATG 2570
Db
2920 GlyTyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAsp-----Gly 2935
Qy
2571 ACCTTCAACTCATTTGGGAGAGCACCATCCGCTGCACAACTGACCCCTCATGGGAATGG 2630
Db
2936 AsnTrpAspAlaGluIleProLeuCys-----LysProValAsnCysGlyPro 2951
Qy
2631 GTTTGGAGCAGCCCTGCTCGCTGTCAACTTTCTGTCTGTGTGTGTGTGTGTGTGTGTGT 2690
Db
2952 ProGluAspLeuAlaHisGlyPhePro-----AsnGlyPheSerPheIleHis 2967
Qy
2691 CCAAGCAGATTTCCATTTGCCAGTCTTACGATCCCAATTAATGACTTTGAGTTCCAGTC 2750
Db
2968 GlyGlyHisIleGlnTyrGlnCysPheProGlyTyr-----LysLeuHisGlyAsnSer 2985
Qy
2751 GGGACATCTTTGAATTAATGATGCGTCTGGTATTTTGGGAAATAATCTCTCTATCTCC 2810
Db
2986 SerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerProSerCysLeuProCys 3005
Qy
2811 -----TGCCTAGAAACTTGTGCTGTCTGTCAAGTGTGAAGACAACTGTAGACGAAA 2861
Db
3006 ArgCysSerThrProValIleGluTyr---GlyThrValAsn---GlyThrAspPheAsp 3023
Qy
2862 TCATGTGGACTCCACAGAACCTTTCATNGAATGTGTGCATATAACACAGATACACAG 2921
Db
3024 CysGlyLysAlaAlaArgIleGlnCysPheLysGlyPheLysLeuLeuGlyLeuSerGlu 3043
Qy
2922 TTTGGATCAACAGTTAATTAATCTTGTAAAGGGTTTCGACTCATTTGGTTCCCACTCT 2981
Db
3044 IleThrCysGluAlaAspGlyGln-----TrpSerSerGlyPhePheProHisCysGlu 3060
Qy
2982 ACTACTGTCTGTCTCAGGCAATAATGTCACTGGGATAGAAGGCCACTATTATTGTGAG 3041
Db
3061 HisThrSerCysGlySerLeuProMetIleProAsnAla---PheIleSer-----Glu 3077
Qy
3042 ATCATATCTTGTGAGCCACTCCAAACCATATCCATGTGAGACTTCTTACAGCAACATAGA 3101
Db
3078 ThrSerSerTrpLysGluAsnValIleThrTyrSerCysArgSerGly----- 3093
Qy
3102 ACATCTTTTCAATGGAACGGTGTGTAATTTTACCAGTGCCACACTGGACAGATGGAGAA 3161
Db
3094 -----TyrValIleGlnGlySerSerAspLeuIleCysThrGluLys----- 3107
Qy
3162 CAGCTGTTTGTGCTTGTGGGAGAACGGTCAATATATTTGACCAGCAAGATGATCAAGTT 3221
Db

Qy	1996	AlaGlyLeuAspThrIleGluCysLeuAlaAspGlyLysTrpSerArgSerAspGln	2015
Db	444	GGAGGGAGAAAGGTGTTGAGCTGTGGGT	473
Qy	2016	CysLeuAlaValSerCysAspGluProProIleValAspHisAlaSerProGluThrAla	2035
Db	474	-----GAGCCCTCCATA-----	485
Qy	2036	HisArgLeuPheGlyAspIleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAsp	2055
Db	486	-----TACTGCACC-----AGCAAT	500
Qy	2056	AsnSerGlnLeuLeuCysAsnAlaGlnGlyLysTrpValProProGluGlyGlnAspMet	2075
Db	501	GACCATCAAGTG-----GGCATCTGGAGCGGCCCG-----GCC	533
Qy	2076	ProArgCysIleAlaHisPheCysGluLysProProSerValSerTyrSerIleLeuGlu	2095
Db	534	CCTCAGTGCATTATACCTAAACAAATGACGCGCTCCAAATGTGGAATGGAATATATGGTA	593
Qy	2096	SerValSerLysAlaLysPheAlaAlaGlySerValSerPheLysCysMetGluGly	2115
Db	594	TCTGACAAACAGAGCTATTCTTCTTAATGAAGTTGTGGAGTTTAGGTGTGCAGCTGGC	653
Qy	2116	PheValLeuAsnThrSerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSer	2135
Db	654	TTTGTGCATGAAGAGACCCCGCTGTGAAGTGCACGCGCTTGAAACAAATGGAGCCGGAG	713
Qy	2136	ProMetSerIleGlnCysIleProValArgCysGlyGluProProSerIleMetAsnGly	2155
Db	714	CTACCAAGC-----TGCTCCAGGTA-----TGTCAGCCACCTCCAGATGCTCTGCATGCT	764
Qy	2156	-----TyrAlaSerGlySerAsnTyrSerPheGlyAlaMetValAlaTyrSerCys	2172
Db	765	GAGCGTACCCAAAGGCAAGCAACACTTTTTCACCCGCGCAGGAAGTGTCTACAGCTGT	824
Qy	2173	AsnLysGlyPheTyrIleLysGlyGluLysSerThrCysGluAlaThrGlyGlnTrp	2192
Db	825	GAGCCCGGCTATGACCTCAGAGGGGCTGCGTCTAGCGCTGCACACCCAGGAGACATGG	884
Qy	2193	SerSerProIleProThrCysHisProValSerCysGlyGluProProLysValGluAsn	2212
Db	885	AGCCTGCAGCCCCACACATGTGAAGTGAATCTCTGTGATGAC-----	926
Qy	2213	GlyPheLeuGluHisThrThrGlyArgIlePheGluSerGluValArgTyrGlnCysAsn	2232
Db	927	---TTCATG-----GGCCAACTCTTAATGCGCGTGTGCTATTT-----	962
Qy	2233	ProGlyTyrLysSerValGlySerProValPheValCysGlnAlaAsnArgHisTrpHis	2252
Db	963	-----CCAGTA-----	968
Qy	2253	SerGluSerProLeuMetCysValProLeuAspCysGlyLysProProIleGlnAsn	2272
Db	968	-----	968
Qy	2273	GlyPheMetLysGlyGluAsnPheGluValGlySerLysValGlnPhePheCysAsnGlu	2292
Db	969	-----AATCTCCAGCTTGAGCAAAAGTGAATTTTGTGTGATGAA	1010
Qy	2293	GlyTyrGluLeuValGlyAspSerSerTrpThrCysGlnLysSerGlyLysTrpAsnLys	2312
Db	1011	GGATTCAATTAAGAGGAGCTCTCTAGTTATTGT-----	1046
Qy	2313	LysSerAsnProLysCysMetProAlaLysCysProGluProProLeuLeuGluAsnGln	2332
Db	1046	-----	1046
Qy	2333	LeuValLeuLysGluLeuThrThrGluValGlyValValThrPheSerCysLysGluGly	2352
Db	1046	-----	1046

Qy	2353	HisValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnGlnTrpAsnAspSer	2372
Db	1047	---GTCTGGCTGGAAATGGGAAGCCTT-----TGGAAATAGCAGT	1082
Qy	2373	PheProValCysLysIleValLeuCysThrProProLeuIleSerPheGly	2390
Db	1083	GTTCACAGTGTGAACAAATCTTTTGTCCAAGTCTCCAGTTATTTCTAATGGGAGAC	1142
Qy	2391	ValProIleProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCys	2408
Db	1143	ACAGGAACCTCTGGGAAGCTTTCCCTTTTGGAAAGACAGTAATTACACATGCGACCC	1202
Qy	2409	-----ValGlyGlyPhePheLeuArgGlyAsnSerThrThrLeuCys	2422
Db	1203	CACCCAGACAGAGGACAGCTTCGACCTCATTTGGAGAGACCATTCGCTGCACAAGT	1262
Qy	2423	-----GlnProAspGlyThrTrpSerSerProLeuProGluCys	2439
Db	1263	GACCTCAAGGGAATGGGTTTGAGCAGCCCTGCCCTCGCTGGGAATTTCTGGGTAC	1322
Qy	2440	CysProGlnProGluGluIleProAsnGlyIleIleAspValGlnGlyLeuAlaTyr	2458
Db	1323	TGTCAGCCCGCAGATCATTTTCTGTGGCCAGTTGGAACCCCAACCAATGCATCTGAC	1382
Qy	2459	-----LeuSerThrAlaLeu-----TyrThrCysLysProGlyPheGluLeuValGlyAsn	2475
Db	1383	TTTCCCATTTGGACATCTTTAAAGTACCAATGCGCTCT-----GAGTACTACGGGAG	1436
Qy	2476	ThrThrThrLeu-----CysGlyGluAsnGlyHisTrpLeuGlyGlyLysProThrCysLys	2494
Db	1437	CCATTCTCTATACATGCTAGATAACCTGGTCTGGTCAAGTCCCAAGATGTCGTGAAA	1496
Qy	2495	AlaIleGluCysLeuLysProLysGlyIleLeuAsnGlyLysPheSer---TyrThrAsp	2513
Db	1497	CGTAATCATGTAAACCTCTCCAGTCCAGTGAATGGCATGGTGCATGATCATCACAGAC	1556
Qy	2514	LeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyPro	2533
Db	1557	ATCCAGGTGGATCCAGAAATCAACTATTTGTACTACAGGGCACCGACTCATTTGGTCCAC	1616
Qy	2534	SerAlaLeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAla	2553
Db	1617	TCATCTCTCAATGTATCTCTCAGGC-----AAACT	1649
Qy	2554	IleHisCysAspSerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSer	2573
Db	1650	GCCCAT-----	1655
Qy	2574	TyrGlyAlaIleIleIleTyrSerCysPheProGlyPheGlnValAlaGlyHisAlaMet	2593
Db	1655	-----	1655
Qy	2594	GlnThrCysGluGluSerGlyTrpSerSerIleProThrCysMetProIleAspCys	2613
Db	1656	-----TGAGCAGCAAGCCGCAATTTGTCAACGAATTTCTCTGT	1694
Qy	2614	GlyLeuProHisIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyr	2633
Db	1695	GGGTACCCCAACCATTCGCAATGGAGATTTTCAT	1730
Qy	2634	PheGluGlnGluAspAspMetMetGluValProTyrValThrProHisProProTyrHis	2653
Db	1730	-----	1730
Qy	2654	LeuGlyAlaValAlaLysThrTrpGluAsnThrLysGluSerProAlaThrHisSerSer	2673
Db	1731	-----AGCACCAACAGAGAG	1745
Qy	2674	AsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProGly	2688
Db	1746	AAATTTCACTATGATCAGTGGGACCTACGCTGCATCTTTGGACAGAGGGAGAAG	1805
Qy	2689	---TyrGluLeuLeuGlyAsnProValIleLeuCysGlnGluAsp-----Gly	2703

Db 1806 GTGTTTGAGCTTGTGGGTGAGCCCTCCATATCTACTGACACGACATGACATGAGTGGGC 1865
Qy 2704 ThrTyrAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuProThrAlaPro 2723
Db 1866 ATCTGGAGCGGCCCGCCCTCAGTGCAATTAACCTAACAAATGACAGCCCTCCAAATGTG 1925
Qy 2724 GluAsnGlyPheLeuArgPheThrGluThrSerMetGlySer-----AlaValGln 2740
Db 1926 GAAATATGGAATATTTGATCTGACACAGAACCTTATTTCTTAAATGAAGTTGTGGAG 1985
Qy 2741 TyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsn 2760
Db 1986 TTAGGTGTGACCTTGCTTGTCTGATGAAGAGACCCCGCGTGTGAAGTGCAGGCCCTG 2045
Qy 2761 ArgLysTrpSerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProAsnPro 2780
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Qy 2781 ValMetAsnGlySerIleLysGlySer-----AsnTyrThrTyrLeuSerThrLeu 2797
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Qy 2798 TyrTyrGluCysAspProGlyTyrValLeuAsnGlyThrGluArgArgThrCysGlnAsp 2817
Db 2163 TTTCTACAGCTGTGAGCCTTGCTATGACCTCAGAGGGCTGCTCTGCACTGCACACC 2222
Qy 2818 AspLysAsnTrpAspGluAspProIleCysIleProValAspCysSerSerProPro 2837
Db 2223 CGAGGAGACTGGAGCCCTGGAAGCCCGAGATGTGCAGTGAATCTCTGTGAT 2273
Qy 2838 ValSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGln----- 2852
Db 2274 ---GACTTCTGGGTCAACTCCCTCATGCGCCGTGTCTTATTTCCACTTAACTCCAGCTT 2330
Qy 2853 ---LysGluIleGluTyrThrCysAsnGluGlyPheLeuLeuGluGlyAlaArgSerArg 2871
Db 2331 GGGCAAGAGTGTCTTGTCTGTGATGAAGGTTTCGCTTAAGGGCAGTTCGGTAGT 2390
Qy 2872 ValCysLeuAlaAsnGlySer-----TrpSerGlyAlaThrProAspCysValPro 2888
Db 2391 CATGTGTCTTGGTGAATGAGAGCCCTTGGAAATACAGTGTCTCTGTGTGTAACAT 2450
Qy 2889 ValArgCysAlaThrProProGlnLeuAlaAsnGlyValThrGluGlyLeu----- 2905
Db 2451 ATCTTTGTGTCAAATCTCTCAGTATCTCTTAATGGGAGACACACAGGAACCTCCCTCTGGA 2510
Qy 2906 AspTyrGlyPheMetLysGluValThrPheHisCysHisGlu----- 2919
Db 2511 GATATTCCTATGGAAGAAATATCTACATGTGACCCCAACCCACACAGAGGGATG 2570
Qy 2920 GlyTyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAsp-----Gly 2935
Db 2571 ACCTTCNAACCTCATTTGGGAGAGACCAATCCGCTGCACAAAGTGAACCTCATGGGAATGG 2630
Qy 2936 AsnTrpAspAlaGluIleProLeuCys-----LysProValAsnCysGlyPro 2951
Db 2631 GTTTGGAGCAGCCCTGCCCCCTCGCTGTGAACCTTCTGTGCTGTCTCAGTGTAAACC 2690
Qy 2952 ProGluAspLeuAlaHisGlyPhePro-----AsnGlyPheSerPheIleHis 2967
Db 2691 CCAGAGCAGTTTCCATTTGCCAGTCTACATCCCAATTAATGACTTTTGAGTTCCAGTC 2750
Qy 2968 GlyGlyHisIleGlnTyrGlnCysPheProGlyTyr-----LysLeuHisGlyAsnSer 2985
Db 2751 GGGACATCTTTGAATATGAATGACCGCTCTCGGTATTTTGGGAAATGTTCTCTATCTCC 2810
Qy 2986 SerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerProSerCysLeuProCys 3005
Db 2811 -----TGCTTAGAAACTTGGTCTGGTCAAGTGTGAAGACAACTGTAGACGAA 2861
Qy 3006 ArgCysSerThrProValIleGluTyr---GlyThrValAsn---GlyThrAspPheAsp 3023

Db 2862 TCATGTGGACCTCCACCAGAACCCCTTCAATGGAATGGTGCATATATAACACAGATACACAG 2921
Qy 3024 CysGlyLysAlaAlaArgIleGlnCysPheLysGlyPheLysLeuLeuGlyLeuSerGlu 3043
Db 2922 TTTGGATCAACAGTTAAATTAATTTCTTGTATGAAGGGTTTCGACTCACTATGGTTCCCATCT 2981
Qy 3044 IleThrCysGluAlaAspGlyGln-----TrpSerSerGlyPheProHisCysGlu 3060
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Qy 3078 ThrSerSerTrpLysGluAsnValIleThrTyrSerCysArgSerGly----- 3093
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Qy 3094 -----TyrValIleGlnGlySerAspLeuIleCysThrGluLys----- 3107
Db 3162 CAGCTGTTTGAGCTTGTGGAGAACCGTCAATATATTTGCCAGCAAGATGATCAAGTT 3221
Qy 3108 GlyValTrpSerGlnProTyrProValCysGluProLeuSerCysGlySerProProSer 3127
Db 3222 GGTGTTTGGAGCAGCCCTCCCTCGGTGTATTTCTACTAATAATGACAGCTCCAGAA 3281
Qy 3128 ValAlaAsnAlaValAlaThrGlyGluAlaHisThrTyrGluSer-----GluVal 3144
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Db 3342 AGATTAGATGTGAGCCCGGGTTTGTATG---GTAGGGTCCCACACTGTGCGATGCCAG 3398
Qy 3165 LysAspGlyArgTrpPheProGluArgIleSerCysSerProLysCysProLeuPro 3184
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Qy 3185 GluAsnIle-----ThrHisIleLeuValHisGlyAspAspPheSerValAsnArgGln 3202
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Qy 3203 ValSerValSerCysAlaGluGlyTyrThrPheGluGlyValAsnIleSerValCysGln 3222
Db 3519 GTGTTCTACAGTGTGAGCCAGCTATGACTCAGAGGGGCTCGGTCTCTGCATGCCAG 3578
Qy 3223 LeuAspGlyThrTrpGluProProPheSerAspGluSerCysSerProValSerCysGly 3242
Db 3579 CCCAGGAGAGACTGGAGCCCT-----GAAGCCCTAGATGTACAGTGAATACTCTGTGAT 3632
Qy 3243 Lys-----ProGluSerProGluHisGlyPheVal-----Val 3253
Db 3633 GACTTCTGGGCCAACTCCCT---CATGCCGTGTCTACTTCCACTTAACTCTCCAGCTT 3689
Qy 3254 GlySerLysTyrThrPheGluSerThrIleIleTyrGlnCysGluProGlyTyrGluLeu 3273
Db 3690 GGGCAAGAGTGTCTTT-----GTTTGGATGAAGGGTTCCGATTA 3731
Qy 3274 GluGlyAsnArgGluArgValCys-----GlnGluAsnArgGlnTrpSerGlyGly 3290
Db 3732 AAAGGCAGGTCTGTAGTCACTTGTGTCTTGGCTGGATGAAGGCCCTTTGGATATAGCAT 3791
Qy 3291 ValAlaIleCysLysGluThrArgCysGluThrProLeuGluPheLeuAsnGlyLys--- 3309
Db 3792 GTTCCAGTGTGGAACAATCTTTTGTCCAAATCTCTCCAGTATCTTATATGGAGACAC 3851
Qy 3310 -----AlaAspIleGluAsnArgThrThrGlyProAsnValValTyrSer 3324
Db 3852 ACAGGAATCTCCCTTTTGGAGATAT-----CCCTATGGAAGAAATATCTTACGCA 3902
Qy 3325 Cys-----AsnArgGly-----TyrSerLeuGluGlyProSerGluAlaHis 3338
Db 3903 TGGACACCCCAACCCAGACAGAGGATGACCTTCACTTCACTGGGGAGAGCTCCATCCGC 3962

3339	QY	CysThrGlu	-----AsnGlyThrTrpSerHisProValProLeuCysLys---	3353
3363	Db	TGCACAGTGACCTCAAGGAAATGGGTTTGAGCAGCCCTGCCCCCTCGCTGTGAAC	4022	
3354	QY	-----ProAsnProCysProValProPheValIleProGluAsnAlaLeuLeuSerGlu	3371	
4023	Db	TCTGTTCTCTGCTGCCTGCCACATCCACCACGATC-----CA	4061	
3372	QY	LysGluPheTyValAspGlnAsnValSerIle-----	3382	
4062	Db	AACGGCGATTACATTTGGAGACACGATCTCTATATCTTCTGGGATGCAATCAGCTAC	4121	
3383	QY	LysCysArgGluGlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAsnProAspGlu	3402	
4122	Db	ACTTGTGACCCCGCTACCTGTTAGTGGGAAGGGCTTCATTTCTGTACAGACCAGGA	4181	
3403	QY	ThrTrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProProAlaHisVal	3422	
4182	Db	ATCTGGGACCAATTGGATCATTTTGCAAAAGAGTAAATTTGTAGCTTCCCACTGTTTATG	4241	
3423	QY	GluAsnAlaIleAlaArgGlyValHis-----TyrGlnTyGlyAspMetIle	3438	
4242	Db	---AATGGAAATTCGAAGGAGTTAGAAATCAAAAAGTATATCACTATGAGGATTATGTG	4298	
3439	QY	ThrTySerCysTySerGlyTyMetLeuGluGlyPheLeuArgSerValCysLeuGlu	3458	
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3459	QY	AsnGlyThrTrpThrSerProTolCysArgAlaValCysArg	3473	
4359	Db	GATGACAGATGG---GACCCCTCTCTGCGCAAAATGTACCTCTCTGT	4400	

RESUM. T 10

US-09-023-655-1066
Sequence 1066, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
Prior Application Data:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
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INFORMATION FOR SEQ ID NO: 1066:
SEQUENCE CHARACTERISTICS:

Db 772 GGTGTA-----ACTGCAAACTTTTCTGTGATGAAGGGTATCGACTGCAAGGC 819
Qy 1940 ProSerIleIleGluCysThrAlaSerGly-----IleTrpAspArgAlaProPro 1956
Db 820 CCACCTTCTAGTCGGTGTGTAATTCGTGCAAGGAGGTGCTTGGACCAAAATG---CCA 876
Qy 1957 AlaCysHisLeuValPheCysGlyGluProProAlaIleLeuAspAlaValIleThrGly 1976
Db 877 GTATGTGAAGAAATTTTGGCCCATCACCTCCCTTATTTCTCAATGGAAGACATATATAGC 936
Qy 1977 Asn-----AsnPheThrPheArgAsnThrValThrThrCys----- 1989
Db 937 AACTCACTAGCAAAATGCTCATATGGAAGCATAGTACTTACTGTGACCCGGACCCA 996
Qy 1990 LysGluGly-----TyrThrLeuAlaGlyLeuAspThrIleGluCysLeuAlaAsp--- 2006
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Qy 2007 -----GlyLysTrpSerArgSerAspGlnCys-----LeuAlaVal 2019
Db 1057 CAGAAAGACTGGGACCTGGAGTGGCCCTGCCACGCTGTGAACCTTCTACTTCTCGGGTT 1116
Qy 2020 SerCysAspGluProProIleVal-----AspHisAlaSerProGluThrAlaHisArg 2037
Db 1117 CAGTGTCCACATCCCGACAGTCTTAAGAGGCCGATGATCTGGCAGAAAGATCGATAT 1176
Qy 2038 LeuPheGlyAspIleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSer 2057
Db 1177 ACCTATAACGACACACTGTGATATTTGCTTGCATGTTTGGCTTCACCTTGAAGGGCAGCAAG 1236
Qy 2058 GlnLeuLeuCysAsnAlaGlnGlyLysTrpValProProGluGlyGlnAspMetProArg 2077
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Qy 2078 CysIleAlaHisPheCysGluLysProProSerValSerTyrSerIleLeuGluSerVal 2097
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Qy 2098 SerLysAlaLysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheVal 2117
Db 1293 ----- 1293
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Db 1294 -----GAATGCCAGGCCCCCTCTCTAACATCTCAATGCGCAAAAG 1332
Qy 2158 SerGlySerAsn-----TyrSerPheGlyAlaMetValAlaTyrSerCysAsnLys 2174
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Db 1483 -----GAAGCTACAGGAAG----- 1497
Qy 2235 TyrLysSerValGlySerProValPheValCysGlnAlaAsnArgHisTrpHisSerGlu 2254
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Qy 2295 GluLeuValGlyAspSerSerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSer 2314
Db 1567 AAGTTAAGTGGGAGTGTATTCAGGAGTGTCAAGGCACAAATTCCTTGG----- 1614
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Qy 2395 SerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGlyPhePheLeu 2414
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Qy 2415 ArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerProLeuProGlu 2434
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Qy 2435 CysValProValGluCysProGlnProGluGluIleProAsnGlyIleIleAspValGln 2454
Db 1699 -----GAAGATTTTCCATATGCA----- 1716
Qy 2455 GlyLeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGly----- 2469
Db 1717 -----ACCACGGTCACTTACACATGTAACTTTCCCTCCTGCTGTCAGTGC--- 1761
Qy 2470 ---PheGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsn-----Gly 2484
Db 1762 GAATTCAGCTCATTTGGAGAGAGACCATCCCGTTGTACAAGCAATGATCAAGAAGAGGC 1821
Qy 2485 HisTrpLeuGlyGlyLysProThrCysLys-----AlaIleGluCysLeuLys 2500
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Qy 2538 CysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAsp 2557
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Qy 2558 SerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIle 2577
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QY 2382 ----- 2382
DB ||||| ||||| |||||
QY 2735 MetGlySerAlaValGlnTyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeu 2754
DB ||||| ||||| |||||
QY 2382 ----- 2382
DB ||||| ||||| |||||
QY 2755 ArgLeuCysLeuGluAsnArgLysTrpSerGlyAlaSerProArgCys----- 2770
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QY 2383 -----TGAGCGGGCGCTTCCCCACAGTGTCTTACGATCTCT 2418
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QY 2771 GluAlaIleSerCysLysLysProAsnProValMetAsnGlySerIleLys----- 2787
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QY 2419 CTTGCTGACTGCTGC-----CCTAATCCAGAGTCAAAATGGGTACAGCTCAATAAA 2472
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US-09-230-652-1
; Sequence 1, Application US/09230652A
; Patent No. 6537775
; GENERAL INFORMATION:
; APPLICANT: Joutel, Anne
; APPLICANT: Bousser, Marie-Germaine
; APPLICANT: Bach, Jean-Francois
; TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
; TITLE OF INVENTION: THERAPEUTIC APPLICATION
; FILE REFERENCE: 03715.0048-00000
; CURRENT APPLICATION NUMBER: US/09/230,652A
; CURRENT FILING DATE: 1999-05-17
; EARLIER FILING DATE: 1996-08-01
; EARLIER FILING DATE: 1997-04-16
; EARLIER FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8091
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(7041)
; OTHER INFORMATION: human ADNC No. 6537775sch 3
US-09-230-652-1
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Alignment Scores:

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Pred. No.: 4,87e-72 Length: 8091
Score: 1004.00 Matches: 651
Percent Similarity: 31.12% Conservative: 234
Best Local Similarity: 22.89% Mismatches: 931
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DB: 4 Gaps: 157
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US-09-977-053-4 (1-3571) x US-09-230-652-1 (1-8091)

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QY 1002 -----CysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSer--- 1017
DB 622 CGCTGCCAGTGTCCAGCTGCTACAGAGGCCACTA-----TGTGAGAACCC 669
QY 1018 -----CysArgIleGlySerTyrGlnAspGluGluGln 1029
DB 670 GCGGTGCTGTGGCCCTCCACCATGCGTAAACGGGGGCACCTGCAGGCAGAGTGGCGAC 729
QY 1030 Leu-----GluCysLysLeuCysPro-----SerGlyMetTyrThrGluTyrIleHis 1045
DB 730 CTCCTTACAGTGTGCTCTCTCTCTGGGTTTGAGGGTTCAGAAATGTGAAGT----- 783
QY 1046 SerArgAsnIleSerAspCysLysAlaGln-----CysLysGln 1058
DB 784 -----AACGTGACGACTGTCCAGGACACCGATGTCTCAATGGGGGACATGCTGGAT 837
QY 1059 GlyThrTyrSerTyrSer-----GlyLeuGlu 1067
DB 838 GGCGTCAACACCTATAACTGCCAGTGCCTCTGAGTGGACAGGCCAGTTCTTGCACGGAG 897
QY 1068 ThrCysGluSerCysProLeu-----GlyThrTyrGlnPro 1079
DB 898 GACCTGATGAGTGTCTGAGCTGACGCCCAACCGCTGCCACCAATGGGGGTACTCTGCTTCAAC 957
QY 1080 LysPheGlySerArgSerCysLeu-----SerCysProGlu 1091
DB 958 ACCTGGTGGGCCACAGCTGCTGTGTGTGTCAATGGGTGGACAGGTGAGAGCTGACGTGAC 1017
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Qy	1092	Asn	-----ThrSerThrValLysArgGlyAlaVal-----AsnIle	1101
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Qy	1104	SerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCys	1123	1108
Db	1078	GCATTCTTTACTGTGCTGCCCATGGGCAAG-----ACTGACCTTCTGCTG	1125	1112
Qy	1124	His	-----ProCysProArgAspTyrTyr-----Gln	1132
Db	1126	CACCTGGATGACGCTGTGTCTGACGAAACCCCTGCCAGGAGTGTATCTGTGACACAAT	1185	1130
Qy	1133	ProAsnAlaGlyLysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAla	1152	1136
Db	1186	CCGCTGAACGCGCGGCATTGTC-----ACCTGTCTCT--CCGCGCTTCAACGGGTGGGCA	1239	1140
Qy	1153	GlySerArgSerIleThrGluCysSerPheSerSerThrPheSerThrPheSerAlaAlaGluGlu	1172	1156
Db	1240	TGTACACGAGTATGGACGAGTGTCTTCTATGCGCGCCACCCCTCGCAGCACTTGGGCGAG	1299	1160
Qy	1173	SerValValProProAlaSerLeu-----GlyHisIleLysLysArg	1186	1176
Db	1300	TGCGTGAACACGACGAGGCTCTCTCTGTGCCAGTGCGGTCTGTGCTACACTGGACCTCGC	1359	1180
Qy	1187	HisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHisAsnSerGly	1206	1190
Db	1360	TGTGAGACCGAT-----GTCAACGAGTGTCTGTGGGGCCCTGCCGAACACGAGCC	1410	1194
Qy	1207	ThrCys---GlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrThrGly	1225	1200
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Qy	1226	LeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsnGlyVal	1245	1208
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Db	1528	TGCAGGACCGAGTCAATGGCTTCAGCTGCACCTGCCCTCGGCTTCAGCGGCTCCACG	1587	1220
Qy	1266	CysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLysGlyIleCysVal	1285	1224
Db	1588	TGTCACTGGACGTGGACGAATGCGCCAGACGCTTCGAGGAATGGCGCAATGGCTG	1647	1228
Qy	1286	AspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHisCysGlu	1305	1232
Db	1648	GACCAGCCGATGGCTACGAGTGCCTGTGCCAGGGCTTTGAGGGCACTCTGTGTAT	1707	1236
Qy	1306	ThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaValCysGluAspGln	1325	1240
Db	1708	CGCAACGTGGACGACTGCTCCCTGACCCATGC---CACCATGTGCTGCGTGGATGGC	1764	1244
Qy	1326	ValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCysGlyLysAsn	1345	1248
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Qy	1346	ValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsn	1365	1256
Db	1825	GTGACGAAATCCGACGACCCCTTCGCCCATGGCGCAATGCTTAGACCTGCTGGAC	1884	1260
Qy	1366	SerPheArgCysLeuAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsn	1385	1264
Db	1885	AAGTACCTCTCGCGTGCCTTCTGGGACCAACAGGTGAACTGCGAAGTGAACTTGAC	1944	1268
Qy	1386	GluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyr	1405	1272
Db	1945	GACTGTGCACGAACCCCTGTC---ACCTTTGGAGTCTGCGGTGATGCATCAACCGCTAC	2001	1276
Qy	1406	SerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlnSerThrGly	1425	1280
Db	2002	GACTGTGTCTCCCAACCTGGCTTTCACAGGGCCCTTTGTAACTGGAG-----	2049	1284
Qy	1426	PheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAsp-GlyMetLe	1445	1288

Db	2050 -ATCAATGAGTGTGCT	2064
Qy	1445	uProSerLeuHieAlaLeuThrCysThrPheTrpMetLysSerAspMetAenTy	1465
Db	2065	: : TCAGCCCATCGCGGAGGAGGTTCCTGTGTGATG-	2101
Qy	1465	rgIyThrProIleSerTyralaValaAspAanGlySerAspAanThrLeuLeuLeuThrAs	1485
Db	2102	-GGGAAATGGCTTCGCTGCC-	2122
Qy	1485	pTyAsnGlyTrpValLeuTyrrValaAsnGlyAargGluLysIleThrAsnCysProSerVa	1505
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Qy	1505	laSnAspGlyArgTrpHisIleAlaIleThrTrpThrSerAlaAsnGlyIleTrpLy	1525
Db	2152	TGCCTCCCCCGA-	2164
Qy	1525	sValTyrrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeuProIl	1545
Db	2165	-GCCATCCCTGT	2175
Qy	1545	eProGlyGlyAlaLeuValLeuGlyGlnGlnAspLysLysGlyGlyGlyPheSe	1565
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Db	2185	CCCTGCA- -GTACGGCATCTGTATGATGCACCTG- -GCGGG	2223
Qy	1585	rProGlnGlnValIysSerLeuAlaThrSerCysProGluGluLeuSerLysGlyAsnVa	1605
Db	2224	TTCCGCTGTGTGTGAGCTGGCTGGGATGGGCCCC- -GCTGCAGC	2268
Qy	1605	lLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValIysIleAspSerLysSe	1625
Db	2269	CAGAGCCTGGCCCGAG-	2284
Qy	1625	rIlePheCysSerAspCysPro- -ArgLeuGlyGlySerValProHisLeuArgThrAl	1644
Db	2285	-ACGCC-TGTGAGTCCCGAGCGGTGCAGGGCGGGTGGG- -ACATG	2324
Qy	1644	aSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGlyPheGlnLe	1664
Db	2325	CAGCAGCGAT- -GGAAATGGGTTCACCTGCACCTGGCCCGCTGTGTGTC-	2370
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Db	2371	: : -CAGGGAGCT-	2381
Qy	1684	sCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPheHisSerAlaAs	1704
Db	2382	GTGTGAATCTCTCCCTCCGACCCCGACCCCTGTGACATGGG- -GGCCGCTG	2435
Qy	1704	pAspPheTyrrAlaGlySerThrValThrTyrrGlnCysAsnAsnGlyTyrrTyrrLeuLeuGl	1724
Db	2436	CGAGTCTGCCCTGGCCAGCTGCTGTCTCTCTCTGCCCCCAGGGC-	2481
Qy	1724	yAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSerProSerCys--	1743
Db	2482	TGGCAAGGC-	2501
Qy	1744	-LeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAs	1763
Db	2502	GCAGATGTGACGAGTGTCTGGCCCGGACCCCTGTGGCCCTCATGTATGTGCACAA	2561
Qy	1763	nValAspGlySerTyrrIleCysSerCysValProProTyrrThrGly	1778
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2679	DB	C-----	GTGGGC-----	TCCTTTCTCTGCTCC-----	2700
1818	QY	YTYRGlnLeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluTrpAsnHisLe	 		1838
2701	DB	-----	TGCTCTCCTCGTTTCGCGCGCCCAAGATGCGCCGCGAT-----		2739
1838	QY	UILEPROTYRCysLysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIle	 		1858
2740	DB	-----	GTGATGAGTGCCTGAGCAACCCCTGCGC-----	CGGGCACCTGTATC	2783
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2784	DB	CGACCACGTGGCC-----	TCCTTCACCTGCACCTGCCGCGCGGCTAC-----		2826
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1998	QY	oValCysGluProValLysCysSerSerProGluAsnIleAsnHengLysTyrIleLe	 		1918
2856	DB	CGACTGCAGCCCCAGCTCCTGCTTC-----	-----	AATGGCGGACCTGTGT	2897
1918	QY	USERGlyLeuThrTyrLeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuG	 ::: :::		1938
2898	DB	GGACGGC-----	GTGAAGTTCGTTACAGTGTGCTGTGCGTCCGGCTAC-----		2940
1938	QY	nGlyProSerIleIleGluCysThrAlaSerGlyIleTrpAspArgAlaProAlaCy	 ::: :::		1958
2941	DB	-----	ACAGGAGCCCACTGCCCAACATCAGGCAGACCCC-----		2973
1958	QY	sHisLeuValPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAs	 ::: :::		1978
2974	DB	-----	TGCTCTCGCGCCCTGCTACAGCGGGGGCTCTGACGGCGCGGCCCA		3020
1978	QY	nPheThrPheArgAsnThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLe	 ::: :::		1998
3021	DB	CCCTGGCTTCGC-----	TGCACCTGCTCGAGAGCTTCACGGCGCCGCGCAGTG		3068
1998	QY	uAspThrIle-----	GluCysLeuAlaAspGlyLysTrpSerAr		2011
3069	DB	CCAGACGCTGTGGATTTGGTGCAGCGCCAGCCTTGTCAAAACGGGGGTGGTGC	 ::: :::		3128
2011	QY	gSerAspGlnGlnCysLeuAlaValSerCysAspGluProIleValAspHisAlaSe	 ::: :::		2031
3129	DB	GACTGGGGCCATTGGCTTT-----	-----	TGTCC	3152
2031	QY	rProGluThrAlaHisArgLeuPheGlyAspIleAlaPheTyrTyrCysSerAspGlyTy	 ::: :::		2051
3153	DB	CCCTGGATGGAGCGAGCCTCTGT-----	GACATCCGAAGCTTGCCTTCAGGAGGGCGCGC		3209
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3270	DB	AGACAGC-----	TCCACTACTGC-----		3288
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3288	DB	-----	-----		3288
2110	QY	eLysCysMetGluGlyPheValLeuAsnThrSerAlaLysIleGlu	 		2125
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2126	QY	-----	CysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleG		2140
3339	DB	CTGCTGGCCCGACCCCTGCCAGCATGGGGGG-----	-----		3369

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QY	2160	rAsnTyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysG	2180
DB	3394	-----TACATGTGTGAG-----	3416
QY	2180	yGluLysSerThrCysGluAlaThrGlyGlnTrpSerSerProIleProThrCysHi	2200
DB	3417	CTACATGGTGTATAACTGTGGAGCAGCAGCTGGACGAGTGTGCTCCCTCCAGCGCCTGCCACGA	3476
QY	2200	sProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrThrG	2220
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QY	2220	yArgIlePheGluSerGluValArgTyrGlnCysAsn-----ProGlyTyrLysSerVa	2238
DB	3490	-----ATTGACCTCGTGGCGCCGCTATCTGTCTCTGCTCCCCACGGAACGCTGGGGGT	3542
QY	2238	lGlySerProValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMe	2258
DB	3543	G-----CTCTCCGAGATTAATGAGGAT-----	3564
QY	2258	tCysValProLeuAspCysGlyLysProProIleGlnAsnGlyPheMetLysGlyG	2278
DB	3565	-----GACTTCGGGCCCGACGCCACCGCTGAGACTCAGGGCCCCCGGTGCCTACA	3611
QY	2278	uAsnPheGluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValG	2298
DB	3612	CAAT-----GCCACCTCGGTG-----	3638
QY	2298	yAspSerSerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCy	2318
DB	3639	TGGTTTCGCTGCACCTGTCCC-----CAGGATA	3668
QY	2318	sMetProAlaLysCysProGluProProLeuLeuAsnGlnLeuValLysGluLe	2338
DB	3669	CACCTGGTTTGGCTGC-----GAGGCAGACATCAATAGTGTGCG-----	3708
QY	2338	uThrThrGluValGlyValThrPheSerCysLysGluGlyHisVal-----Le	2355
DB	3709	-----TCAGTGCTGTCCACGCGGCACACACC CGGAGCTGCCT	3746
QY	2355	uGlnGlyPro---SerValLeuLysCysLeuProSerGlnGlnTrpAsnAspSerPhePr	2374
DB	3747	GCAGGACCCAGCGGAGGTTTCGGTTCCTTTGTCATGCTGGCTTC-----TCAGTCC	3800
QY	2374	oValCysAlaIleValLeu-----CysThrProProProLeuIleSerPheGlyValPr	2392
DB	3801	TCGCTGTACAGACTGTCTGTCTCCCTCGAGTCCCGACCATGCGCAGCATGGAGGCCAGTG	3860
QY	2392	oIleProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGlyPh	2412
DB	3861	CCGTCTAGCCCGGTCTCGGGGTGGCTGACCTTCACTGTCTGTCGCCAGCGGTT	3920
QY	2412	ePhe-LeuArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerProL	2432
DB	3921	CTGGGGTCCGGTTTCGAGC-----GGGTGGCGCGCTCCTG	3956
QY	2432	eUProGluCys-ValProValGluCysProGlnProGluLeuLeuProAsnGlyIleIle	2451
DB	3957	CCGGAGACTCGAGTCCCGGTGGCGGTGCCCATGCCACGACAGCCCGCGCG-----	4007
QY	2452	AspValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyr-ThrCysLysProGlyPheG	2471
DB	4008	-----GCCGCGCTGGCGCTGCCCCCAGGG-----	4032
QY	2471	uLeuValGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyLysPr	2491
DB	4033	-----TTGTCCGAGACCTCTGCGCAGAGTCTCCCGGGTCGCC	4070

Qy	1030	Leu	-----GluCysLysLeuCysPro-----SerGlyMetTyrThrGluTyrIleHis	1045
Db	730	CTCACTTACGACTGCTGCTCTCTTCTGGGGTTTGAGGCTCAGAATTGTGAAGT-	783	
Qy	1046	SerArgAsnIleSerAspCysLysAlaGln-----CysLysGln	1058	
Db	784	-----AACGTGGACGACTGTCCAGGACCGATGTCTCAATGGGGGACATGCTGGAT	837	
Qy	1059	GlyThrTyrSerTyrSer-----GlyLeuGlu	1067	
Db	838	GGCGTCAACACCTATACTGCCAGTGCCTCTGAGTGGACAGGCCAGTTCTTGCACGGAG	897	
Qy	1068	ThrCysGluSerCysProLeu-----GlyThrTyrGlnPro	1079	
Db	898	GACGTGGATGAGTGTCACTGCTCAGCCCAACGCTTCCACCAATGGGGGTACTGCTTCAAC	957	
Qy	1080	LysPheGlySerArgSerCysLeu-----SerCysProGlu	1091	
Db	958	ACGCTGGGTGGCCACAGCTGGTGTGTGTCAATGGCTGGACAGCGAGAGCTGCAGTCAG	1017	
Qy	1092	Asn-----ThrSerThrValLysArgGlyAlaVal-----AsnIle	1103	
Db	1018	AATATCGATGACTGTGCCACAGCGCTGTGCTTCCATGGGGCCACTGCCATGACCGCGTG	1077	
Qy	1104	SerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCys	1123	
Db	1078	GCCTTCTTTACTGTGCTGCGCCCATGGGCAAG-----ACTGGCTCTCCTG---TGT	1125	
Qy	1124	His-----ProCysProArgAspTyrTyr-----Gln	1132	
Db	1126	CACCTGGATGACGCTGTGTGACGACACCCCTGCCACGAGGATGCTATCTGTGACACAAT	1185	
Qy	1133	ProAsnAlaGlyLysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAla	1152	
Db	1186	COGCTGAACGCCCGGCCCATTTGC---ACCTGTCTCT---CCCGGCTTCACGGTGGGGCA	1239	
Qy	1153	GlySerArgSerIleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluGlu	1172	
Db	1240	TGTACCAAGATGTGGACGAGTGTCTATCGCGCCCAACCCCTCCGAGCACTTGGGCGAG	1299	
Qy	1173	SerValValProProAlaSerLeu-----GlyHisIleLysLysArg	1186	
Db	1300	TGCGTGAACACGACGAGGCTCTCTCTGTGCCAGTGGGGTGTGCTACTGACCTCGC	1359	
Qy	1187	HisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHisAsnSerGly	1206	
Db	1360	TGTGACAGCCGAT-----GTCAACAGATGTCTGTGCGGGCCCTGCCGAACACAGGCC	1410	
Qy	1207	ThrCys---GlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrThrGly	1225	
Db	1411	ACGTGCTCTCGACCCATAGGCCAG---TTCACTGTATCTGTATGGCAGGCTTTCACAGGA	1467	
Qy	1226	LeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsnGlyVal	1245	
Db	1468	ACCTATTGGCAGGTGGACATTGACAGTGTGACAGTAGCCCTCTGTGTCAACGTGGGGTC	1527	
Qy	1246	CysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGlyGlnArg	1265	
Db	1528	TGCAGGACCCGAGTCAATGGCTTCAGCTGCACCTGCCCTCTGGGCTTCAGCGGCTCCACG	1587	
Qy	1266	CysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLysGlyIleCysVal	1285	
Db	1588	TGTCACTGGACGTGGACGAATGCCACGACGCCCTCTCGAGGAATGGCGCCCAATGGGTG	1647	
Qy	1286	AspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHisCysGlu	1305	
Db	1648	GACCAGCCCGATGCTACGAGTGGCGCTGTGCCAGGGCTTTGAGGGCGACGCTGTGTGAT	1707	
Qy	1306	ThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGluAspGln	1325	
Db	1708	CGCAACGTGGACGACTGCTCCCTGACCCATGCG---CACCATGTGTGGTGGATGGC	1764	
Qy	1326	ValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCysGlyLysAsn	1345	

Db	1765	ATGCCAGCTTCTCATGTGCTCTGCTCTCTGCTCTACAGGGCAACAGCTCCGAGAGCCAG	1824
Qy	1346	ValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsn	1365
Db	1825	GTGGAGCAATGCCAGCAGCCCTCGCCGATGGCGGCAATGCTAGACCTGGTGGAC	1884
Qy	1366	SerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsn	1385
Db	1885	AAGTACCTCTCGCGCTGCTCCCTTCTGGGACCACACAGGTGTGAACCTCGAAGTGAACATTGAC	1944
Qy	1386	GluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyr	1405
Db	1945	GACTGTGCCAGCAACCCCTGC---ACCTTTGGAGTCTGCGGTGATGCATCAACCGCTAC	2001
Qy	1406	SerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlnGlnSerThrGly	1425
Db	2002	GACTGTGTCTGCCAACCTTGCTTTCACAGGGCCCCCTTTGTAACTGGAG---	2049
Qy	1426	PheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAsp-GlyMetLe	1445
Db	2050	-----ATCAATGAGTGTGCT	2064
Qy	1445	uProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspAspMetAsnTyr	1465
Db	2065	TCCAGCCCATCGCGCAGGAGGTCTCTGTGTGATG---	2101
Qy	1465	rGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeuThrAs	1485
Db	2102	GGGAAATGGCTTCCGCTGCC---	2122
Qy	1485	pTyrAsnGlyTyrpValLeuTyrValAsnGlyArgGluLysIleThrAsnCysProSerVa	1505
Db	2123	-----TCTGCCCGCTGCTCTTTCGCCCCCACTC	2151
Qy	1505	AsnAspGlyArgTrpHisIleAlaIleThrThrThrSerAlaAsnGlyIleTrpLys	1525
Db	2152	TGCTCTCCCCCGA---	2164
Qy	1525	sValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeuProIle	1545
Db	2165	-----GCCATCCCTGT	2175
Qy	1545	eProGlyGlyGlyAlaLeuValLeuGlyGlnGlnAsnLysGlyGlyGlyPheSe	1565
Db	2176	GCCC-----ATGAG	2184
Qy	1565	rProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrpAspTyrValLeuSe	1585
Db	2185	CCCTGCA-----GTACGGCATCTGTATGATGCACCTG---	2223
Qy	1585	rProGlnGlnValLysSerLeuAlaThrSerCysProGluLeuSerLysGlyAsnVa	1605
Db	2224	TTCCGCTGTGTGTGTGAGCTGCTGGTGGTGGCCCCC---	2268
Qy	1605	LleuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLysIleAspSerLysSe	1625
Db	2269	CAGAGCTTGCCCGAG---	2284
Qy	1625	rIlePheCysSerAspCysPro---ArgLeuGlyGlySerValProHisLeuArgThrAl	1644
Db	2285	ACGCC-TGTGATGCCAGCGGTGCAGGGCGGTGGG---	2324
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Db	2325	CAGCAGCGAT-----GGATGGGTTCCTACCTGCACCTGCCCGCTGTGTGC---	2370
Qy	1664	uValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTrpThrGlnProLeuProHi	1684
Db	2371	-----CAGGGACGT---	2381
Qy	1684	sCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPheHisSerAlaAs	1704

Qy	2392	oileProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGlyPh	2411
Db	3661	CCGTCCTAGCTCGGGTCTCGGGGTGGGCTGACCTTCACCTGTCACTGTGTCCACCGGTT	3920
Qy	2412	ePhe-LeuArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerProL	2432
Db	3921	CTGGGGTCCGGCTTGGCAGC-----GGTGGCGCGCTCCCTCG	3956
Qy	2432	euProGluCys-ValProValGluCysProGlnProGluGluLeuProAsnGlyIleIle	2451
Db	3957	CCGGGAGCTGAGTGCCTCCGGTGGCGTCCATGTCGACGACAGCCCGCGGG-----	4007
Qy	2452	AspValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyr-ThrCysLysProGlyPheGl	2471
Db	4008	-----GCCGCGTGGCGCTCTGCCCCCAGGG-----	4032
Qy	2471	uLeuValGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyLysPr	2491
Db	4033	-----TTGTGGGAGCCCTCTCTGCGCAGCTTCCCGGGGTGCGC	4070
Qy	2491	o-----ThrCysLysAlaIleGluCysLeuLysProLysGluIleLe	2505
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Qy	2505	uAsnGlyLysPheSerTyrThrAspLeuHisTyrGlyGlnThr-----	2519
Db	4111	-----CTCCAGCGGGGCTCTCTGCGCGCCCGCGCGCTGCG	4145
Qy	2520	ValThrTyrSerCysAsnArgGlyPhe-----ArgLeuGluGlyProse	2534
Db	4146	GCCCTTCTCCGCTGCGCTTCGCGCAGGGCTGGACCGGGCCGCGCTGCGAGCGCGCCG	4205
Qy	2534	rAlaLeuThrCysLeuGluThrGlyAspValAspValAlaProSerCysAsnAlaIle	2554
Db	4206	CGCGGACCCGAGTCTCG-----GAGAGCGCGGTGTCGCGCGCGC	4247
Qy	2554	eHisCysAspSerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTy	2574
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Qy	2574	rGlyAlaIleIleIleTyrSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGl	2594
Db	4258	-----GCCAAGCGCGGGGACCA	4274
Qy	2594	nThrCysGluGluSerGlyTrpSerSerSerIleProThrCysMetProIleAspCysGl	2614
Db	4275	CGCTGTGACCGCGAG-----TGCACAGCCCGAGCTGCGG	4310
Qy	2614	yLeuProProHisiIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPh	2634
Db	4311	CTGG-----GACGCGCGGACTGTCTGCTGAGGTGGCGAC-----	4347
Qy	2634	eGluGlnGluAspAspMetMetGluValProTyrValThrProHisProTyrHisLe	2654
Db	4348	-----CCCTGGGGGCGCA	4358
Qy	2654	uGlyAlaValAlaLysThrTrp-----GluAsnThrLysGluSerProAlaThrHi	2671
Db	4359	ATGCGAGCGCTGAGTGTCTGGCGCTCTTCACACACAGCGGTGCGACCCCGCTCGAG	4418
Qy	2671	sSerSerAsnPheLeuTyrGlyThrMetValSerTyr-----ThrCy	2685
Db	4419	CTGCGCGCTGCTCTACGACAACTTCGACTGCCAGCGGGTGGCGCGGCGCACTTG	4478
Qy	2685	sAsnProGlyTyrGluLeuLeu-----GlyAsnProValLeuIle	2698
Db	4479	CAACCCGGTGTACGAGAAGTACTCGCGCGACCACTTTGCGAGCGCGCTGCGCACCGAGG	4538
Qy	2698	eCysGln--GluAspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGluCy	2717
Db	4539	CTGCACACGAGGAGTGGCGCTGGATGG-----CTGGATTG	4577
Qy	2717	s-----AspLeuProThrAlaProGluAsnGlyPheLeuArgPheThr-----	2731

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4638	Db	GCGGAGGAGCTACTGCTTCAGCGCGGACTTTCGAGGGCTCAGCGCCATCTCGG	4697
2750	Qy	aglySerAspLeuArgLeuCysLeuGlu	2760
4698	Db	CACCTCG---CTGGCTTCGCTCGACGCGCACGCGCCAGCCCATGCTCTTCCTTACCA	4754
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2780	Qy	oValMetAsnGlySerIleIysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrG1	2800
4803	Db	CGAGGTGATCGGCTCGGTA---GTAATGCTGGA	4832
2800	Qy	uCysAspProGlyTyrValLeuAsnGlyThrGluArgThrCysGlnAspAspIysAs	2820
4833	Db	GATTGACACACCGCTCTGCTGCGCTGAGATGATCACTGCTTCCCCGATGCCCA	4892
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2838	Qy	lSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGlnIysGluIleGluTyrTh	2858
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2858	Qy	rCysAsnGluGlyPheLeuLeuGluGlyAlaArgSerArgValCys---LeuAlaAsnGlyS	2878
4985	Db	---CTCCAGAACCCAGCGCTCCCGCTGCTGCGCACTGCTAGTGGCG	5025
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5026	Db	GG---CGCTGT---CTTG	5037
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5038	Db	CTGCTGT---CATTC	5052
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5053	Db	GTCTGG---TGTCATGTGGCGCGCAAGCGCGAGCACAGCACACCCCTCTGGTTC	5106
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2944	Qy	ysIysProValAsnCysGlyProProGluAspLeuAlaHisGly---PheProA	2961
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2981	Qy	euhisGlyAsnSerSerArgArg---CysLeuSerAsnGlySerTrpSerGlyS	2998
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5299	Db	GCTGAGGAGGCTGTGGATTGCTCGCTGAGTCAACACCATCTGCTGCTGCTGACATC	5358
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5359	Db	CGGCTGCCACGACCATGGCACTGACACCAACGAGCGGACGAGATGCTGATGGCATG	5418
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5916 TGC-----GGCTGTGAACAACGTGGA 5936
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5997 GACCCCTTATCTCTGGCGCGCGCGAGGACCTATGAGCTGCCAGTGTGTGTG-- 6054
3193 sGlyAspAspPheSerValAsnArgGlnValSer-----Valse 3206
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6330 GAGCTGGGCTGCGCGGGGCTTGTGCTGACAGCTCGGTCAAGCTG-----TCGCGCGT 6383
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6384 GGACTCGCTGGACTCCCGCGGCGCTTTCGGTGGGGCGCGCTTCCCTGTGT----- 6435

3323 rSerCysAsnArgGlyTyrsrLeuGluGlyPro-----SerGluAlaHisCysTh 3340
6436 -----GGCTTCCCTTGGGGGCGCTATGACAGTCCAC-TGCCACTGCAG 6481
3340 rGluAsnGlyThr-----TrpSerHisProValProLeuCysLysProAsnPro----- 3356
6482 TGTCTCTGGCAGACTTGGTGGCCAGCGCGGGGGTCTAGGGCGCGCAGCCCCCTGGGA 6541
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6711 -----ACCTGGCAGTCCCGACATGGCGAGGATACCCG 6745
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6860 CCTCTCTCTCAGACTGGTCCGAATCCACGCTAGCCCGACCA-----CTGCC 6907
3523 oProGly-----TrpThrGlySerArgCysHisThrAlaValCysGlnSerProCysLeuAs 3542
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RESULT 13

US-08-083-590A-21
Sequence 21, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.


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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..7419
; US-08-083-590A-21

Alignment Scores:
Pred. No.: 9,768-70 Length: 9723
Score: 978.00 Matches: 636
Percent Similarity: 30.26% Conservative: 263
Best Local Similarity: 21.41% Mismatches: 881
Query Match: 4.90% Indels: 1196
DB: 1 Gaps: 167

US-09-977-053-4 (1-3571) x US-08-083-590A-21 (1-9723)
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DB 571 CCAGGACACTGCCAGCATGGTGGACCTGCTCCCTCACTGCTCT- 612
QY 1010 LeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAspGluGluGln 1029
DB 613 -----GGTTCTCTACAG 624
QY 1030 LeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAsnIle 1049
DB 625 -----TGCCAG--TGCCCTCAGGCTTCACAGGCCAGTACTGTGCACAGCTGTATGTG 675
QY 1050 SerAspCysLysAlaGlnCys---LysGlnGlyThrTyrSerTyrSerGlyLeuGluThr 1068
DB 676 CCTGTGCACCTCCTACCTTGTGTCAATGAGGAGCACCTGTGCGCAGACTGCTGACTTCCT 735
QY 1069 CysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySerArgSerCysLeuSer 1088
DB 736 TTGTAGTCAACTGCTCTCCAGGTTTGTGAAGGAGCACCTGTGTGAGGAGGAATTTGATGAC 795
QY 1089 CysProGluAsnThrSerThrValLysArgGlyAlaVal-----AsnIleSerAla 1105
DB 796 TGCCCTTACCAC-----AGGTGTCAAGATGAGGGGTTTGTGTGATGGGCTCAACT 849
QY 1106 CysGlyValProCysPro-----GluGlyLysPheSerArgSerGlyLeuMetPro 1122
DB 850 TACAACTGCGCTGTCTCCCAATGGACAGACAGTCTGTGCACAGAGATGTGGATGAA 909
QY 1123 CysHisProCysProArgAspTyrTyrGlnProAsnAla----- 1135
DB 910 TGC-----CTGTGCGAGCCCAATGCTGTCAAAATGGGGCCACTGT 951
QY 1136 -----GlyLysAlaPheCysLeuAla----- 1142

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1011 GCGAAGCGCAATGGAGGCTATGCTGTGTATGTGTCAACGGCTGGAGTGGAGTACTGTC 1011
1143 -----CysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
1012 AGTGAGAACATTTGATGATTTGCTTGGCTTCTGCTACTTCA-----GGTCCACCTGTC 1065
1157 IleThrGluCysSerSerPheSerThrPheSerAlaAlaGluGluSerValPro 1176
1066 ATGACCGGTGTGGCTCTCTCTCT-----TCATGTGTCCTCA 1101
1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
1102 GAGGGGAAGCAGGT-----CTCCTGTGTCTATCTGGATGATGCA 1140
1197 CysPhePheAsnProCysHisAsnSerGlyThrCys-----GlnGlnLeuGlyArgGly 1214
1141 TGCATCAGCAATCTTGGCCACCAAGGGGCGACTGTGTGACACCAACCCCTTAATGGGCNA 1200
1215 TyrValCysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGlu 1234
1201 TATATTTGCACCTTCCCAACAGCTTACAAGGGGCTGACTGCACAGAGATGTGGATGAA 1260
1235 CysSerProLeu-----ProCysLeuAsnAsnGlyValCysLysAspLeuValGly 1251
1261 TGTGCCATGGCCAATAGCAATCTTGTGTGAGCATGTCAGGAAATGTGTGAACACGGATGGC 1320
1252 GluPheIleCysGluCysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsn 1271
1321 GCTTTCCACTGTGAGTGTCTGAAGGGTTATGACAGGACCTGTTGTGAGATGGACATCAAT 1380
1272 GluCysSerSerProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyr 1291
1381 GAGTGCCATTCAGACCTTCCAGAAATGATGACTACTCTGTCTGGATTAAGATGGAGGCTTC 1440
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1372 AlaAlaGlyPheThrGlySerHisCysGlyLysAsnValAspGluCysLeuSer 1383
1681 GCCACAGGTTTCACTGCTGTGTGTGTGTGAGGAGAACATTTGACAACTGTGTGACCCGATCCT 1740
1383 ----- 1383
1741 TGCCACCATGGTCACTGTGCGAGTGTATTTGATTCTCTACACCTGTCATCTGCAATCCCGGG 1800
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1921 GGGGTTAATTTGAA-----ATTAAATTTGATGCTGTGCAAGTAAC 1962
1435 -----IleTyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThr 1452

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QY 2053 uAlaasp-----AsnSerGlnLeuLeuCy 2061
DB 3612 TATTGACCTTGGAACATTTCAGTGTCTTGGCCACGAGCACTCGGGGCTACTCTG 3671
QY 2061 sAsn-----AlaGlnGlyLysTrpValProProGluGlyGlnAspMe 2075
DB 3672 TGAAGAGAACATTGATGACTGTGCCGGGGTCCCATTTAGTGTGTTGAGTGCAT 3731
QY 2075 tProArgCysIleAlaHisPheCysGluLysProProSerValSerTrpSerIleLeuG1 2095
DB 3732 CGATAGCATTCGAGGCTACAGTTGT----- 3756
QY 2095 uSerValSerLysAlaLysPheAlaAlaGlySerValValSerPheLysCysMetGluG1 2115
DB 3757 -----CGCTGCTTCCCTGG 3770
QY 2115 yPheVal-----LeuAsnThrSerAlaLysIleGluCysMetAr 2128
DB 3771 CTTTGTGGGAGCGTGTGAGGGAGACATCAAC-----GAGTGCCTCTC 3815
QY 2128 sGlyGlyGlnTrpAsnPro-----SerProMetSerIleGlnCysIleProValArgCy 2146
DB 3816 C-----AACCCCTGCGAGCTCTGAGGGCAGCCTGGAGCTGTATA----- 3852
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DB 3853 -----CAGCTCACCAATGACTACTGTGT----- 3876
QY 2166 aMetValAlaTyrSerCysAsnLysGlyPheTyriLysGlyLysLysSerThrCy 2186
DB 3877 -----GTTTGGCGTAGTGCTTT-----ACTGGCCGCACTG 3908
QY 2186 sGluAlaThrGlyGlnTrpSerSerProIleProThrCysHisProValSerCysGlyG1 2206
DB 3909 TGAACCTTCGTCGATGTGTGCCAGATGCCCTGCCATGAGGAGCTGTGCTGT 3968
QY 2206 uProProLysValGluAsnGlyPheLeuGluHisThrGlyAlyGlePheGluSerG1 2226
DB 3969 GGCCAGTACATGCTGCTGATGGTTTCAT----- 3996
QY 2226 uValArgTyrGlnCysAsnProGlyTyriLysSerValGlySerProValPheValCysG1 2246
DB 3997 -----TGCCGCTGTCCCGGGATTTTCGGGGCAAGG-----TGCCA 4034
QY 2246 nAlaAsnArgHisTrpHisSerGluSerProLeuMetCysValProLeuAspCysGlyLys 2266
DB 4035 GAGCAGC-----TGTTGA-- 4047
QY 2266 sProProIleGlnAsnGlyPheMetLysGlyGluAsnPheGluValGlySerLysVa 2286
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DB 4048 -CAAGTGAATCTAGGAAGGGGGAGCAGTGTG----- 4080
QY 2306 sSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAlaLysCysProGluPr 2326
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DB 4119 C-----CGGGACTGCGAGTCCAGCTGTCAG 4145
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QY 2363 sLeuProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeuCysThrPr 2383
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QY 2484 lYHisTrpLeuGlyGlyLysProThrCysLysAlaIleGluCysLeuLysProLysGluI 2504
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DB 4559 GTAACCAAGGTGCAACAGTGA-----GAGTGTGTT--T 4591
QY 2544 rPAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGlnProIleGluA 2564
DB 4592 GGGAT-----GGGCTGAGCTGTGCTGTGCTGCAACCT--GAGA 4627
QY 2564 sNGlyPheValGluGlyAlaAspTyrSerTyriGlyAlaIleIleIleTyrSerCysPheP 2584
DB 4628 AC-----CTGGCAAGAGGTACCTGTGTATTGTGGTATTGATGTC 4666
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DB 4667 CACCTGACAACTGTCTCCAGGATGTGCGAGTCTCTTC-----GGGCATCG----- 4714
QY 2604 SerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAspPheGlyAsp 2623
DB 4715 -----GTACCCTGCTCCACACCA-----ACC 4735
QY 2624 CysThrLysLeuLysAspAspGlnGlyTyriPheGluGlnGluAspAspMetGluVal 2643
DB 4736 TCGGCATT-AAGCGGAGCTCCAGGG-----GAACCTCATGTGTGTAC 4776
QY 2644 ProTyriValThrProHisProTyriHisLeuGlyAlaValAlaLysThrTrpGluAsn 2663
DB 4777 CCTATTATGTT-----GAGAAGTCAGCTGCTATGAAGAAACAGAGATG 4821
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DB 4822 ACACGCGAGATCC----- 4833
QY 2684 ThrCysAsnProGly-----TyriGluLeuLeuGlyAsnProValLeuIle----- 2698
DB 4834 -----CTTCTGGTGAACAGACAGGAGGTGGTGGCTCTTAAGTCTTCTTGGAAATT 4887
QY 2699 -----CysGlnGluAspGlyThrTrp-----AsnGlySerAlaProSer 2711
DB 4888 GACAACCGCAGTGTGTTCAGACTCAGACCACTGCTTCAAGAACACGAGTGCAGCAGCA 4947
QY 2712 CysIleSerIleGluCysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThr 2731

3360	Qy	oPheValIleProGlu---	AsnAlaLeuLeuSerGluLysGluPheTyrValAspGlnAs	3379
3605	Db	CTTTTCTAACCTTCATGAATGCAGCCTTGGC-		6638
3379	Qy	nValSerIleLysCysArgGluGlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAs	3399	
6638	Db	-----		6638
3399	Qy	nProAspGluThrTrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProPr	3419	
6639	Db	-----ACATGGGCCAGCACTGTGTCTCTCCCTCAGTGAGCCAGTGTCTATCCACC	6688	
3419	Qy	oAlaHisValGluAsnAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleTh	3439	
6689	Db	ACCACAT-----TGTCCTCCAGG-	CA 6709	
3439	Qy	rTyrSerCysTyrSerGlyTyrMetIleuGluGlyPheLeuArgSerValCysIleuGlu-	3458	
6710	Db	GTGGCAGTGTCTGGAAG-	CTTGAGTA 6733	
3458	Qy	-----		3458
6734	Db	GGTCCATCAGTCCCACTCCACGATGGGATGAACCCGATGGAGGTGAATGAGACCC	6793	
3459	Qy	-----	AsnGlyThrTrpThrSe 3464	
6794	Db	AGTACAATGAGATGTTTGGTATGTGCTCTGCTCCAGCTGAGGGGCACCCATCTCTGGCATAG	6853	
3464	Qy	rProPro-----	IleCysArgAl 3470	
6854	Db	CTCCCAAGACAGCGCCACTGAAGGGAGCACATAACCAACCCCTCGGAGCCCTTGCCCC	6913	
3470	Qy	aValCysArgPhePro-----	CysGlnAsnGlyGly----- 3480	
6914	Db	CCATTGTGACTTTCACGCTCATCTCTAAAGGCAGTATTGCCCAACACGCGGGGCTCCCC	6973	
3481	Qy	-----IleCysGlnArgProAsnAlaCysSerCysProGluGlyTrpMetGlyArgLeuCy	3499	
6974	Db	AGCCTCAGTCCACCTGGCCCTCCAGCTGT-----	TG 7003	
3499	Qy	sGluGluProIleCysIleLeuProCysLeuAsnGlyGly-----	ArgCysValAl 3516	
7004	Db	CGGGCCCCCTGGCCACCATGTACCAGATCCAGAAATGGCCCGTGTGCCCATGTGGCTT	7063	
3516	Qy	aProTyrGlnCysAspCysProProGlyTrpThrGlySerArgCysHisThrAlaValCy	3536	
7064	Db	TCCCATGTGCATGATGCCCCAGCAGGACGGGCAGGTAGTTCAGACCATTTCTCCAGCCT	7123	
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7124	Db	ATCATCTCTTCCAGCCTCTGTGGG	7148	

RESULT 14

RES. 14
 US-08-532-384-21
 ; Sequence 21, Application US/08532384
 ; Patent No. 6083904
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Artavanis-Teakonas, S. et al.
 ; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
 ; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
 ; TITLE OF INVENTION: Nucleic Acids
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

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Qy	1157	IleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluGluSerValValPro	1176
Db	1066	ATTCACCGTGTGGCTCTCTCTCT-----TCGATGTGCCCA	1101
Qy	1177	ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu	1196
Db	1102	GAGGGGAAGGCAGGT-----CTCCCTGTGTCTATCTGGATGATGCA	1140
Qy	1197	CysPhePheAsnProCysHisAsnSerGlyThrCys-----GlnGlnLeuGlyArgGly	1214
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Qy	1215	TyrValCysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGlu	1234
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Db	1261	TGTCCCATGGCCAAATAGCAATCTTGTGAGCATCAGCAAAATGTGTGACACGGATGGC	1320
Qy	1252	GluPheIleCysGluCysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsn	1271
Db	1321	GCCTTCACACTGTGAGTGTCTGAAGGGTTATGCAGGACTCTGTTGTGAGATGGACATCAAT	1380
Qy	1272	GluCysSerSerSerProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyr	1291
Db	1381	GAGTGCATTTAGACCCCTGCCAGATGATGTACTCTCTCGGATAGATGGAGGCTTC	1440
Qy	1292	ArgCysThrCysValLysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCys	1311
Db	1441	ACATGTCGTGTCATGCCAGGTTTCAAGGTTGTGCAATTTGTAATAGAAATAGATGT	1500
Qy	1312	GlnSerAsnProCysLeuAsnAsnAlaValCysGluAspGlnValGlyGlyPheLeuCys	1331
Db	1501	CAGAGCAACCCCTGTGTGAACAAATGGGCAGTGTGTGGATAAGTCAATGCTTTCCAGTGC	1560
Qy	1332	LysCysProProGlyPheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSer	1351
Db	1561	CTGTGTCTCTGTGTTTCACTGGGCCAGTTTGCAGATGATGATGATGATGATGATGAT	1620
Qy	1352	GlnProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCys	1371
Db	1621	ACTCCGTGTCGAATGGGCAAGTGTATCGATCACCCGGAATGGCTATGAATGCCAGTGT	1680
Qy	1372	AlaAlaGlyPheThrGlySerHisCysGluLeuAsn-----	1383
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Qy	1383	-----	1383
Db	1741	TGCCACCATGGTCAGTGTGAGATGTTGATTCTCTACCTGCATCTGCAATCCCGGG	1800
Qy	1384	-----IleAsnGluCysGlnSerAsnProCysArgAsn	1394
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Qy	1395	GlnAlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSer	1414
Db	1861	GATGGTCGCTGCAATGACCTGGTCAATGGCTACAGTGCACACTGCCAGCCAGGACGTCA	1920
Qy	1415	GlyGlnArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGly	1434
Db	1921	GGGGTTAATTGTGAA-----ATTAAATTTGATGATCTGTGCAAGTAAC	1962
Qy	1435	-----IleTyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThr	1452
Db	1963	CTTTGATCATGGA-----ATCTGTATGATGATGGCAAT-----AATCGTACAGATGTGTC	2013

QY	1453	CysThrPheTrpMetIlySerSerAspMetAsnTyrGlyThrProIleSerTyrAla	1472
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QY	1511	HisHisIleAlaIleThrTrpThrSerAlaAsnGlyIleTrpLysValTyrIleAspGly	1530
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QY	1531	LysLeuSerAspGlyAlaGlyLeuSerValClyLeuProIleProGlyGlyGlyAla	1550
DB	2148	-----	2148
QY	1551	LeuValLeuGlyGlnGlnAspLysGlyGluGlyPheSerProAlaGluSerPhe	1570
DB	2148	-----	2148
QY	1571	ValGlySerIleSerGlnLeuAsnLeuTrpAspTyrValLeuSerProGlnGlnValLys	1590
DB	2149	CCCAGCTGCTACTCACAGGTGAAC-----GAA	2175
QY	1591	SerLeuAlaThrSerCysProGluGluLeuSerIlyGlyAsnValLeuAlaTrpProAsp	1610
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QY	1649	LysProGlySerLysValAsnLeuPhe-----CysAspProGlyPhe-----	1662
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QY	1663	-----GlnLeuValGlyAsnProValGlnTyrCysLeuAsnGln	1675
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QY	1676	GlyGlnTrpThrGlnPro-----LeuProHis-----	1684
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QY	1685	-----CysGluArgIle-----SerCysGlyValProProLeuGluAsnGlyPhe	1700
DB	2488	AAGAATTTGTACAGACAGTATTGGCTCCCTGTTC---CCNAACCTTGTGAGAATGTGCT	2544
QY	1701	HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr	1720
DB	2545	GTTTGCAAAGAG-----TCACCAATTTTGAGAGTTATACTTCG-----	2583
QY	1721	TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSer	1740
DB	2584	-----TTGTGTGCTCT-----GGCTGGCAAGGT---CAG	2610
QY	1741	ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer	1760
DB	2611	CGGTGTACCATTTGACATTCAGAGTGT---ATCTCCAAGCCCTTCATGAACCATGGTCTC	2667
QY	1761	CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGly-----	1778
DB	2668	TGCCATAACACCCAGGCGAGCTACATGTGTGAATGTCCACAGCGCTTCAGTGGTATGGAC	2727
QY	1779	-----AspGlyLysAsnCysAla	1784

2403 rVallySerSerCysValGly-----GlyPhePheLe 2414
 Db CCTCTGCGCAGCTGTGTGAGCCAGTATTGTGCGCAAAAGCTCGGAGGGCTCTGTGA 4325
 2414 uArgGlyAsnSerThrThrLeuCysGlnProAspGly-----Thr-Tips 2429
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 2449 lYleileaspValGlnGlyLeuAlaTyrrLeuSerThrAlaLeuTyrrThrCysLysProG 2469
 Db GGATTTATATCAACAACACAGGTGTGATGAGTGTGCAACACGCTGAGTGCCTGTTT-GACA 4483
 2469 lYpPheGluLeuValGlyAsnThrThr-----LeuCysGlyGluAsnG 2484
 Db ACTTTGATGCCAGGGGACAGCAGACATGCAAGTATGCAATATACTGTGCAGACCAC- 4542
 2484 lYHisTrpLeuGlyGlyLysProThrCysLysAlaileGluCysLeuLysProLysGluI 2504
 Db ----- 4542
 2504 leLeuAsnGlyLysPheSerTyrrThrAspLeuHisTyrrGlyGlnThrValThrTyrrSerC 2524
 Db TTTCAAGACAAACAC-----T 4558
 2524 yAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAspT 2544
 Db GTAACCGGGTCCACAGTGA-----GAGTGTGGT-T 4591
 2544 rPaspValAspAlaProSerCysAsnAlaileHisCysAspSerProGlnProileGluA 2564
 Db CGGAT-----GGGCTGACTGTGCTGTGACCAACCT--GAGA 4627
 2564 snGlyPheValGluGlyAlaAspTyrrSerTyrrGlyAlailellelleTyrrSerCysPheP 2584
 Db -----CTGCAGAGGATACCTGGTTATTTGGTATTCATGTC 4666
 2584 roGlyPheGlnValAlaGlyHisAlaMetGln-ThrCysGluGluSerGlyTrpSerSer 2603
 Db CACCTGAACAACATGCTCCAGGATGCTCGCAGCTTCTTC-----GGGCACTGG----- 4714
 2604 SerileProThrCysMetProileAspCysGlyLeuProProHisileaspPheGlyAsp 2623
 Db -----GTACCCTGCTCCACACCA-----ACC 4735
 2624 CysThrLysLeuLysAspAspGlnGlyTyrrPheGluGlnGluAspMetMetGluVal 2643
 Db TGGCGAAT-AAGCGGACTCCCGAGG-----GAATCATGGGTGTAC 4776
 2644 ProTyrrValThrProHisProTyrrHisLeuGlyAlaValAlaLysThrTrpGluAsn 2663
 Db CCTATTATGCT-----GAGAAGTCAGCTCTATGAAGAACAAGAGGATG 4821
 2664 ThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrrGlyThrMetValSerTyrr 2683
 Db ACACGAGATCC----- 4833
 2684 ThrCysAsnProGly-----TyrrGluLeuLeuGlyAsnProValleulle----- 2698
 Db CTTCTTGGTGAAACAAGAACAGGAGGTGGCTCTTAAGTCTTTCTGGAAAT 4887
 2699 -----CysGlnGluAspGlyThrTrp-----AsnGlySerAlaProSer 2711
 Db GACAACCGCCAGTGTCTTCAAGACTCAGACCCTGCTTCAAGAACACAGGATGCAGCAGCA 4947
 2712 CysileSerileCysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThr 2731
 Db -----CTGGCTCTCAGCCATACAGGGGACCTGTCTATAC--- 4989
 4948 GCTCTC-----

2732 GluThrSerMetGlySerAlaValGlnTyrrSerCysLysProGly----- 2746
 Db -----CCTCTTGTGTCTGTGTCAGTGAATCCCTGACTCCAGAACGCACTCAGCTCTC 5043
 2747 HisileLeuAlaGlySerAsp-----LeuArgLeuCysLeu 2758
 Db TATCTCTCTGCTGTGCTGTGTCATCATCTCTCTTTATTATTCTCTGGGGTAAATCATG 5103
 2759 GluAsnArgLys-----Tip-----SerGlyAlaSerProArgCys 2770
 Db GCAAAACGAAAGGTAAGCATGGCTCTCTGCTGGCTGCTGAAGGTTTCACTCTTCGCCGA 5163
 2771 GluAlaileSerCysLysLysProAsnProValMetAsnGlySerileLysGlySerAsn 2790
 Db ----- 5223
 2791 TyrThrTyrrLeuSerThrLeuTyrrTyrrGluCysAspProGlyTyrrValLeuAsnGlyThr 2810
 Db -----CTCTCAGTGAAGTCTCAGAAAGCTAAC-----CTAATTGGTACT 5262
 2811 GluArgArgThrCysGlnAspAspLysAsnTrpAspGluAspGluProileCysilePro 2830
 Db -----GGAACACAGTGAACACTGGGTGATGATGAA----- 5292
 2831 ValAspCysSerSerProProValSerAlaAsnGlyGlnValArgGlyAspGluTyrrThr 2850
 Db -----GGGCCCCAGCCAAAGAAAGTAAGGCTGAA-----GATGAGCCTTA 5334
 2851 PheGlnLysGluLeuGlu-----TyrrThrCysAsnGluGlyPheLeu 2864
 Db CTCTCAGAAAGATGACCCCATTTGATCGACGGCCATGGACACAGCAGCAC- 5385
 2865 LeuGluGlyAla-----ArgSerArgValCysLeuAlaAsnGlySerTrpSerGly 2881
 Db CTTGAAGTCTCAGACATCCGTAGGACACC-ATGCTGGCTCTCACCCCTCTCCAGGCAGA 5444
 2882 AlaThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGlyVal 2901
 Db GAGGAGGTGGATGTGTAGATGTGATGTCCTGGGCCAGATGGCTG----- 5492
 2902 ThrGluGlyLeuAspTyrrGlyPhe-----MetLysGluValThrPhe----- 2915
 Db -----CACCCCATGATGTGGCTTCTCTCCGAGGAGGAGCAGCTCAGATTTAGTGTGAAGA 5549
 2916 ---HisCysHisGluGlyTyrrileLeuHis-----GlyAlaProLysLeuThr 2930
 Db TGAAGATGCAAGAGACTTTCTTCTGCTAACATCATCAGACATGCTGGTCTACCA-----GGG 5603
 2931 CysGlnSerAspGly-----AsnTrp---AspAlaGluileProLeuCysLys 2945
 Db TGCACCTCCAGGCCGACAGACAGCCGAGTGTGTAGATGGCTTCGACCT---TGCAGC 5660
 2946 ProValAsnCysGly-----ProProGluAspLeuAlaHisGlyPhePro 2960
 Db CCGCTACTCAGGGCTGATGCTGCCAAGCGTCTCT----- 5696
 2961 AsnGlyPheSerPheileHisGlyGlyHisileGlnTyrrGlnCysPheProGlyTyrrLys 2980
 Db -----GGATGAGTGCAGATGCACATGC-----CAGAGCAAA--- 5729
 2981 LeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySer---Ser 2999
 Db -----CATGGCCGCTGTCTCACTCCATCTGTC-----AGTGGCAGTGTGATGC 5771
 3000 ProSerCysLeuPro-----CysArgCysSer----- 3008
 Db CCAAGGTGCTTCCAGATCTGTATGCGAACCGAGTAACATGATAGATGCCAGATGAA 5831
 3009 -----ThrProValilleGluTyrrGlyThrValAsnGlyThrAspPheAspCys 3024
 Db TGATGTACTACACCTT-----GATCCT 5855
 3025 GlyLysAlaAlaArgileGlnCysPheLysGlyPheLysLeuLeuGlyLeuSerGluile 3044

Alignment Scores:

Pred. No.: 4,546-60 Length: 763
Score: 838.00 Matches: 148
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.20% Indels: 0
DB: Gaps: 0

US-09-977-053-4 (1-3571) x US-09-484-9708-110 (1-763)

QY 720 ileValileLysGlySerProCysGluileProPheThrProValleAsnGlyAspPhele 739
DB 763 ATTGTCATAAAAGGCTTCCTCGTGAATTCACCTCTGAAATGCCATTCACACCTGTAATGGGATTTTATA 704
QY 740 CysThrProAsnThrGlyValaAsnCysThrLeuThrCysLeuGluGlyTyrAspPhe 759
DB 703 TGCACCTCCAGATAATACTGGAGTCAACTGTACATTAACTTGTGGAGGCTATGATTTC 644
QY 760 ThrGluGlySerThrAspLysTyrCysAlaTyrGluAspGlyValTrpLysProThr 779
DB 643 ACAGAGGGTCTACTGACAGTATATTGTCTATGAGATGGCTCTGGAACCAACA 584
QY 780 TyrThrThrGluTrpProAsnCysAlaLysLysArgPheAlaAsnHisGlyPheLysSer 799
DB 583 TATACCACTGAATGGCCAGACTGTGCCAAAAAAGTTTTCAAAACCAACCGGTTCAAGTCC 524
QY 800 PheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSer 819
DB 523 TTTCAGATGTTCTACAAAGCAGCTGCTGTGTGATGACACAGATCTGTATGAAGAAGTTTCT 464
QY 820 GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
DB 463 GAAGCAATTGAGACGACCTGGGAAAAATGTTCCCATCATTTTGTAGTGATGACAGGAC 404
QY 840 ileAspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAsp 859
DB 403 ATTGACTGCAGACTGGAGGAGAACCTGACCAAAAAATATTGCTTAGAATAATAATTATGAC 344
QY 860 TyrGluAsnGlyPheAlaIleGly 867
DB 343 TATGAAATGGCTTTGCAATTGGT 320

RESULT 16

US-08-939-366-27

Sequence 27, Application US/08939366

Patent No. 6355415

GENERAL INFORMATION:

APPLICANT: Wagner, Thomas E.

APPLICANT: Xie, Yuesheng

TITLE OF INVENTION: Compositions and Methods for the Use of

TITLE OF INVENTION: Ribozymes to Determine Gene Function

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,366

FILING DATE: 29-SEP-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Carroll, Peter G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: OHU-02749

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 6677 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-939-366-27

Alignment Scores:

Pred. No.: 4,616-58 Length: 6677
Score: 834.00 Matches: 540
Percent Similarity: 31.42% Conservative: 205
Best Local Similarity: 22.78% Mismatches: 784
Query Match: 4.18% Indels: 848
DB: Gaps: 122

US-09-977-053-4 (1-3571) x US-08-939-366-27 (1-6677)

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QY 947 GluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyrSerPheGln 966
DB 590 CCCACACCCCAAGCTCCCGTAGTCTCTCTCCACTGACCCCTCACTTCTCTCTGTCACC 649
QY 967 LeuAlaSerGluLeuLeuAlaAspSerAsnSerLeuGluThrLysLysAlaSerPro 986
DB 650 TGGCCCTCTGGC---TTCACCGGTGATCGATGCCAAACCCCATCTGGAAGAGCTCTGTCCA 706
QY 987 -----PheCysArgProGlySer-----ValLeuArgGlyArgMetCysVal 1000
DB 707 CCTTCTTTCTTCTTCCACACGGGGTCACTGTATGTTTTCAGGCTCAGGCCCGCCACAGTGC 766
QY 1001 AsnCysProLeuGlyThrTyrAsnLeuGluHisPheThrCysGluSerCysArgile 1020
DB 767 TCTTGGGCGCTGGG-----TGGACAGGTGAGCAATGCCAGCTC 805
QY 1021 GlySerTyrGlnAspGluGlu-----Gly 1028
DB 806 CGAGACTTCTCTCAGCAACCCCTGTGCGAACGGAGCGGTGCTGCCGCCACATACCCCC 865
QY 1029 GlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAsn 1048
DB 866 CAGATCCAGTGGCGC---TGTCCACCTGGG---TTCAGAGGTGCACACTGTGGAACGCCGAC 919
QY 1049 IleSerAspCys-----LysAlaGlnCysLysGlnGlyThrTyrSerTyrSerGly 1065
DB 920 ATCAACAGATGCTTCTCTGGAGCCGGGACCTGCGCTCAGGCGCACCTCTCTGCCATAACACC 979
QY 1066 LeuGluThrCysGluSer---CysProLeuGlyThrTyrGlnProLysPheGlySerArg 1084
DB 980 TTGGGTTCCTACCAGTGTCTCTGCCCTGTGGGCGAGGAAGTCCCGCAGCTCAGGCTCAGG 1039
QY 1085 -----SerCysLeuSer-----CysProGlu 1091
DB 1040 AAGGGAGCTTCCCTCTCTGGAAGCTGTCTCAATGGGGGCGACCTGCCAGCTGCTGCCAGAG 1099
QY 1092 AsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGlyValPro----- 1109
DB 1100 GGACACTCCACC-----TTTCATCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 1138
QY 1110 -----CysProGlu 1112
DB 1139 TTCACGGGGCTGAGCTGTGAGATGAACCCAGATCACTGTGTGTGTCAGGCGACCACTGTGCA 1198
QY 1113 GlyLysPheSerArgSerGlyLeu-----MetProCysHisProCysProArgAspTyr 1130
DB 1199 GGGGCCACCTGTCTGGATGGGCTGGATACCTACACCTGC-----CCCTGCCCCCAAGACATGG 1255

QY 1130 ----- 1130
DB 1256 AAGGCTGGAGTCTCTGAAGATAGATGAATGTGAAGCCGGGGTCCCCCTCGCTGC 1315
QY 1131 ----- TyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysProPhe 1145
DB 1316 AGGAACGGTGGACCTGCCAGAACACAGCTGGCAGCTTTCACCTGTGTGGCTGAGTGGC 1375
QY 1146 TyrGly----- ThrThrProPheAla 1152
DB 1376 TGGGAGGTGGCAGGCTGTGAGGAGAACCTGGATGACTGTGCAGCTGCCACCTGTGCCCG 1435
QY 1153 GlySerArgSerIleThrGluCysSerSerPheSerThrPheSerAlaAlaGluGlu 1172
DB 1436 GGATCCACCTGCATCGACCGTGTGGCTCTTTCTCC----- 1471
QY 1173 SerValValProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGln 1192
DB 1472 TGCCTCTGCCACCTGGACGCACAGGCTCTCTGTGCCACCTGGAAGACATG----- 1522
QY 1193 ValPheHisGluCysPhePheAsnProCysHisAsnSerGlyThrCys----- GlnGln 1210
DB 1523 ----- TGTTCAGTCAGCGCTGCCACGCTGAATGCCAGTGCAGCACCAACCCCT 1570
QY 1211 LeuGlyArgGlyTyTyValCysLeuCysProLeuGlyTyThrGlyLeuLysCysGluThr 1230
DB 1571 CTGACAGGCTCCACCTCTGCATATAGCCAGCTGCTACTCAGGATCCACCTGTGCACCA 1630
QY 1231 AsnIleAspGluCys----- SerProLeuProCysLeuAsnAsnGlyVal 1245
DB 1631 GATCTGGATGAGTGCMAATGGCCAGCAAGGACCCAGTCCCTGCGAACTGGGGGTCC 1690
QY 1246 CysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyThrGlyGlnArg 1265
DB 1691 TGCATCAACACCCCTGGCTCTTCACTGCCTCTGCCTGCTGCTGTACAGGGCTCCCGC 1750
QY 1266 CysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLysGlyIleCysVal 1285
DB 1751 TGTGAAGTTCACCAATAGTGGCTCTTCACTGCCTCTGCCTGCTGCTGTACAGGGCTCCCGC 1810
QY 1286 AspGlyValAlaGlyTyArgCysThrCysValLysGlyPheValGlyLeuHisCysGlu 1305
DB 1811 GACCTGTGCAACCTTCCACTGCTCTGCTGCCACCCAGGCTTGGAGGGGAGACTCTGTGAG 1870
QY 1306 ThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGluAspGln 1325
DB 1871 GTGGAGTCAATGAGTGCACCTCTAATCCCTGCCTGAAACCAAGCTGCCTGCCATGACCTG 1930
QY 1326 ValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCysGlyLysAsn 1345
DB 1931 CTCAACGGCTTCCAGTGCCTCTGCTTCTGATTCACGGGGCCCGATGTGAGAAAGAC 1990
QY 1346 ValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsn 1365
DB 1991 ATGGACGAGTGTAGCAGCACCCCTCTGCCATGGGGGGCTGCGGACCCAGCTCGA 2050
QY 1366 SerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsn 1385
DB 2051 GCCTTCTACTGCGAGTGTCTCCAGGCTTTGAAGGGGCCACACTGTGAGAAAGAGTGGAC 2110
QY 1386 GluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTy 1405
DB 2111 GAATGCTGAGTGAACCCCTGTCCCGTGGAGGAGCAGCTGTGTGATCTCCCGGAGCATTC 2170
QY 1406 SerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSerThr--- 1424
DB 2171 TTCTGTCTCGCTCTGCTGTTTTCACAGGTCAACTTTGTGAGGTTCCCTGTGTCACCC 2230
QY 1425 ----- GlyPheAsnLeuAspPheGlu----- 1431
DB 2231 AACATGTGCCAACCTGGACGACGAATGCCAAGGTTCAGGAACACACAGAGCCCTGCTTGC 2290
QY 1432 ValSerGlyIleTyTyValMetLeuAspGlyMetLeuProSerLeuHis-AlaLe 1451

DB 2291 CCTGACGGAAGTCTCTGGCTGTGTCTCTGCGAGGACAACTGCCCTGTCCACCATGCCAT 2350
QY 1451 uThr----- CysThrPheTrpMetLysSerSerAspAspMetAsnTyrglyThrPr 1468
DB 2351 TGCCAGAGATCTCTGT 2399
QY 1468 oileSerTyAlaValAspAsnGlySerAspAsnThrLeuLeuThrAspTyArgGln 1488
DB 2400 ----- GCGAGACAGAAC----- 2411
QY 1488 YTrpVal-LeuTyValAsnGlyArgGluLysIleThrAsnCysProSerValAsnAspG 1508
DB 2412 -TGGTGGCTGCATCTCCAC----- ACCCTGTGCCA----- 2442
QY 1508 LysArgTrpHisIleAlaIleThrTrpThrSerAlaAsnGlyIleTrp--- LysValT 1527
DB 2443 ----- TGGGGGACCTGCCACCCACA-----GCCATCTGGCTACAACTGT 2482
QY 1527 YrIleAspGlyLysLeuSerAsp----- GlyGlyAlaGlyLeuSerVal- 1541
DB 2483 ACCTGCCCTGCGAGCTTACATGGGGTTGACCTGTAGTGAGAGGTGACAGCTTGTACTCA 2542
QY 1542 ----- GlyLeu----- 1543
DB 2543 GGGCCCTGTCTCAATGGTGGCTCTCTGCAGCATCCGTCTCTGAGGGCTATTCTCTGCCACTGC 2602
QY 1544 ----- ProIleProGly----- 1547
DB 2603 CTTCCAAGTTCACACAGCTGCCACTGCCAGACTGCCGTGGACCACTGTGTGTCTGCTCG 2662
QY 1547 ----- 1547
DB 2663 TGCCTCAATGGGGGTACCTGTGTGAACAGCTGGCACTTCTTCTGCTCTGTGTGCCACT 2722
QY 1548 ----- GlyGlyAlaLeuValLeuGlyGlnGlu----- GlnAspLysL 1560
DB 2723 GCTTCCAGGGCTGCACCTGTGTGAGGAGAGACTAACCCAGCTGTGCAGACAGCCCTGC 2782
QY 1560 YrGlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuT 1580
DB 2783 AGGAACAAGGCAACCTGCCAAGACACACTCGAGGGGGCCGCTG--- CCTCTGACGCCCT 2839
QY 1580 TrpAspTyValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluL 1600
DB 2840 GGTATATC----- AGAAGACAGCTGCCAGACTCTGTATAGACTTGTGTGCCCGAAGCCC 2893
QY 1600 euserLysGlyAsnValLeu----- AlaTrp-ProAspPhe----- LeuSer 1613
DB 2894 TGTCCACACACTGCTCGAGCTCCAGAGTGGGGCTCTGTCAGTGCCTCTCCAGTCCAG 2953
QY 1614 GlyIleValGlyLysVal----- LysIleAspSerLys 1624
DB 2954 GGATGACAGAGGGGCTCTGTGTGACTTCCACTGTCTGTCAGAGCCCGGATGAGCCAA 3013
QY 1625 SerIlePheCysSerAspCysProArgLeuGlyGlySerValProHisLeuArgThrAla 1644
DB 3014 GGCATAGAGATCTTGGCTGTGCCAGATGAGGGCTCTGT----- 3055
QY 1645 SerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGlyPheGln--- 1663
DB 3056 ----- ATTGACACGGGCTCTCTATTTCTGCGCTGCCCTCTCTGATTTCCAAGGC 3106
QY 1664 --- LeuValGlyAsnProValGlnTyCysLeuAsnGlnGlyGlnTrpThrGlnProLeu 1682
DB 3107 AAGTTATGCCAGATAAATGTGAACCCCTGC-----GAGCCCAAT 3145
QY 1683 ProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPheHisSer 1702
DB 3146 CCC---TGCCATCAGGGTCTACTCTGTGTGCTCAGCCC----- 3181
QY 1703 AlaAspAspPheTyAlaGlySerThrValThrTyGlnCysAsnAsnGlyTyTyTyLeu 1722

QY 2339 hrThrGluVal-----GlyValValThrPheSer---CysLysGluGlyH 2353
 DB 4878 ACCAGAGCCCGCAAGTGGATGAGGTGGCCATGTCTCGGCCCTGAAGAGGAG 4937
 QY 2353 isValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnGlnTrpAsnAspSerP 2373
 DB 4938 AGGCTGAAGAAACAGCCTCAGCCTCAGGTGC-----CAGCTTTGG----- 4978
 QY 2373 heProValCysLysIleValLeuCysThrProProLeuIleSerPheGlyValProI 2393
 DB 4979 -----CAGCTCAGCAGCGCTGTGGAGAGC 5003
 QY 2393 leProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGlyPheP 2413
 DB 5004 TCCCCCAGCAGCCATG----- 5020
 QY 2413 heLeuArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerProLeuP 2433
 DB 5020 ----- 5020
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 QY 2453 alGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluLeuV 2473
 DB 5061 TGGAC-----ACCTGTGGACCTGATGGGGTGGACAC 5090
 QY 2473 alGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyLysProThrC 2493
 DB 5091 CCTGTATGTCAGCGCTCTCTGTGGGGAGTGCAGTCCACGACTGGGGTAGTCCACAGA 5150
 QY 2493 ysLysAlaIleGluCysLeuLysProLysGluIleLeuAsnGlyLysPheSerTyrThra 2513
 DB 5151 GACTGGGGCTAGGAAATCTGGAACTCTGGAAACCACTG----- 5188
 QY 2513 spLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyP 2533
 DB 5189 -----CTGGATAGGCG-----GCTGCC 5207
 QY 2533 roSerAlaLeuThrCysLeuGluThrGlyAspTrp---AspValAspAlaProSerCys- 2551
 DB 5208 CCCAGGCTCA-CACGT-----GGGCACTGGAGAGCGCTCTGCACCTAGCTGCC 5257
 QY 2552 -----AsnAlaIleHisCys-----AspSerProGlnProI 2562
 DB 5258 AGATTCTCTCGGCCCAACCGCTGCCCGCGCTCTTGGAGGCTGGAGCCCAACCCCAACAG 5317
 QY 2562 leGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIleIleTyrSerC 2582
 DB 5318 CCAGACCGCGCTGGCGCGCACCCACCTTCACACTGCTGTGGC----- 5358
 QY 2582 ysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrps 2602
 DB 5359 -----TGGCGACGCTCGGCA---G 5374
 QY 2602 erSerSerIleProThrCysMetProIleAspCysGlyLeuProProHis----- 2618
 DB 5375 GTTTGCCAGCTCTATTATGGCCAGCAGACAGACTACGGTGGACGCCCGCCACAGAGACCGG 5434
 QY 2619 -----IleAspPheGlyAspCysThrLysLeuLysAspAspGlnGly---TyrPheG 2635
 DB 5435 ACTACACCTTTGATGCTGCG---TGCCAGGCTGGCGCTGGAGGACCTGGTGAAGAAATG 5491
 QY 2635 luGlnGluAspAspMetMetGluValProTyrVal----- 2646
 DB 5492 ATCG-CAGCCCGCAGCATGTAGGAGCCAGGCGATAAAGGGGAAAAATCGCACTGCACCTG 5550
 QY 2647 -----ThrProHisProProTyrHisLeuGlyAlaValAlaLys----- 2659
 DB 5551 GCGCGCTGCTGTAACAACGCCCGAGCGCGCTCTCTCTCCAGGCTGGAGCGGATAA 5610
 QY 2660 -----ThrTrpGluAsnThrLysGluSerP 2668

DB 5611 AGATCCCGCAGGACACTGAGGAACAGACGCGCTTTCTTGGCAGCGCGGAGAGCGGT 5670
 QY 2668 roAlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProG 2688
 DB 5671 CGAGGTGGCGCAGCTGTGTCTGGAGCTCGGGCGCGCCCGGGAGCTCGAGACCAGCGCG 5730
 QY 2688 lyTyrGluLeuLeuGlyAsnProValLeuIleCysGlnGlu----- 2701
 DB 5731 GCTGGCCC-----CAGGAGATGTGGCGCGCCGCGCAGCGCAG 5763
 QY 2702 --AspGlyThr-----TrpAsnGlySerAlaProSerCysIleSerIleGluC 2717
 DB 5764 TCACCTGGGACCTGTCTAAGCTCTGGAA-GGGCTGGACCGACTACGAGGAGCCCGTG 5822
 QY 2717 ysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlyS 2737
 DB 5823 CGCAGCGCAGCACCACGCGCGGGGCG-----GGGT 5852
 QY 2737 erAlaValGlnTyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArg----- 2755
 DB 5853 CGGCCCCCGCG-----TGC CGGACG-----CTGTCTCGGGAGCGCGCCCGCGGGG 5900
 QY 2756 -----LeuCysLeuGluAsnArgLysTrpSer-----GlyAlaSer----- 2767
 DB 5901 GCGGAGCCTGTCTGCGAGCTCGCACTTGGTGGTGGAGCGCGCGGAGGGAAG 5960
 QY 2768 -----ProArgCysGluAlaIle-----SerCysLysLysProAsnProValMetAsnG 2784
 DB 5961 TGTATGCTCGCTGCGGAGCGCATCTGGAAGCTCGGG-AGGCCCCACACCGCGCGCGCG 6019
 QY 2784 lySerIleIleGlySerAsnTyrThr-----TyrLeus 2795
 DB 6020 AGTTCTCCGCGGGCTCCCGTGGACGACGCGGGGCTAGGGCATCACAGATGACTGGCCT 6079
 QY 2795 erThrLeuTyrTyrGluCysAspProGlyTyrValLeuAsnGlyThrGluArgArgThrc 2815
 DB 6080 CGCGACTG-----GGTGGCCCTGGGAAGCTG-----CGGCTCGCGCTGCAGT 6121
 QY 2815 ysGlnAspAspLysAsnTrpAspGluAspGluPro---IleCysIleProValAspCys- 2833
 DB 6122 GCGCGCATCCCGCTCCCGAGCTGACCCCGCTGCCAGAACGCTGGATCCCTCAAGTTGCC 6181
 QY 2834 -----SerSerPro-ProValSerAlaAsnGlyGlnValArg----- 2845
 DB 6182 TGGGCTCTTCAGTTTCCACAGAGATTCCCTTAACTCGGTTGTAGAAATCTGAAGTAG 6241
 QY 2846 -----GlyAspGluTyr-----ThrPheGln 2852
 DB 6242 GCAGCTCGGTGGAGAGGAGGAGCGACGCTAGGAGCTCGGAAGACTCCGGAAGCTTTTAAG 6301
 QY 2853 LysGluIle-----GluTyrThrCysAsnGluGlyPheLeuLeuGluGlyAlaArgSer 2870
 DB 6302 GCCAAATAACCGTTAAGCTCACTTGT-----CTCCCCCAT 6337
 QY 2871 ArgValCysLeuAlaAsnGly 2877
 DB 6338 AGATGATGACAGCAATGGGA 6358

RESULT 17

US-09-467-997-6
 ; Sequence 6, Application US/09467997
 ; Patent No. 6379925
 ; GENERAL INFORMATION:
 ; APPLICANT: Kitajewski, Jan
 ; APPLICANT: Uyttendaele, Hendrik
 ; TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
 ; FILE REFERENCE: 53863-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/467,997
 ; CURRENT FILING DATE: 1999-12-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6


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; LENGTH: 6677
; TYPE: DNA
; ORGANISM: mouse
; US-09-467-997-6

Alignment Scores:
Pred. No.: 4,61e-58 Length: 6677
Score: 834.00 Matches: 539
Percent Similarity: 31.24% Conservative: 203
Best Local Similarity: 22.69% Mismatches: 784
Query Match: 4.18% Indels: 854
DB: 4 Gaps: 119

US-09-977-053-4 (1-3571) x US-09-467-997-6 (1-6677)
QY 927 ProAspGluAArgAsnAphrLeuGluTrpGluAsnGlnGlnArgLeuLeuGlnThrLeu 946
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530 CCTGACCCCTGCAGGAGATCCCAACTCTGCAGAGATGGTGGCAGCTGCCAAGCCCTGCTC 589
QY 947 GluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyrSerPheGln 966
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
590 CCCACACCCCAAGCTCCCGTAGTCTTCTTCTCCACTGACCCCTCACTTCTCTCTGCACC 649
QY 967 LeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSerPro 986
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
650 TGCCTCTCTGCGC---TTCACCGGTGATCGATGCCAAACCCATCTGGAGAGCTCTGTCCA 706
QY 987 -----PheCysArgProGlySer-----ValLeuArgGlyArgMetCysVal 1000
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
707 CTTCTCTCTGTTCCAAAGGGGTCACTGTATGTTTCAGGCTCAGCGCCGCCACAGTGC 766
QY 1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
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767 TCCTGCGAGCTGGG-----TGCACAGGTGAGCAATGCCAGCTC 805
QY 1021 GlySerTyrGlnAspGluGlu-----Gly 1028
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
806 CGAGACTTCTGCTCAGCAACCCCTGTGCCAAGGAGGTGTGCTGCGCCACATACCCC 865
QY 1029 GlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAsn 1048
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
866 CAGATCCAGTGGCG---TGTCCACCTGGG---TTCGAGGGTCCACACTGTGAAGCGGAC 919
QY 1049 IleSerAspCys-----LysAlaGlnCysLysGlnGlyThrTyrSerTyrSerGly 1065
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920 ATCAACAGAGTGTCTCTCGAGCGCGGACCCCTGCCCTCAGGGCACCTCTGCCATAACACC 979
QY 1066 LeuGluThrCysGluSer---CysProLeuGlyThrTyrGlnProLysPheGlySerArg 1084
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
980 TTGGTTCCTACCAAGTGTCTCTGCTCTGCTGCGGCGAGGAGTCCCGAGTGCAGCTCAGG 1039
QY 1085 -----SerCysLeuSer-----CysProGlu 1091
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1040 AAGGAGCTGCTCCTCTGCAAGCTGTCTCAATGGGGGCACCTGCCAGCTGTGCCAGAG 1099
QY 1092 AsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGlyValPro----- 1109
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1100 GGACACTCCACC-----TTTCATCTCTGCTCTCTGCCCCAGGT 1138
QY 1110 -----CysProGlu 1112
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1139 TTCAGGGGCTGAGCTGTGAGATGAACCCAGATGACTGTGTGAGGACCACTGTGCAGAAC 1198
QY 1113 GlyLysPheSerArgSerGlyLeu-----MetProCysHisProCysProArgAspTyr 1130
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1199 GGGGCCACCTGTCTGGATGGCTGGATACCTACACCTGC---CCCTGCCCCCAAGACATGG 1255
QY 1130 ----- 1130
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1256 AAGGGCTGGACTGTCTCTGAAGATATAGATGAATGTGAAGCCCGGGGTCCCTCGCTGC 1315
QY 1131 -----TyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysProPhe 1145
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1316 AGNAAGGTGGCAGCTGCTGCCAGAACACAGCTGGCAGCTTTCTACTGTGTGTGTGAGTGGC 1375
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1436 GATCCACCTGCATCGACCGTGTGGGTCTTTCTCC----- 1471
QY SerValValProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGln 1192
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1472 TGCCTCTGCCACCTGGAGCGCACAGGCTCTGTGTGCCACCTGGAGACATG----- 1522
QY ValPheHisGluCysPheAsnProCysHisAsnSerGlyThrCys-----GlnGln 1210
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1523 -----TGTTTGAGTCAGCCGCTGCCACGTGAATGCCAGTGCAGCACCAACCT 1570
QY LeuGlyArgGlyTyrValCysLeuProLeuGlyTyrThrGlyLeuLysCysGluThr 1230
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1571 CTGACAGCTCCACCCTCTGCATATGACCGCTGCTACTCAGGATCCACCTGTCCACCA 1630
QY AspIleAspGluCys-----SerProLeuProCysLeuAsnAsnGlyVal 1245
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1631 GATCTGATGAGTGCACAAATGGCCAGCAGGACCCAGTCCCTTGCAGACATGGGGGTCC 1690
QY CysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGlyGlnArg 1265
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1691 TGCATCAACACCCCTGCTTCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1750
QY CysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLysGlyIleCysVal 1285
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1751 TGTGAGCTGACCAATAGTGTCTGTACAGCCCTGCCACCCAGGACGACCTGCTGCTG 1810
QY AspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHisCysGlu 1305
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1811 GACCTGCTTGCAGGTTTCCACTGCTCTGCCACCCAGGCTTGGAGGGAGACTCTGTGAG 1870
QY ThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGluAspGln 1325
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1871 GTGAGGTCAATGAGTGCACCTTAATCTCTGCTGACCAAGCTGCTGCCATGACCTG 1930
QY ValGlyGlyLeuCysLysCysProProGlyPheLeuGlyThrArgCysGlyLysAsn 1345
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1931 CTCACGGCTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1990
QY ValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsn 1365
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1991 ATGAGCAGGTGTAGCAGCAGCCCCCTGTGCCAATGGGGGCGCTGCCAGAGACGAGCTGGA 2050
QY SerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsnIleAsn 1385
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2051 GCCTTCTACTGCGAGTGTCTCCAGGCTTGAAGGGCCACACTGTGAGAAAGAGTGGAC 2110
QY GluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyr 1405
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2111 GAATGCTGAGTGCACCTGCTGCCGTGGAGCCAGTGTCTGTGATCTCCCGGAGCATTC 2170
QY SerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSerThr--- 1424
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2171 TTCTGTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2230
QY -----GlyPheAsnLeuAspPheGlu----- 1431
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2231 AACATGTGCCAACCTGGACAGCAATGCCAGGTGAGGAACACAGAGCCCCCTGCTTGC 2290
QY ValSerGlyIleTyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHis-AlaIle 1451
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2291 CCTGACGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2350
QY uThr-----CysThrPheTrpMetLysSerSerAspAspMetAsnTyrGlyThrPr 1468
DB ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy nGlyLysTrp-----ValProProGluGlyGlnAsp-----MetProAr 2077
Db 4162 ATGTGGCTGGAGCGGGAGAGACTGCAGACCAAGAGGGAAGACTCAGAGGGGAGGCGCTC 4221
Qy 2077 gCyLeAlaHisPheCysGluLysProProSerValSerTyrSerIleLeuGluSerVa 2097
Db 4222 CTTGGCCCTGTGGTGGTGTGAGGCGGCCCGAGCCCTGGATCAGCAGCTGCTT----- 4273
Qy 2097 lSerLysAlaLysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheVa 2117
Db 4274 -----GCCCTGSCACAGTGTCTGCTCTG----- 4297
Qy 2117 lleuAenThrSerAlaLysIleGluCysMetArgGlyGlnTrpAsnProSerProMe 2137
Db 4298 -----ACTCTGAGGGTCTGCTCTG----- 4318
Qy 2137 tSerIleGlnCysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAl 2157
Db 4319 -----GTGAGGAAGGACAG 4332
Qy 2157 aSerGlySerAsnTyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTy 2177
Db 4333 TGAAGCAGACACATGTGTTC-----CCCTATCTCTGGGACCGGGCC----- 4375
Qy 2177 rIleLysGlyGluLysLysSerThrCysGluAlaThrGlyGlnTrpSerProIlePr 2197
Db 4376 -----AAAGAGGAGTGTAGTGGAGTGGAGTCTCTTCATCTGGGAAGACAAAGCCCC 4428
Qy 2197 oThrCysHisProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHi 2217
Db 4429 TCCACTCAGCCCTGGGC---AAGGAGACAGAGTCTCTTGGTGCGAGGTTTGTG----- 4480
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Db 4480 ----- 4480
Qy 2237 rValGlySerProValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLe 2257
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Qy 2257 uMetCysValProLeuAspCysGlyLysProProIleGluAsnGlyPheMetLysGl 2277
Db 4525 ---TGGTCTCCCTGCCCCCTGGGACTCTGGACTCTCTGCTGCGCTCTCTTGGAGCAATGG 4580
Qy 2277 yGluAsnPheGluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuVa 2297
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Qy 2297 lGlyAspSerSerTrpThrCysGlnLysSer----- 2307
Db 4641 CAGGAGACCAGGCC---CCCTGCCAACAGCTCTCCCTGGCCCATTTCTATGTTTACCAGTGG 4697
Qy 2308 -----GlyLysTrpAsnLysLysSerAsnProLysCysMet----- 2319
Db 4698 TTGGGGTGTCTTCTCTGGCCCTTGGGGCCCTTCTGCTCTCCAGCTCATTTGGCGGAGCGG 4757
Qy 2320 -----ProAlaLysCysPro----- 2324
Db 4758 GACGAGAACATGGGGCCCTGTGGCTGCCCTGTTTCATTCGAGGCCCTCAGACACAGC 4817
Qy 2325 -----Glu-ProProLeuLeuGluAsnGlnLeuValLeuLysGluLeuTr 2339
Db 4818 AGGCACCCACCGCGGAGGCCCCCACTTGGCGGAGGACACATTTGTTCTTAAGGCACCTGA 4877
Qy 2339 hThrGluVal-----GlyValValPheSer---CysLysGluGlyH 2353
Db 4878 AGCCAGAGGCCGGAAGTGAAGATGGAGTGGAGTGGCCATGTGCTCGGGCCCTGGAAGGGAG 4937
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Db 4979 -----CCGCTCAACAGCGCGCTGTGTGAGAGC 5003
Qy 2393 leProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGlyPheP 2413
Db 5004 TCCCCAGGAGCCATG----- 5020
Qy 2413 heLeuArgGlyAsnSerThrLeuCysGlnProAspGlyThrTrpSerSerProLeup 2433
Db 5020 ----- 5020
Qy 2433 roGluCysValProValGluCysProGlnProGluGluIleProAsnGlyIleIleAspV 2453
Db 5021 -----CTGACCCCTCTCTAGGAGTGTGAATCGGAGGTCTTGGATG 5060
Qy 2453 alGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluLeuV 2473
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Db 5091 CCCTGATGTTCAGCGCTCTCTGTGGGGAGTGCAGTCCACGACTGGGGCTAGTCCACAGA 5150
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Qy 2513 sPLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyP 2533
Db 5189 -----CTGGATAGAGG-----GCCTGCC 5207
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Qy 2562 leGluAenGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIleTyrSerC 2582
Db 5318 CCAGACCGCTGGCGCACCCCACTTCACACTCTCTGTC----- 5358
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Db 5359 -----TGCCGACGCTCGGA---G 5374
Qy 2602 erSerSerIleProThrCysMetProIleAspCysGlyLeuProProHis----- 2618
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Qy 2619 -----IleAspPheGlyAspCysThrLysLysAspAspGlnGly---TyrPheG 2635
Db 5435 ACTACACCTTTGATGCTGGC---TGCCAGGCTGGCGCTGGAGGACCTGGTTGAAGAATTG 5491
Qy 2635 luGlnGluAspAspMetMetGluValProTyrVal----- 2646
Db 5492 ATCG-CAGCCGAGCAGATGTAGCAGCCAGGGATAAAGGGGAAAACTGCACTGCACCTG 5550
Qy 2647 -----ThrProHisProProTyrHisLeuGlyAlaValAlaLys----- 2659
Db 5551 GGCGCTGTGTGAACAAACCCCGAGCCCGCTCTCTCTCTCCAGGCTGGAGCGGATAA 5610
Qy 2660 -----ThrTrpGluAsnThrLysGluSerP 2668
Db 5611 AGATGCCAGGACAGTAGGGAACAGACCGCGCTTTTCTTGGCAGCGCGCGAAGGAGCGCT 5670
Qy 2668 roAlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProG 2686
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1288 -----GACAAAGATCTCAATTACTGTGGG 1311
QY 1108 val-----ProCysProGluGly-----LysPheSer 1116
1312 ACTCATCAGCGGTCTCAACGGGGGAACTGTAGCAACACAGGCCCTGACAAATATACAG 1371
QY 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
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QY 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
1407 ----- 1407
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QY 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
1408 -----GAAATTCCTGAG-----CAGCC 1425
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QY 1357 GlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysValLeuAlaGlyPheThr 1376
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QY 1377 GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
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2131 -----ATTGAC-----AGCTGCACAGTGCC 2151
QY 1457 MetLysSerSerAspAspMetAsnTyrThrPro-----IleSerTyrAlaValAsp 1474
2152 ATGCTTCCACAC-----ACACCTGAAGGGTGCCTATATTTCTCTCC 2196
QY 1475 AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn 1494
2197 AAC-----GTCGTGGTCTCTCAC 2214
QY 1495 GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTyrHisIleAla 1514
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QY 1515 IleThrTyrThrSerAlaAsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAsp 1534
2248 -----ACCTGTGACTGTAAACAAAGCTTCACGGGAACATCTGCCCATGAATAATTAATGAC 2304
QY 1535 GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyGlyAlaLeuValLeuGly 1554
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QY 1555 GlnGluAsnLysLysGlyGluGlyPheSerProAlaGluSerPheValGlySerIle 1574
2350 GTCAACTCTCTACAG-----TGCACTGTGTAGTACGGCTGGAGGGCCCTAC 2397
QY 1575 SerGlnLeuAsnLeuTyrAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr 1594
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QY 1595 SerCysProGluGluSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGly 1614
2434 ---TGCCACAAT----- 2442
QY 1615 IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg--- 1633
2443 -----GGGGGCGACGTGCGGACCTGGTCAATGACTTCTACTGTGACTGTAAAAATGGG 2496
QY 1634 LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653
2497 TGAAGAAGAAAGACCTCCACTCAGTGACAGTCAGTGTGATGAGGCCACCTGCAACAC 2556
QY 1654 ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr 1671
2557 GGTGGCACCTGCTATGATGAGGGGAGTCTTTTAAG----- 2592
QY 1672 CysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGluArgIleSerCysGly 1691
2593 TGCATGTCTCTGCGCGCTGGGAAGAACCTGTAACTAGCCCGAACACAGTAGCTGC 2652
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2653 CTGCCCCAACCCCTGCCATATGCG----- 2676
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2677 -----GGCACATGTGTGTCAACGGCGAGTCTCTTACGTGCGCTC 2715
QY 1732 AspAsnGlySerTyrPheGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
2716 TGCAGAAGAGGCTGGGAGGG-----CCCATCTGTGCTCAGAAATACC----- 2757
QY 1752 GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
2758 ---AATGACTGAGCCCTCATCTCTGTTACACAGCGGACCTGTGTGGATGGAGACAC 2814
QY 1767 SerTyrIleCysSerCysValProProTyrThrGlyAsp----- 1779
2815 TGTACCGGTGCGAATGTGCCCCGGGTTTGTGTCGGCCGAGTGCAGATAAATCAATCAAT 2874


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QY 1780 -----GlyLysAsnCysAlaGluProLeu----- 1787
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QY 1788 LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluLeuLeuThrVal 1807
DB 2935 CGGTGTCTGCTGCTT-----CCAGGCGACAGTGGTGCCCAAG----- 2970
QY 1808 GlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeuMetGlyValThrLysIle 1827
DB 2971 -----TGCCAGGAA-----GTTTCAGGAGGA 2991
QY 1828 ThrCysLeuGluSerGlyGluThrPheHisLeuLeuPro----- 1840
DB 2992 CCTTGATCACCATTGGGAGT-----GTGATACAGATGGGCGCCAAATGGGATGAT 3042
QY 1841 -----TyrCysLysAlaValSerCysGly 1848
DB 3043 GACTGTATATACCTGCCAGTGCCTGTAATGACGGATCGCTCTCAAGGTCTGGTGTGGC 3102
QY 1849 ---LysProAlaIleProGluAsnGly-----CysIle 1858
DB 3103 CTTGACCTTGTCTGCTCCACAAGGGCACAGGAGTGGCCCGGCGAGCTGCATC 3162
QY 1859 -----GluGluLeuAlaPheThrPheGlySerLysValThrTyrArgCysAsnLys 1875
DB 3163 CCCATCTCGGACGACCGAGTCTTC-----GTCCACCCCTGC----- 3198
QY 1876 GlyTyrThrLeuAlaGlyAspLysGluSerSerCysLeu----- 1888
DB 3199 -----ACTGGTGTGGCGAGTGTGCTTTCAGTCTCCAGCGGTGAAGACAAGTGC 3252
QY 1889 -----AlaAsnSerSerTrpSerHis----- 1895
DB 3253 ACCTCTGACTCTTATPACCAGGATACCTGTGGGAACATCACATTTACCTTTAAACAGGAG 3312
QY 1896 -----SerProValCysGluProValLysCysSerSerProGluAsnLeuAsn 1913
DB 3313 ATGATGTACACAGGCTTACTACGGAGCACATTTGCAGTGAATTGAGGAATTGAAT--- 3369
QY 1914 GlyLysTyrIleLeuSerGlyLeuThrTyrLeuSerThrAlaSerTyrSerCysAspThr 1933
DB 3370 -----ATTGTGAAGAAATGTTCCGCTGAATATTCAATCTACATCGCTTCCGAGCCT 3420
QY 1934 GlyTyrSerLeuGlnGlyProSerIleIleGluCysThrAlaSerGlyIleTrpAspArg 1953
DB 3421 TCCCTCTCAGCGAACAATGAATACATGTGGCCATTCTCTGCTGAAGATATACGGATGAT 3480
QY 1954 AlaProPro 1956
DB 3481 GGGAAACCG 3489

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RESULT 19
US-09-855-722-6
; Sequence 6, Application US/09855722
; Patent No. 6638741
; GENERAL INFORMATION:
; APPLICANT: Sakado, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 4208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (409)..(4062)
; NAME/KEY: sig_peptide
; LOCATION: (409)..(501)
; NAME/KEY: mat_peptide
; LOCATION: (502)..(4062)
US-09-855-722-6

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Alignment Scores:
Pred. No.: 1,61e-52 Length: 4208
Score: 763.00 Matches: 288
Percent Similarity: 34.28% Conservative: 145
Best Local Similarity: 22.80% Mismatches: 400
Query Match: 3.82% Indels: 430
DB: 4 Gaps: 57

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US-09-977-053-4 (1-3571) x US-09-855-722-6 (1-4208)

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QY 834 CysSerAspAlaGlu-----AspIleAspCysArgLeuGluGluAsnLeuThrLys 850
DB 571 TCGCGCGCGCCCGGAACCCCGGAGACCCGAGTGCACCCGCGACGAGTCTGCACATAC 630
QY 851 ---LysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe---AlaIleGlyPro 868
DB 631 TTCAAAGTGTGCTCAAG-----GAGTATCAGTCCCGCTCAGCGCGCGGGGCC 681
QY 869 GlyGlyTrpGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrVal 888
DB 682 TGCAGCTTCGGCTCAGG----- 699
QY 889 GlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaPro 908
DB 700 -----TCCACGCTGTGTCATCGGGGGCAACACCTTCACCTCAGGCCACCGCGGC 750
QY 909 LeuSerAspTyrLysIleLysLeuIlePheAsnIle-----ThrAla 922
DB 751 AACGACCGCAACCGCATCTGCTGCTTCAGTTTCGCTGCGCGAGGTCCTATACGTTG 810
QY 923 SerValProLeuProAspGluArgAsnAspThrLeuGluTrpGlu----- 937
DB 811 CTTGTGAGGCGTGGGANTTCCAGTATGACACCGTTCAACCTGACAGCTATATTGAAAG 870
QY 938 -----AsnGlnAlaArgLeuLeuGlnThrLeuGluThrIleThr 950
DB 871 GCTTCTACTCGGGCATGATCAACCCCGCGCAGTGGCAGACGCTGAGCAGACACG 930
QY 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspPrometTyrSerPhe 965
DB 931 GCGGTGCCCCACTTTGAGTATCAGATCCGCGTGACCTGTGATGACTACTATGGCTTT 990
QY 966 GlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSer 985
DB 991 -----GCGTGCAT 999
QY 986 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
DB 1000 AAGTTCTGCGCCCGCAGAGATGACTTCTTTGGA----- 1032
QY 1006 ThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAsp 1025
DB 1033 -----CACTATGCTGTGAC-----CAGAAATGGCAACAAATTCG 1068
QY 1026 GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr 1041
DB 1069 ATGGAAGGCTGGATGGGCCCGCAATGTAACAGAGCTATTTGGCCGACAGAGCTCGAGTCT 1128
QY 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
DB 1129 AAGCATGGGTCTTGCAAACTCCAGGTGACTCCAGGTGCTGAGTGCAG-----TAC 1173
QY 1062 SerTyrSerGlyLeuGluThrCysGluSerCys-----ProLeuGlyThrTyr--- 1077
DB 1174 GGCTGGCAAGGCTG---TACTGTGATAAGTGCATCCACCCCGGAGTCCGTCACGCG 1230

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1078 QY -----GlnProLysPheGlySerArgSerCysLeu 1087
1231 DB ATCTGTAATGAGCCCTGGCAGTGCCTCTGTGAGACCAACTGGCGCGCCAGCTCTGT--- 1287
1088 QY SerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGly 1107
1288 DB -----GACAAGATCTCAATTACTGTGG 1311
1108 QY Val-----ProCysProGluGly-----LysPheSer 1116
1312 DB ACTCATCAGCGGTCTCAACGGGGAACTGTAGCAACACAGCGCCCTGACAAATATACG 1371
1117 QY ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
1372 DB TGTTC-----TGCCTTGAAGGGGTATTTCAGGACCCAACTCT--- 1407
1137 QY LysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
1407 DB ----- 1407
1157 QY IleThrGluCysSerSerPheSerThrPheSerAlaAlaGluGluSerValPro 1176
1407 DB ----- 1407
1177 QY ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
1408 DB -----GAAATTGCTGAG-----CACGCC 1425
1197 QY CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
1426 DB TGCCTCTGATCCTCTGTCACACAGGGCAGCTGTAAAGAGACCTCCCTGGGGCTTTGAG 1485
1217 QY CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGlyCysSer 1236
1486 DB TGTGAGTGTTCCTCCAGCGCTGACCGCGCCACCATGCTCTACAAACATTGATGACTGTCT 1545
1237 QY ProLeuProCysLeuAsnAnglyValCysLysAspLeuValGlyGluPheIleCysGlu 1256
1546 DB CCTAATAACTGTTCCTCCAGCGGGCACCCTGCGGACCTGGTTAAACGGATTAAAGTGTGTG 1605
1257 QY CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSer 1276
1606 DB TGCCTCCAGTGGACTGGGAAACCTGCAGTAGTACGATGCAATGATGATGAGGCCAAA 1665
1277 QY ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
1666 DB CTTTGTGTAAACGCCAAATCCTGTAAAGAACTCTCATTCAGCTACTACTGCGACTGTCTT 1725
1297 QY LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
1726 DB CCGCGCTGGATGGTTCAGAAATTGACATAAATAATTAATGACTGCTTGGCCAG---TGT 1782
1317 QY LeuAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGly 1336
1783 DB CAGAAAGACCTCTCTCGGATTGGTAAATGGTTATCGCTGTATCTGTCCACTGGC 1842
1337 QY PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
1843 DB TATGCAGCGCATCATCTGTGAGAGAGACATCGATGAATGTGCCAACCCCTGTGTGAAT 1902
1357 QY GlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThr 1376
1903 DB GGGGGTCACTGTTCAGATGAATAACACAGATTCCAGTGTCTGTGTGCCACTGGTTTCTCT 1962
1377 QY GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
1963 DB GGAACCTCTGTAGCTGGACATCGATTATGTGAGCTTAATCTCTGCCAGACGGTGC 2022
1397 QY ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGln 1416
2023 DB CAGTGTCTACAAACCGTGCAGTGACTATTCTTCTCAAGTGTCCCGGAGGACTATGAGGGCAAG 2082

1417 QY ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr 1436
2083 DB AACTGCTCACACTGAAAGACCACTGCCCGCACGACCCCTGTGTGAAGTG--- 2130
1437 QY GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyr 1456
2131 DB -----ATTGAC-----AGCTGCACAGTGGCC 2151
1457 QY MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp 1474
2152 DB ATGGCTTCCACAGC-----ACACCTGAAGGGTGCCTATATTTCCTCC 2196
1475 QY AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn 1494
2197 DB AAC-----GCTGTGGTCTCTCAG 2214
1495 QY GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTyrHisHisIleAla 1514
2215 DB GCGAAG-----TGCACAGATCAGTCCGGAGGCAAAATTC--- 2247
1515 QY IleThrTyrThrSerAlaAsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAsp 1534
2248 DB ACCTGTGACTGTACAAAGGCTTCACGGGAACATACCTGCCATGAATAATTAATGAC 2304
1535 QY GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyGlyAlaLeuValLeuGly 1554
2305 DB TGTGAGAGCAAC-----CCTGTAGAAACGGTGGCAGCTTGTGATCGATGT 2349
1555 QY GlnGluAsnLysLysGlyGlyGlyPheSerProAlaGluSerPheValGlySerIle 1574
2350 DB GTCAACTCTCTACAG-----TGCACTCTGTAGTACGGCTGGGAGGGCGCTAC 2397
1575 QY SerGlnLeuAsnLeuThrAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr 1594
2398 DB TGTGAACCAATTAATGACTCGACGCCAGAACCCC----- 2433
1595 QY SerCysProGluGluLeuSerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGly 1614
2434 DB TGCACCAAT----- 2442
1615 QY IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg--- 1633
2443 DB -----GGGGGCGACGTGCGGACCTGGTCAATCACTTCTACTGTGACTGTAAATAATGG 2496
1634 QY LeuGlyCysSerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653
2497 DB TGGAAAGGAAGACCTCCCACTCAGTGCAGCAGTCAGTGTGATGAGGCCACCTGCAACAC 2556
1654 QY ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr 1671
2557 DB GTTGGGACCTGCTATGATGAGGGGGATGCTTTTAAG----- 2592
1672 QY CysLeuAsnGlnGlyGlnTyrThrGlnProLeuProHisCysGluArgIleSerCysGly 1691
2593 DB TGCATGTGCTCTGGCGCTGGGAAGGAACAACCTGTAACATAGATGCCGAACAGTAGCTGC 2652
1692 QY ValProProLeuLeuAsnGlyPheHisSerAlaAspAspPheTyrAlaGlySerThr 1711
2653 DB CTGCCCCAACCCCTGCCATAATGGG----- 2676
1712 QY ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThr 1731
2677 DB -----GGCACATGTGTGTGTCACGGCGGAGTCTTTACGTGCGTC 2715
1732 QY AsnAsnGlySerTyrAsnGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
2716 DB TGCAGGAAGCGCTGGAGGGG-----CCCATCTGTGCTCAGAAATACC--- 2757
1752 QY GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
2758 DB AATGACTGCAGCCCTCATCTCCCTGTTACAAACAGCGCACCTGTGTGGATGAGAGAAC 2814
1767 QY SerTyrIleCysSerCysValProProTyrThrGlyAsp----- 1779

[illegible]

RESULT 20

US-08-110-158-3

US 00 110 158 ; Sequence 3, Application US/08110158

; Patent No. 5605821

GENERAL INFORMATION:

APPLICANT: McEVer, Rodger P.

APPLICANT: Pan, Junliang

TITLE OF INVENTION: Expression Control Sequences of the

TITLE OF INVENTION: P-Selectin Gene

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 1100 Peachtree Street, Suite 2800

CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-4530

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

Alignment Scores:

Alignment Scores:	
Pred. No.:	1.05e-52
Score:	762.50
Percent Similarity:	32.49%
Best Local Similarity:	22.41%
Query Match:	3.82%
DB:	1
Length:	3142
Matches:	311
Conservative:	140
Mismatches:	421
Indels:	517
Gaps:	60

US-09-977-053-4 (1-3571) x US-08-110-158-3 (1-3142)

1556	Qy	GlulnAspLysLysGlyGluGlyPheSerProAlaGluSerPheValGlySerIleSer	1575
20	Db	CAGCAGGTCCACAGAGGATGGCCAACTGCCCAAATAGCCATCTCTGTACAGAGATTCCA	79
1576	Qy	GlulnAsnLeuTrpAspTyrValLeuSerProGlnValLysSerLeuAlaThrSer	1595
80	Db	GAGAGTGTCTTTGGAAATTTCCCACTCTCTTCTCAGTGCCTGATCTCTGAACTAAC	139
1596	Qy	CysProGlu-GluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIrl	1615
140	Db	AAACCCAGAGAGA-----GTGCAGCATGGACTTATCATTCAGCACACAA	184
1615	Qy	eValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArgLeuGl	1635
185	Db	AGCATACTCATGAATATTTCCTGATA-----TACTGCCAG-----	221
1635	Qy	yGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLysValas	1655
222	Db	-----AA-----	223
1655	Qy	nLeuPheCysAspProGlyPheGlnLeuValGly-----AsnProValGlnTy	1671
224	Db	TCGCTACACAGAC-----TTATGGCCATCCAGATAAATAAGAAATTGATTA	271
1671	Qy	rCys-----LeuAsnGl	1675
272	Db	CCTCAATAAGGTCTTACCCTACTACAGCTCTACTTGGGATTCGGAAGAACAA	331
1675	Qy	nGlyGlnTrpThrGlnProLeuProHisCysGluArgIleSerCysGlyValProPro	1695
332	Db	TAAGACATGGACATGG-----GTGGACACCAAAAGGC	364
1695	Qy	oLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrl	1715
365	Db	TCTACCAAC-----GAGGCTGAGAAC---TGGGCTGATAATGAACCTAACACAA	412
1715	Qy	nCysAsnAsn-----GlyTyrTyrLeuLeuGlyAspSerArgMetPheCysTh	1731


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Db      413  AGGAACACAGGAGCTCGTGGAGATATACATCAAGAGTCCGTCAGCC----- 461
Qy      1731  rAspAenGlySerTrpAenGly-----ValSe 1740
Db      462  -----CCTGGCAAGTGGAAATGATGAGCACTGCTTGAAGAAAAAGACGACCATTTGTTATCAC 517
Qy      1740  rProSerGlyLeuAaspValAaspGlyCysAlaValGlySerAaspCysSerGluHisAlaSe 1760
Db      518  AGCTCTCTCCAGGACATG-----TCTCGACGCAAAACAGGAGA 556
Qy      1760  rCysLeuAenValAaspGlySerTrpAenGlyCysSerCysValProProTrpThrGlyAaspG1 1780
Db      557  GTGCGCTCGAGACCATCGGAGAACTACACCTGCTCTCTGTTACCTCGGATTCTATGCGCCAGA 616
Qy      1780  y-----LysAenCy 1783
Db      617  ATGTGAATACGTGAGAGAGTGTGGAGAACTTGAGCTCCCTCAACACAGTGCTCATGAACCTG 676
Qy      1783  sAlaGluProIleLysCysAlaProGlyAenProGluAenGlyHisSerSerGlyG1 1803
Db      677  GAGCCACCTCTG-----GGAAC----- 695
Qy      1803  uIleTyThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyThrGlnLeuMetG1 1823
Db      696  ----TTCTCTTTAACTCGCAGTGCAGCTTCCACTGCAGCTGACGGGTACCAAGTAAATGG 751
Qy      1823  yValThrLysIleThrCysLeuGluSerGlyGluTrpAenHisLeuIleProTyThrCysLy 1843
Db      752  GCCCAAGAGCTGGAATGCTTGCTTCTGGAATCTGGACAAATAAGCCTCCACAGTGT 811
Qy      1843  sAlaValSerCysGlyLysProAlaIleProGluAenGlyCysIleGluLeuAlaPh 1863
Db      812  AGCTGCCAGTGCACCCCTGGAAGATTCTGACGAGGA----- 851
Qy      1863  eThrPheGlySerLysValThrTyArgCysAenLysGlyTyThrLeuAlaGlyAaspLy 1883
Db      851  ----- 851
Qy      1883  sGluSerSerCysLeuAlaAenSerSerTrpSerHisSerProProValCysGluProVa 1903
Db      852  -AACATGATCTGCCTT-----CATCT----- 872
Qy      1903  lLysCysSerSerProGluAenIleAenAenGlyLysTyIleLeuSerGlyLeuThrTy 1923
Db      873  -----GAAAAGCATTCAGCA 889
Qy      1923  rLeuSerThrAlaSerTySerCysAaspThrGlyTySerLeuGlnGlyProSerIle1 1943
Db      890  TCAGTCTAGCTCAGCTTCAGTTGTGAAGAGGGAATTTGCATTAGTTGGACCGGAAGTGT 949
Qy      1943  eGluCysThrAlaSerGlyIleTrpAaspArgAlaProProAlaCysHisLeuValPheCy 1963
Db      950  GCAATGCACAGCTCGGGGGTATGGACAGCCCCCAGCTGTGTAAAGCTGTGCAGTG 1009
Qy      1963  sGly-----GluProProAla-----IleLysAaspAlaValIleThrGlyAenAenPh 1979
Db      1010  TCAGCACCTGGAAAGCCCCCAGTGAAGAACCATGGACTGTGTTCATCCGCTCACTGCTTT 1069
Qy      1979  eThrPheArgAenThrValThrTyThrCysLysGluGlyTyThrThrLeuAlaGlyLeuAs 1999
Db      1070  TGCCTATGGCTCCAGCTGCAGAAATTTGAGTGCCAGCCCGCTACAGAGTGGGGGCTTGA 1129
Qy      1999  pThrIleGluCysLeuAlaAaspGlyLysTrpSerArgSerAaspGlnGlnCysLeuAlaVa 2019
Db      1130  CATGCTCCGCTGCATTTGACTCTGGACACTGCTGCACCTCTGCCAACCTTGCCAGCTAT 1189
Qy      2019  lSerCysAasp-----GluProProIleValAaspHisAlaSerProGluThrAlaHisAr 2037
Db      1190  TTCGTGTGAGCGCTGGAGAGTCTCTC-----CACGAAGCATGGAT----- 1232
Qy      2037  gLeuPheGlyAaspIleAlaPheTyThrTySerAaspGlyTyThrSerLeuAlaAaspAenSe 2057

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Db      1233  -----TGCTCT----- 1238
Qy      2057  rGlnLeuLeuCysAenAlaGlnGlyLysTrpValProProGluGlyGlnAaspMetProAr 2077
Db      1238  ----- 1238
Qy      2077  gCysIleAlaHisPheCysGluLysProProSerValSerTySerIleLeuGluSerVa 2097
Db      1239  -----CCATCCTTG----- 1247
Qy      2097  lSerLysAlaLysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheVa 2117
Db      1248  -----AGAGCGCTTTCAGTATGACACCACTGTAGCTTCGCTGTGCTGAAGGTTTCAT 1300
Qy      2117  lLeuAenThrSerAlaLysIleGluCysMetAsgGlyGlyGlnTrpAen-----ProSerPr 2136
Db      1301  GCTGAGAGGAGCCGATATAGTTGCGGTGTGATACTTGGAGACAGTGGACAGCACCAGCCCC 1360
Qy      2136  oMetSerIleGlnCysIleProValArgCysGlyGluProProSerIleMetAenGlyTy 2156
Db      1361  AGTC-----TGTCAGCTTTGCAGTGCAGGATCTCCCA-----GTTCCAAATGAGGC 1408
Qy      2156  rAlaSerGlySerAenTySerPheGlyAla-----MetValAlaTySe 2171
Db      1409  CCGGTGCAACTGCTCCACACCCCTTCGGTGCTTTAGGTACCAGTCAGTCTGCAGCTTCAC 1468
Qy      2171  rCysAenLysGlyPheTyThrIleLysGlyGluLysLysSerThrCysGluAlaTrpGlyG1 2191
Db      1469  CTCGAATGAAGGCTTGCTCTCTGTTGGAGCAAGTGTCTACAGTCTGTTGGTACTGGAAA 1528
Qy      2191  nTrpSerSerProIleProThrCysHisProValSerCysGlyGluProProLysAvalG1 2211
Db      1529  CTGGAATTTGTTCTCCAGAAATGCCAAGCCATTCCCTGACACACTTTGCTAAGCCCTCA 1588
Qy      2211  uAenGlyPheLeuGluHisThrThrGlyArgIlePheGluSerGluValArgTyGlnCy 2231
Db      1589  GAATGGA----- 1595
Qy      2231  sAenProGlyTyLysSerValGlySerProValPheValCysGlnAlaAenAsgHisTr 2251
Db      1595  ----- 1595
Qy      2251  pHisSerGluSerProLeuMetCysValProLeuAaspCysGlyLysProProIleG1 2271
Db      1596  -----ACATGACCTGTGT-----CAACCTCTTG 1621
Qy      2271  nAenGlyPheMetLysGlyGluAenPheGluValGlySerLysAvalGlnPhePheCysAs 2291
Db      1622  AAGTTCAGCTTATAAA-----TCCACATGTCAATTCATCTGTGA 1660
Qy      2291  nGluGlyTyThrGluLeuValGlyAaspSerSerTrpThrCysGlnLysSerGlyLysTrpAs 2311
Db      1661  CGAGGATATCTTGTCTGGACCAAGAAATTTGATTTGCTGATCGGAGACCTGGAC 1720
Qy      2311  nLysLysSerAenProLysCysMetProAlaLysCysProGlu-----ProProLe 2328
Db      1721  A---GACTCCCCCACTAATGTGTGAAGCCATCAAGTGCACAGACTCTTTTGGCCCCAGAG-- 1775
Qy      2328  uLeuGluAenGlnLeuValLeuLysGluLeuThrThrGluValGlyValValThr----- 2346
Db      1776  -----CAGGCGAGCTGTGATTTGTTCTGACACTCTGTGGAGAAATTCAAATTTGGCTCCACCTG 1831
Qy      2347  -----PheSerCysLysGluGlyHisValLeuGlnGlyProSerValLeuLysCysLeuPr 2365
Db      1832  TCATTTCTCTTGTAACAATGGCTTTTAAGCTGGAGGGGCCCAATANTGTGAATGCACAC 1891
Qy      2365  oSerGlnGlnTrpAenAaspSerPheProValCysLysIleValLeuCysThrProProPr 2385
Db      1892  TTCGGAAGATGTGCTAGCTACTCCACCACTGCAAAGGCATAGCATCACTTCTCTACTCC 1951
Qy      2385  oLeuIleSerPheGlyValProIleProSer----- 2395
Db      1952  A-----GGGTTCGAATGTCCAGCCCTCACCACTCTCTGGGCGAGGAACCATGTA 1999

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QY 2396 -----SerAlaLeuHisPheGlySerThrValLysTyrSerCysValG1 2410
Db 2000 CTGTAGGCATCATCGGAAACCTTTGGTTTAAATACCACTTGTACTTTGGCTGCAAGC 2059
QY 2410 yGlyPhePheLeuArgGlyAsnSerThrLeuCysGlnProAspGlyThrTrpSerSe 2430
Db 2060 TGGATTTCACCTATAGAGAGACGACCTCTGCTGCGAGACCTTCAGAGCAATGACAGC 2119
QY 2430 rProLeuProGluCysValProValGluCysProGlnProGluGluLeuProAsnGlyI1 2450
Db 2120 AGTAACTCCAGCATGACAGCTGTCAATGCTCAGAA----- 2156
QY 2450 eIleaspValGlnGlyLeuAlaIleTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPh 2470
Db 2157 -----CTACATGTTAATAAGCCA----- 2174
QY 2470 eGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyL 2490
Db 2175 ----ATAGCATGAACCTGCTCAACCTC-----TGG----- 2201
QY 2490 sProThrCysLysAlaIleGluCysLeuLysProLysGluLeuLeuAsnGlyLysPheSe 2510
Db 2202 -----GGAAACTTCAG 2212
QY 2510 rTyrThrAspLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLe 2530
Db 2213 T-----TATGATCAATCTGCTCTTTTCCATCTCTAGAGGGCCAGTTACT 2257
QY 2530 uGluGlyProSerAlaLeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSe 2550
Db 2258 TAATGGCTCTGCAAAACAGCATGCTCAAGAGAAATGGCCACTGTCTCACTACCTGCTCCAC 2317
QY 2550 rCysAsnAlaIleHisCysAspSerProGlnProIleGlu-----AsnG1 2565
Db 2318 CTGCCAAGCAGG-ACCATTGACTATCCAGGAGCCCTGACTTACTTTGTGTGAGCGGTGG 2376
QY 2565 yPheValGluGlyAlaAspTyrSerTyrGlyAlaIlelleIleTyrSerCysPheProG1 2585
Db 2377 CTCTTACAATAGCTGTGATAATGGTGGGACGCT-----CCTGG 2415
QY 2585 yPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrpSerSerI1 2605
Db 2416 CTTT-----GCTAAGAAGCGTTTCAGACA-----AAAGATGATGGAA 2455
QY 2605 eProThrCysMetProIleAspCysGlyLeuProHis----- 2618
Db 2456 -----ATGCCCTTGAATCTCTCAGCCACCTAGAACATATGGAGTTTTCACAA 2505
QY 2618 ----- 2618
Db 2506 ACGCTCATTTGACCCGAGTCTTAAGGTTTCCATAAAACCCATCAATCAAGACATGG 2565
QY 2619 -----Ileasp----- 2620
Db 2566 AATTACCTTAGATTAGCTCTGACACGAGCTGTGACCGCTCTGACCAACCCCTGTTTC 2625
QY 2621 ----PheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspAs 2639
Db 2626 CTGAGTTTGGGATTGTGGTACAAATCTCAATCTCRACT----- 2665
QY 2639 pMetMetGluValProTyrValThrProHisProProTyrHisLeuGlyAlaValAlaI 2659
Db 2666 -----ACCACCCCTTCCTGTCCTC----- 2683
QY 2659 sThrTrpGluAsnThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyTh 2679
Db 2684 -----ACCTCTCTCTCTCTGTAACAGCCACAGAGCCAGAGCGCAATG 2730
QY 2679 rMetValSerTyrCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCy 2699
Db 2731 TTTCTGCAAGTAGTCTCTGTGCTTCACTCACCCTGTACTTGAATACCACTG-----AA 2784

QY 2699 sGlnGluAspGlyThrTrpAsn-----GlySerAlaProSerCysIleSerIleG1 2716
Db 2705 CCAAGAGAC-----TGAGCATCTGACTCAAGAAGACCACTGTGGAGAAATAAA 2838
QY 2716 uCysAspLeuProThrAlaProGlu-AsnGlyPheLeuArgPheThrGluThrSerMetG 2736
Db 2839 AATACCTCTTATTATTTTGAATTGAAGGAAGTTTCTCCACTTTGTGGAAAGCAGGTGG 2898
QY 2736 lYserAlaVal---GlnTyrSerCysLys-ProGlyHisIleLeuAlaGlySerAspLeu 2754
Db 2899 CATCTCTAATTGAAGAAATTCCTCTAGCATCTCTGGAGTCTCCAGTGGT----- 2949
QY 2755 ArgLeuCys-LeuGluAsnArgLysTrpSerGlyAla-----SerProAr 2769
Db 2950 -----TGCTGTGATGAGGCTCTTGGACCTCTCTGAGGCTTCCAGAGTCTCT 3003
QY 2769 gCysGluAlaIleSerCysLysLeuProAsnProValMetAsnGlySerIleLysGlySe 2789
Db 3004 GGATGGCACCAGAGCTGCAAGAGCCCAAGATCAAGCTAGAAGGCCACATG-----TC 3057
QY 2789 rAsnTyrThrTyrLeu 2794
Db 3058 ACCGTGGACCTTCCTG 3073

RESULT 21
US-09-023-655-1090
; Sequence 1090, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1090:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g183390
US-09-023-655-1090

Qy	2171	rCysAsnLysGlyPheTyrIleLysGlyGluLysLysSerThrCysGluAlaThrGlyG	2191
Db	1469	CTGCAATGAAGGCTTGCCTCGTGGGAGCAAGTGTGTACAGTGTGCTACTCGAAA	1528
Qy	2191	nTrpSerSerProIleProThrCysHisProValSerCysGlyGluProProLysValG	2211
Db	1529	CTGGAATTCTGCTCTCCGAAGTCCCAAGCCANTTCCCTGCACACCTTGTCTAAGCCCTCA	1588
Qy	2211	uAsnGlyPheLeuGluHisThrThrGlyArgIlePheGluSerGluValArgTyrGlnCy	2231
Db	1589	GAATGGA-----	1595
Qy	2231	sAsnProGlyTyrLysSerValGlySerProValPheValCysGlnAlaAsnArgHisTr	2251
Db	1595	-----	1595
Qy	2251	pHisSerGluSerProLeuMetCysValProLeuAspCysGlyLysProProIleG	2271
Db	1596	---ACAAATGACCTGTGTT-----CAACCTCTTGG	1622
Qy	2271	nAsnGlyPheMetLysGlyGluAsnPheGluValGlySerLysValGlnPhePheCysAs	2291
Db	1622	AAAGTCCAGTTATAA-----TCCACATGTCATTCATCTGTGA	1660
Qy	2291	nGluGlyTyrGluLeuValGlyAspSerSerTrpThrCysGlnLysSerGlyLysTrpAs	2311
Db	1661	CGAGGATATCTTTGTCTGACAGCAAGATGGATTGTACTCGATCGGAGCATGGAC	1720
Qy	2311	nLysLysSerAsnProLysCysMetProAlaLysCysProGlu-----ProProLe	2328
Db	1721	A---GACTCCCAACCAATGTGTGAAGCCATCAAGTCCCAAGACTCTTGTCCCAAG--	1775
Qy	2328	uLeuGluAsnGlnLeuValLeuLysGluLeuThrThrGluValGlyValValThr----	2346
Db	1776	---CAGGCGACCTGGATTGTTCTGCACACTCGTGGAGATTCAATGTGGCTCCACCTG	1831
Qy	2347	---PheSerCysLysGluGlyHisValLeuGlnGlyProSerValLeuLysCysLeuPr	2365
Db	1832	TCATTTCTTTGTAACAATGCTTTAAGCTGGAGGGGCCCAATAATGTGGAATGCACAAC	1891
Qy	2365	oSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeuCysThrProProPr	2385
Db	1892	TTCTGGAAGATGTCAGCTACTCCACCACTGCAAAAGGCATAGCATCTTCTACTCC	1951
Qy	2385	oLeuLeSerPheGlyValProIleProSer-----	2395
Db	1952	A-----GGTGTCAATGTCAGGCCTCACCCCTCACCTCTGGGCGAGAACCATGTA	1999
Qy	2396	---SerAlaLeuHisPheGlySerThrValLysTyrSerCysValG	2410
Db	2000	CTGTAGGCATCATCGGGAACCTTTGGTTTTTAATACCACCTGTGTACTTGGCTGCAACGC	2059
Qy	2410	yGlyPhePheLeuArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSe	2430
Db	2060	TGGATTACACTCATAGGAGACAGCACTCTCAGCTGCAGACCTTCAGGACAATGGACAGC	2119
Qy	2430	rProLeuProGluCysValProValGluCysProGlnProGluIleuLeuProAsnGlyI	2450
Db	2120	AGTAACTCCAGCATGCAGAGCTGTGAATGCTCAGA-----	2156
Qy	2450	eIleAspValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPh	2470
Db	2157	-----CTACATGTTAATAAGCCA-----	2174
Qy	2470	eGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyLy	2490
Db	2175	---ATACCGATGAACCTCTCCAACTC-----TGG-----	2201
Qy	2490	sProThrCysLysAlaIleGluCysLeuLysProLysGluIleLeuAsnGlyLysPheSe	2510
Db	2202	-----GGAACTTCAG	2212
Qy	2510	rTyrThrAspLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLe	2530

RESULT 22
US-09-199

QY 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
DB 1405 TATGACGGCGATCACTGTGAGAGAGACATCGATGAATGTGCAGCAACCCCTGTTGAAT 1464
QY 1357 GlyAlaThrCysLysAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThr 1376
DB 1465 GGGGTCACTGTCAAGATGAATCAACAGATTCAGTGTCTGTGTCCACTGGTTCTCT 1524
QY 1377 GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
DB 1525 GGAACCTCTGTCACTGGACATGATTAATTTGTGAGCCTAATCTCTGCAGAACGGTGCC 1584
QY 1397 ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGln 1416
DB 1585 CAGTGTCAACACCGTGCAGTCACTATTCTCAAGTGTCCCGAGGACTATGAGGGCAAG 1644
QY 1417 ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr 1436
DB 1645 AACTGCTCACCTGAAAGACCACTGCCCGCAGACCCCTGTGAAGTG----- 1692
QY 1437 GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyr 1456
DB 1693 -----ATTGAC-----AGCTGCACAGTGGCC 1713
QY 1457 MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp 1474
DB 1714 ATGGCTTCCACGAC-----ACACCTGAAAGGGGTGGCGGTATATTTCCTCC 1758
QY 1475 AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn 1494
DB 1759 AAC-----GTCTGTGCTCTCTAC 1776
QY 1495 GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTrpHisIleAla 1514
DB 1777 GGGAG-----TGCAAGACTCAGTCGGAGGCAATTC----- 1809
QY 1515 IleThrTrpThrSerAlaAsnGlyIleTrpLysValTyrIleAspGlyLysLeuSerAsp 1534
DB 1810 ---ACCTGTGACTGTAAACAAGGCTTCACGGGAACATATCTGCCATGAAATAATTATGAC 1866
QY 1535 GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyGlyAlaLeuLeuGly 1554
DB 1867 TGTGAGAGCAAC-----CCTGTAGAACGGTGGCACTTGCATCGATGGT 1911
QY 1555 GlnGluGlnAspLysGlyGluGlyPheSerProAlaGluSerPheValGlySerIle 1574
DB 1912 GTCAACTCTACAG-----TGCACTGTGTAGTGACGGCTGGGAGGGGGCTAC 1959
QY 1575 SerGlnLeuAsnLeuTrpAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr 1594
DB 1960 TGTGAACCAATATTAATGACTGCAGCCAGAACCC----- 1995
QY 1595 SerCysProGluGluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGly 1614
DB 1996 ---TGCCACAA----- 2004
QY 1615 IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg--- 1633
DB 2005 -----GGGGGCACGTGTCGGACCTGGTCAATGACTTCTACTGTGACTGTATAAATGGG 2058
QY 1634 LeuGlyGlySerValProHisLeuArgThrAlaSerGluAspLeuLysProGlySerLys 1653
DB 2059 TGGAAAGGAACACCTGCCACTCACGTGACGTGACGTGATGAGGCCACGTGCACACAC 2118
QY 1654 ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr 1671
DB 2119 GTGGCACCCTGTATGATGAGGGGATGCTTTAAG----- 2154
QY 1672 CysLeuAsnGlnGlyGlnTrpThrGlnProLeuProHisCysGluArgIleSerCysGly 1691
DB 2155 TGCATGTGTGCTGGCGCTGGGAAGGAACAACCTGTGAACATAGCCCGAACACAGTAGCTGC 2214

RESULT 23

QY 1692 ValProProLeuGluAsnGlyPheHisSerAlaAspAspPheTyrAlaGlySerThr 1711
DB 2215 CTGCCAACCCCTGCCATATGGG----- 2238
QY 1712 ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThr 1731
DB 2239 -----GGCACATGTGTGGTCAACGGCGAGTCTTTTACGTGGTC 2277
QY 1732 AspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
DB 2278 TGCAGGAGAGCGTGGAGGG-----CCCATCTGTGTCTCAGAAATACC----- 2319
QY 1752 GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
DB 2320 ---AATGACTGCAGCCCTCATCTCCCTGTACACAGCGGCACTGTGTGATGGAGACAAC 2376
QY 1767 SerTyrIleCysSerCysValProTyrThrGlyAsp----- 1779
DB 2377 TGGTACCGGTGCAATGTGCCCGGGTTTGTGTGGCCCGGACTGCAGAAATAAACATCAAT 2436
QY 1780 -----GlyLysAsnCysAlaGluProIle----- 1787
DB 2437 GAATGCCAGTCTTCACTTGTGCTTGTGGAGCGACCTGTGTGATGAGATCAATGGCTAC 2496
QY 1788 LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTyrThrVal 1807
DB 2497 CGGTGTCTGCCCT-----CCAGGCACTGTGTGCCAAG----- 2532
QY 1808 GlyAlaAlaValThrPheSerCysGlnGlyTyrGlnLeuMetGlyValThrLysIle 1827
DB 2533 -----TGCCAGGAA-----GTTTCAGGAGGA 2553
QY 1828 ThrCysLeuGluSerGlyLutTrpAsnHisLeuIlePro----- 1840
DB 2554 CCTTGATCACCATCGGGAGT-----GTGATACCAGATGGGCCCAATGGGATGAT 2604
QY 1841 -----TyrCysLysAlaValSerCysGly 1848
DB 2605 GACTGTATATACCTGCCAGTCCGTGAATGACGGATCGCTCTCAAGGTCTGTGTGGC 2664
QY 1849 ---LysProAlaIleProGluAsnGly-----CysIle 1858
DB 2665 CCTGACCTTGTCTGTCTCCAAAGGGCACAGCGAGTGGCCCGGCGCAGAGTGCATC 2724
QY 1859 -----GluGluLeuAlaPheThrPheGlySerLysValThrTyrArgCysAsnLys 1875
DB 2725 CCCATCTCTGGACGACCGTGTCTC-----GTCCACCCCTGC----- 2760
QY 1876 GlyTyrThrLeuAlaGlyAspLysGluSerSerCysLeu----- 1888
DB 2761 -----ACTGTGTGGCGAGTGTGGTCTTCCAGTCTCCAGCGGTGAAGACAAGTGC 2814
QY 1889 -----AlaAsnSerTrpSerHis----- 1895
DB 2815 ACCTCTGACTCTATTACAGGATAACTGTGCGAACATCACATTTACTTTAAACAGGAG 2874
QY 1896 -----SerProValCysGluProValLysCysSerSerProGluAsnIleAsnAsn 1913
DB 2875 ATGATGTCAACAGGTCTTACTACGGAGCACATTTGCAGTGAATTTGAGGAATTTGAAT--- 2931
QY 1914 GlyLysTyrIleLeuSerGlyLeuThrTyrLeuSerThrAlaSerTyrSerCysAspThr 1933
DB 2932 -----ATTTGAGGAATGTTCCGCTGAATATCAATCTACATCGCTTCGAGCCT 2982
QY 1934 GlyTyrSerLeuGlnGlyProSerIleIleGluCysThrAlaSerGlyIleTrpAspArg 1953
DB 2983 TCCCTTTCAGCAACAATGAATATCATGTGGCCATTTCTGCTGAAGATATACGGGATGAT 3042
QY 1954 AlaProPro 1956
DB 3043 GGGAAACCCG 3051

US-08-400-159-5
 ; Sequence 5, Application US/08400159
 ; Patent No. 5869282
 ; GENERAL INFORMATION:
 ; APPLICANT: Ieh-Horowicz, David
 ; APPLICANT: Henrique, Domingos M.P.
 ; APPLICANT: Lewis, Julian H.
 ; APPLICANT: Myat, Anna M.
 ; APPLICANT: Fleming, Robert J.
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; APPLICANT: Mann, Robert S.
 ; APPLICANT: Gray, Grace B.
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
 ; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/400,159
 ; FILING DATE: 07-MAR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7326-029
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6464 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 371..4027
 ; US-08-400-159-5

Alignment Scores:
 Pred. No.: 7,41e-52 Length: 6464
 Score: 759.00 Matches: 288
 Percent Similarity: 34.13% Conservative: 143
 Best Local Similarity: 22.80% Mismatches: 402
 Query Match: 3.80% Indels: 430
 DB: 2 Gaps: 57

US-09-977-053-4 (1-3571) x US-08-400-159-5 (1-6464)
 QY 834 CysSerAspAlaGlu-----AspIleAspCysArgLeuGluGluAsnLeuThrLys 850
 DB 533 TGGCGGCGCGCCCGGAGACCCCGGAGACCGGAGTGCACCCCGCAGGAGTGTGACATAC 592
 QY 851 ---LysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe---AlaIleGlyPro 868
 DB 593 TTCAAAGTGTGCTCAAG-----GAGTATCAGTCCCGCGTCACGGCGCGGGGGGCC 643
 QY 869 GlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrVal 888
 DB 644 TGCAGCTTGGCTCAGCG----- 661

QY 889 GlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaPro 908
 DB 662 -----TCCACGCTGTATCGGGGGCAACACCTTCAACCTCAAGGCAGCGCGGC 712
 QY 909 LeuSerAspTyrLysIleLysLeuIlePheAsnIle-----ThrAla 922
 DB 713 AACGACCCGAACCGCATCGTCTTTCAGTTTTCCTGCGCGAGGTCTCTATACGTTG 772
 QY 923 SerValProLeuProAspGluArgAsnAspThrLeuGluThrGlu----- 937
 DB 773 CTTTGGAGCGGTGGATTCACAGTATGACACCGTTCACACTGACATATTATTGAAAG 832
 QY 938 -----AsnGlnArgLeuGlnThrLeuGluThrIleThr 950
 DB 833 GCTTCTCCTCGGCGATGATCAACCCGCGAGTGGCAGCGCTGAAGCAGACACG 892
 QY 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTyrSerPhe 965
 DB 893 GCGTTCGCCCATCTTGTGATATCAGATCCGCGTACCTGTGTGATGACTACTATATGGCTTT 952
 QY 966 GlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysAlaSer 985
 DB 953 -----GGCTGTAAT 961
 QY 986 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
 DB 962 AAGTTTTCGCCCGCCAGAGATGACTTCTTTGGA----- 994
 QY 1006 ThrTyrTyrAsnLeuGluHisPheThrCysGlySerCysArgIleGlySerTyrGlnAsp 1025
 DB 995 -----CACTATGCTCTGTAC-----CAGAATGCAACAAACTTGC 1030
 QY 1026 GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr 1041
 DB 1031 ATGGAAGCTGGATGGCGCCCGAATGTAAACAGAGCTATTTGCCGACAGGCTGCAGTCT 1090
 QY 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
 DB 1091 AAGCATGGGTCTTGCAAACTCCAGGTGACTGAGGTGCCAG-----TAC 1135
 QY 1062 SerTyrSerGlyLeuGluThrCysGluSerCys-----ProLeuGlyThrTyr--- 1077
 DB 1136 GGTGCGCAAGGCTG-----TACTGTGATAAGTGCATCCACACCGGATGCGTCCACGCG 1192
 QY 1078 -----GlnProLysPheGlySerArgSerCysLeu 1087
 DB 1193 ATCTGTAATGAGCCCTGGCAGTGCCTCTGTGAGACCACTGGGCGCGCAGCTCTGT--- 1249
 QY 1088 SerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAlaCysGly 1107
 DB 1250 -----GACAAAGATCTCAATTACTGTGG 1273
 QY 1108 Val-----ProCysProGluGly-----LysPheSer 1116
 DB 1274 ACTCATCAGCGGTGTCTCAACCGGGGAACTTTAGCAACACAGCCCTGACAAATATCAG 1333
 QY 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
 DB 1334 TGTTC-----TGCCCTGAGGGGTATTCAGGACCACTGT--- 1369
 QY 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
 DB 1369 ----- 1369
 QY 1157 IleThrGluCysSerSerPheSerSerThrPheSerAlaAlaGluSerValPro 1176
 DB 1369 ----- 1369
 QY 1177 ProAlaSerLeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGlu 1196
 DB 1370 -----GAAATTGCTGAG-----CACGCC 1387
 QY 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216

1308 TCCTCTCGATCCCTGTGTCACACAGGAGCTGTAAAGAGACCTCCCTGGCTTTGAG 1447
 1217 CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236
 1448 TGTGAGTGTCCCGAGGCTGGACCGGCCCCACATGCTCTACAAACATTGATGCTTCT 1507
 1237 ProLeuProCysLeuAsnAsnGlyValCysValAspLeuValGlyGluPheIleCysGlu 1256
 1508 CTAATAACTGTTCACCGGGGACCTCCAGGACCTGTTAAACGGATTTAAGTGTGTG 1567
 1257 CysProSerGlyTyrThrGlyGlnArgCysGluAsnIleAsnGluCysSerSerSer 1276
 1568 TGCCCCCACAGTGGAGCTGGGAAACGTCAGTTAGTCAAAATGAATGTAGGCCAAA 1627
 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
 1628 CCTGTGTAAACGCCAAATCCTGTGAAGATCAATTGCCAGCTACTACTGCCAGCTGTCT 1687
 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
 1688 CCCGCTGGATGGGTGAGAAATGTGACATAAATAATTAATGACTGCTTCGCCAG---TGT 1744
 1317 LeuAsnAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGly 1336
 1745 CAGAAATGAGCTCTCTGTCGGATTTGTTATGTTATGCTGTATCTGTCTCCACTGGC 1804
 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
 1805 TATGAGGCGCATCACTGTGAGAGACATCATGATGTCAGCAGCAACCCCTGTTTGAAT 1864
 1357 GlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThr 1376
 1865 GGGGTCACTGTGACAGAAATCAACAGATTCAGTGTCTGTGTCTCCACTGTTTCTCT 1924
 1377 GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
 1925 GGAACCTCTGTGAGTGGACATGATTAATTTGAGCCTTAATCCCTGCCAGAACGGTGC 1984
 1397 ThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGln 1416
 1985 CAGTGTCAACACCGTCCAGTCACTATTCTGCAAGTGCCTGAGGACTATGAGGGCAAG 2044
 1417 ArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyr 1436
 2045 AACTGCTCACCTGAAGACCACTGCCCGCAGACCCCTGTGAAGTG----- 2092
 1437 GlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrp 1456
 2093 -----ATTGAC-----AGCTGCACAGTGGCC 2113
 1457 MetLysSerSerAspAspMetAsnTyrGlyThrPro-----IleSerTyrAlaValAsp 1474
 2114 ATGGCTTCCACAGC-----ACACCTGAAGGGGTGGCGTATATTCTCTCC 2158
 1475 AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTrpValLeuTyrValAsn 1494
 2159 AAC-----GTCTGTGTCTCTAC 2176
 1495 GlyArgGluLysIleThrAsnCysProSerValAsnAspGlyArgTrpHisIleAla 1514
 2177 GGGAG-----TGCAAGAGTCACTCGGAGGCAAAATTC----- 2209
 1515 IleThrTrpThrSerAlaAsnGlyIleTrpLysValTyrIleAspGlyLysLeuSerAsp 1534
 2210 ---ACCTGTGACTGAACAAAGGCTTACCGGGAACATATCTGCCATGAAATAATTAATGAC 2266
 1535 GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyAlaLeuValLeuGly 1554
 2267 TGTGAGAGCAAC-----CCTGTAGAAACGGTGGCACTTGCATCGATGT 2311
 1555 GlnGluGlnAspLysGlyGluGlyPheSerProAlaGluSerPheValGlySerIle 1574

2312 GTCAACTCCTACAG-----TGCATCTGTAGTGACGCTGGGAGGGGGCCTAC 2359
 1575 SerGlnLeuAsnLeuTrpAspTyrValLeuSerProGlnGlnValLysSerLeuAlaThr 1594
 2360 TGTGAACCAATATTAAATGACTGCAGCCAGAACCCC----- 2395
 1595 SerCysProGluGluLeuSerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGly 1614
 2396 ---TGCCACAAT----- 2404
 1615 IleValGlyLysValLysIleAspSerLysSerIlePheCysSerAspCysProArg--- 1633
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 1654 ValAsnLeuPheCysAspProGly-----PheGlnLeuValGlyAsnProValGlnTyr 1671
 2519 GGTGGCACCTGCTATGATGAGGGGGATGCTTTTAAG----- 2554
 1672 CysLeuAsnGlnGlyGlnTrpThrGlnProLeuProHisCysGluArgIleSerCysGly 1691
 2555 TGCATGTGCTCTGGCGCTGGGAAGACACACCTGTAAACATAGCCGAAACAGTAGCTGC 2614
 1692 ValProProLeuGluAsnGlyPheHisSerAlaAspPheTyrAlaGlySerThr 1711
 2615 CTGCCAACCCCTGCCATAATGG----- 2638
 1712 ValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerArgMetPheCysThr 1731
 2639 -----GGCACATGTGTGGTCAACGGCGAGTCTTTTACGTGGTGC 2677
 1732 AspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspValAspGluCysAlaVal 1751
 2678 TGCAAGGAAGGCTGGGAGGG-----CCCATCTGTGCTCAGAATACC----- 2719
 1752 GlySerAspCysSerGluHis-----AlaSerCysLeuAsnValAspGly 1766
 2720 ---AATGACTGAGCCCTCATCTCTTACACAGCGGACCTGTGTGGATGGAGACAAC 2776
 1767 SerTyrIleCysSerCysValProProTyrThrGlyAsp----- 1779
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 1788 LysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTyrThrVal 1807
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 2933 -----TGCCAGGAA-----GTTTCAGGGAGA 2953
 1828 ThrCysLysLeuGluSerGlyGluTrpAsnHisLeuIlePro----- 1840
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 1841 -----TyrCysLysAlaValSerCysGly 1848
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QY 1876 GlyTyrThrLeuAlaGlyAspLysGluSerSerCysLeu----- 1888
DB 3161 -----ACTGGTGTGGCGAGTGTGGTCTTCAGTCTCCAGCGGTGAAGACAAAGATGC 3214
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QY 1896 -----SerProProValCysGluProValLysCysSerProGluAsnLeuAsn 1913
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DB 3383 TCCCTTCAGCGAACAATGAATACATGTGGCCATTCTGCTGAGATATACGGGATGAT 3442
QY 1954 AlaProPro 1956
DB 3443 GCGAACCOCG 3451

RESULT 24

US-08-611-729A-5
Sequence 5, Application US/08611729A

Patent No. 6004924

GENERAL INFORMATION:

APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE

TITLE OF INVENTION: SERATE GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

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STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/611,729A

FILING DATE: 06-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mierock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-037

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8664

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 6464 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS
LOCATION: 371..4024
US-08-611-729A-5

Alignment Scores:

Score: 7,41e-52 Length: 6464
Pred. No.: 759,00 Matches: 288
Percent Similarity: 34.13% Conservative: 143
Best Local Similarity: 22.80% Mismatches: 402
Query Match: 3.80% Indels: 430
DB: 3 Gaps: 57

US-09-977-053-4 (1-3571) x US-08-611-729A-5 (1-6464)

QY 834 CysSerAspAlaGlu-----AspIleAspCysArgLeuGluAsnLeuThrLys 850
DB 533 TGGCGCGCGCCCGGAACCCCGGAGACCGCAAGTGCACCCCGCAGAGTGTGACACATAC 592
QY 851 ---LysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPhe---AlaIleGlyPro 868
DB 593 TTCAAAGTGTGCTCAAG-----GAGTATCAGTCCCGGTCCACGCGCGGGGGGCC 643
QY 869 GlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrVal 888
DB 644 TGCAGCTTCGGCTCAGGG----- 661
QY 889 GlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaPro 908
DB 662 -----TCCAGCGCTGTCATCGGGGCAACACCTTCAACCTCAAGGCCCGCGCGC 712
QY 909 LeuSerAspTyrLysIleLysLeuIlePheAsnIle-----ThrAla 922
DB 713 AACGCCCGAACCGCATCGCTGCTGCTTTCAGTTTCGCTGCGCGAGTGCCTATACGTTG 772
QY 923 SerValProLeuProAspGluArgAsnAspThrLeuGluTrpGlu----- 937
DB 773 CTGTGGAGGCGTGGGATTCAGTAATAGACACCGTTCAACCTGACAGTATTATTGAAAG 832
QY 938 -----AsnGlnArgLeuLeuGlnThrLeuGluThrIleThr 950
DB 833 GTTCTCAGTGGGCGATGATCAACCCCGCGCGAGTGGCAGACGCTGAACAGACAGACG 892
QY 951 AsnLysLeuLys-----ArgThrLeuAsnLysAspProMetTyrSerPhe 965
DB 893 GGGCTTCCCGCCCTTGTAGTATCAGATCGCGGTGACCTGTGATGACTACTACTATGGCTT 952
QY 966 GlnLeuAlaSerGluIleLeuLeuAlaAspSerAsnSerLeuGluThrLysLysAlaSer 985
DB 953 -----GGCTGTAAT 961
QY 986 ProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGly 1005
DB 962 AGTTTCTCGCGCCCGCAGAGATGACTTCTTTGGA----- 994
QY 1006 ThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAsp 1025
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QY 1026 GluGluGlyGlnLeu-----GluCysLys-----LeuCysProSerGlyMetTyrThr 1041
DB 1031 ATGGAAGGCTGGATGGGCGCCCGAATGTAAACAGAGCTATTTGCCGACAGGTGCGAGTCT 1090
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QY 1078 -----GlnProLysPheGlySerArgSerCysLeu 1087
DB 1193 ATCTGTAATGAGCCCTGGCAGTGCCTCTGTGAGACCAACTGGGCGCGCGCTGT--- 1249

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1274 ACTCATGACCGGTCTCAACGGGGAACCTTGTAGCAACACAGGCCCTGACAAATATACG 1333
QY 1117 ArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGly 1136
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1334 TGTTC-----TGCCCTGAGGGGTATTCAGGACCCCAACTGT--- 1369
QY 1137 LysAlaPheCysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSer 1156
DB : : : : :
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QY 1157 IleThrGluCysSerSerPheSerThrPheSerAlaAlaGluSerValPro 1176
DB : : : : :
1369 ----- 1369
QY 1177 ProAlaSerLeuGlyHisIleLysIysArgHisGluIleSerSerGlnValPheHisGlu 1196
DB : : : : :
1370 -----GAAATTTGCTGAG-----CAGGCC 1387
QY 1197 CysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrVal 1216
DB : : : : :
1388 TGCCTCTCTGATCCCTGTCAACACAGGACGCTGTAAGGAGACCTCCCTGGGCTTTGAG 1447
QY 1217 CysLeuCysProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSer 1236
DB : : : : :
1448 TGTGAGTGTCCCGAGCTGGACCGCCGCCACATGCTCTACAAACATGATGACTGTCT 1507
QY 1237 ProLeuProCysLeuAsnAsnGlyValCysLysAspLeuValGlyPheIleCysGlu 1256
DB : : : : :
1508 CTAATAACTGTTCACAGGGGGACCTGCCAGGACCTGTTAAACGATTAAGTGTGNG 1567
QY 1257 CysProSerGlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSer 1276
DB : : : : :
1568 TGCCCCCAGCAGTGGGAAAACGTCGCCAGTTAGATGCAAAATGAATGTGAGGCCAAA 1627
QY 1277 ProCysLeuAsnLysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysVal 1296
DB : : : : :
1628 CTTGTGTAAACGCCAAATCTGTGAAGATCTCATGTCAGCTACTACTGCACTGTCTT 1687
QY 1297 LysGlyPheValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCys 1316
DB : : : : :
1688 CCGGCTGGTGGTCAAGATTTGCACATAAATATTAATGACTGCTTGGCCAG--TGT 1744
QY 1317 LeuAsnAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGly 1336
DB : : : : :
1745 CAGAAATGACGCTCTCTGTCGGATTTGGTTAATGTTATCGCTGTATCTGTCCACTGCTGC 1804
QY 1337 PheLeuGlyThrArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsn 1356
DB : : : : :
1805 TATGACGGCGATCACTGTGAGAGACATCTGATGAATGTGCCAGCAACCCCTGTTTGAAT 1864
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DB : : : : :
1865 GGGGGTCACTGTCAAGATGAATCAACAGATTCACGTGTCTGTCTCCCACTGGTTCTCT 1924
QY 1377 GlySerHisCysGluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAla 1396
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DB : : : : :
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DB : : : : :
2093 -----ATTGAC-----AGCTGCACAGTGGCC 2113
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QY 1535 GlyGlyAlaGlyLeuSerValGlyLeuProIleProGlyGlyAlaLeuValLeuGly 1554
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2312 GTCAACTCTACAG-----TGCATCTGTGTAGTACCGCTGGGAGGGGCTAC 2359
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DB : : : : :
2360 TGTGAACCAATATTATGACTGACCCAGAACCC----- 2395
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DB : : : : :
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RESULT 25

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PCT-US91-05059-1
; Sequence 1, Application PC/TUS9105059
; GENERAL INFORMATION:
; APPLICANT: Regents of the Board of the, University of
; APPLICANT: Oklahoma
; TITLE OF INVENTION: Functionally Active Selectin-Derived
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Kilpatrick & Cody
; STREET: 100 Peachtree Street, Suite 3100
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/05059
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/320408
; FILING DATE: 08-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554199
; FILING DATE: 17-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR110CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-572-6508
; TELEFAX: 404-572-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3144 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
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; FEATURE:
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; LOCATION: 3124..3130
; OTHER INFORMATION: /note= "Potential polyadenylation
; OTHER INFORMATION: signal"
; PCT-US91-05059-1

Alignment Scores:
Pred. No.: 2,26e-52 Length: 3144
Score: 758.50 Matches: 272
Percent Similarity: 33.42% Conservative: 124
Best Local Similarity: 22.95% Mismatches: 352
Query Match: 3.80% Indels: 438
DB: 5 Gaps: 49

US-09-977-053-4 (1-3571) x PCT-US91-05059-1 (1-3144)

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Qy 1743 CysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeu 1762
Db 525 TGCCAGGACATG-----TCTTCGACGAAACCAAGAGAGTGCCTC 563
Qy 1763 AsnValAspGlySerTyrIleCysSerCysValProTyrThrGlyAspGly-----1780
Db 564 GAGACCATCGGAACCTACACCTGCTCTCTGTTACCTGGATTCTATGGCCAGAAATGTGA 623
Qy 1781 -----LysAsnCysAlaGlu 1785
Db 624 TAGCTGAGAGAGTGTGGAGAACTTGAGCTCCCTCAACACGCTGCTCATGAACCTGACGCCAC 683
Qy 1786 ProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGluIleTyr 1805
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Db 699 TCTTTAACTCCGAGTCTCCACTGACGAGGTACCAAGTAAATGGGCCAGC 758
Qy 1826 LysIleThrCysLeuGluSerGlyGluThrPheHisLeuIleProTyrCysLysAlaVal 1845
Db 759 AAGCTGGAATGCTTGCTTCTGGAATCTGGACAATAAGCCCTCCACAGTGTATTAGCTGCC 818
Qy 1846 SerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGluLeuAlaPheThrPhe 1865
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Qy 1866 GlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAlaGlyAspLysGluSer 1885
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Qy 1982 ArgAsnThrValThrTyrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThrIle 2001
Db 1077 GCCTCCAGCTGCAATTTGAGTGCCAGCCGCTACAGAGTGAGGGGCTTGACATGCTC 1136
Qy 2002 GluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnGlnCysLeuAlaValSerCys 2021
Db 1137 CGCTGCAATGACTCTGGACACTGGTCTGCACCTTGCCCAACCTGTGAGGCTATTTCGTGT 1196
Qy 2022 Asp-----GluProIleValAspHisAlaSerProGluThrAlaHisArgLeuPhe 2039
Db 1197 GAGCGCTGGAGAGTCTCTGTC-----CACGGAAGCATGGAT----- 1232
Qy 2040 GlyAspIleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeu 2059
Db 1233 -----TGCTCT----- 1238
Qy 2060 LeuCysAsnAlaGlnGlyLysTrpValProProGluGlyGlnAspMetProArgCysIle 2079
Db 1238 ----- 1238
Qy 2080 AlaHisPheCysGluLysProProSerValSerTyrSerIleLeuGluSerValSerLys 2099
Db 1239 -----CATCTCTG----- 1247
Qy 2100 AlaLysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsn 2119
Db 1248 AGAGCGTTTCAGTATGACACCACTGATGCTTCCGCTGTGCTGGAAGTTTCATGCTGAGA 1307
Qy 2120 ThrSerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsn---ProSerProMetSer 2138
Db 1308 GGAGCCGATATAGTTGGTGTGATTAACCTGGACAGCTGGACAGCACACGCCCCAGTCT--- 1364
Qy 2139 IleGlnCysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSer 2158
Db 1365 -----TGCAAGCTTTTGAGTGCAGGATCTCCCA---GTTCCAAATGAGCCCGGGTG 1415
Qy 2159 GlySerAsnTyrSerPheGlyAla-----MetValAlaTyrSerCysAsn 2173
Db 2173 ----- 2173

Db 1416 AACTGCTCCACCCCTTGGTGCCTTTAGGTACCAAGTCAGTCTGCAGCTTCACCTGCAAT 1475
Qy 2174 LysGlyPheTyrIleLysGlyGluLysLysSerThrCysGluAlaThrGlyGlnTrpSer 2193
Db 1476 GAAGCTTTGCTCTGCTGGGGAAGAGTGTGTACAGTGTCTGGCTACTGGAACCTGGAAT 1535
Qy 2194 SerProIleProThrCysHisProValSerCysGlyGluProProLysValGluAsnGly 2213
Db 1536 TCTGTCTCTCCAGAAATGCCAAGCCATTCCCTGCACACCTTGTCTAAGCCCTCAGAATGA 1595
Qy 2214 PheLeuGluHisThrThrGlyArgIlePheGluSerGluValArgTyrGlnCysAsnPro 2233
Db 1595 ----- 1595
Qy 2234 GlyTyrLysSerValGlySerProValPheValCysGlnAlaAsnArgHisTrpHisSer 2253
Db 1595 ----- 1595
Qy 2254 GluSerProLeuMetCysValProLeuAspCysGlyLysProProProIleGlnAsnGly 2273
Db 1596 -----ACAATGACCTGTGTT-----CAACCTCTTGGAACTTCC 1628
Qy 2274 PheMetLysGlyGluAsnPheGluValGlySerLysValGlnPhePheCysAsnGluGly 2293
Db 1629 AGTTATAAA-----TCCACATGTCAATTCATCTGTGACGAGGGA 1667
Qy 2294 TyrGluLeuValGlyAspSerSerTrpThrCysGlnLysSerGlyLysTrpAsnLysLys 2313
Db 1668 TATTCTTTGTCTGGACCAAGAAAGATGGATTGTATCGATCGGACCTGGACA---GAC 1724
Qy 2314 SerAsnProLysCysMetProAlaLysCysProGlu-----ProProLeuLeuGlu 2330
Db 1725 TCCCAACCAATGTGTGAAGCCATCAGTGTCCAGAACTCTTTGCCCCAGAG-----CAG 1778
Qy 2331 AsnGlnLeuValLeuLysGluLeuThrThrGluValGlyValValThr-----Phe 2347
Db 1779 GCGAGCTGGATGTCTGACACTCGTGAGAAATCAATGTGGTCTCCACCTGTCTCATTTTC 1838
Qy 2348 SerCysLysGluGlyHisValLeuGlnGlyProSerValLeuLysCysLeuProSerGln 2367
Db 1839 TCTTTGTAACAATGGCTTTTAAGCTGGAGGGGCCAATAATGTGGAATGCACTTCTGGA 1898
Qy 2368 GlnTrpAsnAspSerPheProValCysLysIleValLeuCysThrProProLeuIle 2387
Db 1899 AGATGCTCAGTACTCCACCACTGCAAGCATAGCATCATCTTCTACTCCA----- 1952
Qy 2388 SerPheGlyValProIleProSer----- 2395
Db 1953 -----GGGTTGCAATGTCCAGCCCTCACCACCTCTCGGCGAGGAACCATGTACTGTAGG 2006
Qy 2396 -----SerAlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGlyPhe 2412
Db 2007 CATCATCCGGGAACCTTTGGTTTTTAATACCACTGTGTACTTTGGCTGCAACCGCTGGATTC 2066
Qy 2413 PheLeuArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerProLeu 2432
Db 2067 ACACATATAGGAGACAGCACTCTCAGTGTCCAGACCTTCAGGACAAATGACAGCAGTAAC 2126
Qy 2433 ProGluCysValProValGluCysProGlnProGluGluIleProAsnGlyIleIleAsp 2452
Db 2127 CCAGCATGCAGAGCTGTGAATGCTCAGAA----- 2156
Qy 2453 ValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluLeu 2472
Db 2157 -----CTACATGTTTAATAAGCCA-----ATA 2177
Qy 2473 ValGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyLysProThr 2492
Db 2178 GCGATGAACCTGCTCCACCTC-----TGG----- 2201
Qy 2493 CysLysAlaIleGluCysLeuLysProLysGluIleLeuAsnGlyLysPheSerTyrThr 2512
Db 2202 -----GGAAACTTTCAGT----- 2213

2513	AspLeuHis	TyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGly	2533
2214	-----	-TATGGATCAATCTGCTCTCTTCCATTTGTCTAGAGGCGCATTTACTTTAATGGC	2264
2533	ProSerAla	LeuThrCysLeuGluThrGlyAspTyrAspValAspAlaProSerCysAsn	2552
2265	CTGCGCAACACAGCATGCCAAGAGATGGCCACTGGTCAACTACCGTGCACACTGCCAA	2324	
2553	AlaIleHis	CysAspSerProGlnProIleGlu-----	AsnGlyPheVal 2567
2325	GCAGG-ACCATTGACTATCCAGGAAGCCCTGACTTACTTTGGTGGAGCGGTGCTTCTAC	2383	
2568	GluGlyAla	AspTyrSerTyrGlyAlaIleIleIleTyrSerCysPheProGlyPheGln	2587
2384	AATAGTCTGTGATAATGGGTGGACGCT-----	CCTGGCTTT--- 2419	
2588	ValAlaGlyHis	AlaMetGlnThrCysGluGluSerGlyTyrPheSerSerSerIleProThr	2607
2420	---GCTAAGAAACGGTTTCAGACA-----	AAAAGATGATGGCAA----- 2455	
2608	CysMetProIle	AspCysGlyLeuProHis-----	2618
2456	---ATGCCCTTGGATCTCTACAGCCACCTAGGAACATATGGAGTTT	TACAAAACGCTGC 2512	
2618	-----	-----	2618
2513	ATTGACCGAGTCCTTAGGTTTCCATAAACACCATGATCAAGACATGGAAATTACC	2572	
2619	-----	-----IleAsp-----	Phe 2621
2573	TTAGATTAGCTCGGACAGCCCTGTTGGACCGCTCTGGACCAACCCGTGTTCTCGAGTT	2632	
2622	GlyAspCysThr	IleuLysAspAspGlnGlyTyrPheGluGlnGluAspAspMetMet	2641
2633	TGGGATGTGGTACAAATCTCAAAATCTCAACCT-----	2665	
2642	GluValPro	TyrValThrProHisProProTyrHisLeuGlyAlaValAlaLysThrTyr	2661
2666	-----	-----ACCACCCCTCTCTGTGCC-----	2683
2662	GluAsnThr	LysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetVal	2681
2684	-----	-----ACCTCTTCTCTTCTGTAACACAGCCACAGAGCCAGGACCAAAATGTTTCTGCG	2737
2682	SerTyrThr	CysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCysGlnGlu	2701
2738	AGTAGTCTCTGTCTTGTGACTCACTGTTACTTTGAAATACCACTG-----	-----AACCAAGA 2791	
2702	AspGlyThr	TrpAsn-----GlySerAlaProSerCysIleSerIleGluCysAsp	2718
2792	GAC-----	-----TGGAGCATCTGACTCACAGAAGACCCAGCTGTGGAGAAATAAAATACCT	2845
2719	LeuProThr	AlaProGlu-AsnGlyPheLeuArgPheThrGluThrSerMetGlySerAl	2738
2846	CTTTATTTTGTGATGAGGAAGGTTTCTCCACTTTGTGGAAAGCAGGTGGCATCTCT	2905	
2738	aVal---Gln	TyrSerCysLys-ProGlyHisIleLeuAlaGlySerAspLeuArgLeu	2757
2906	AATTGGAAGAAATCTCTGTAGTACTTCTTGGAGTCTCCAGTGCT-----	-----T 2950	
2757	ys-Leu	GluAsnArgIleTyrSerGlyAla-----	SerProArgCysGlu 2771
2951	GCTGTGTGATGAGCCCTCTTGGACCTCTGCTCTCTGAGGCTTCCAGAGAGTCTCT	TGGATGGC 3010	
2772	AlaIleSer	CysLysLysProAsnProValMetAsnGlySerIleIleLysGlySerAsnTyr	2791
3011	ACCAGAGGCTGCAGAGGCCAAGATCAACACTAGAGGCCACATG-----	-----TCACCGTGG 3064	
2792	ThrTyrLeu	2794	
3065	ACCTTCTG	3073	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 9, 2004, 07:07:47 ; Search time 2398.04 Seconds
(without alignments)
6326.134 Million cell updates/sec

Title: US-09-977-053-4

Perfect score: 19973

Sequence: 1 MWPLRAFCWGLALVSGWAT.....CHCLSSWTGHCNCRKRTGCF 3571

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO spool_p/US09977053/runat_06052004_075942_18178/app_query.fasta_1.5710
-DB=N Geneseq 26Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosu62 -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=25
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09977053 @CGN 1.1 4042 @runat_06052004_075942_18178 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq_29Jan04.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19958	99.9	10878	6	AAD32025 Human C3b
2	19905.5	99.7	11546	8	AAD57253 Human C3b
3	19616	98.2	11152	6	ABT08491 Human nov
4	19566	98.0	11158	6	ABT08490 Human nov
5	16707	83.6	11230	6	AAD32026 Mouse C3b
6	9400	47.1	5421	4	AAK94920 Human ful
7	8427	42.2	6153	6	ABA03880 Human POL
8	8400.5	42.1	6152	7	ABX56476 cDNA enco

9	8391	42.0	6153	9	AAD58963	Human com
10	7537	37.7	5124	4	AAH16667	Human cDN
11	7471	37.4	3991	6	ABK13101	Human REP
12	6950	34.8	4088	4	AAK94919	Human ful
13	6452	32.3	3804	4	AAS28968	CDNA enco
14	6452	32.3	3804	4	AAS26868	Human cDN
15	6452	32.3	3804	4	ABA06548	Human cDN
16	6452	32.3	3804	4	AAS31587	CDNA enco
17	6452	32.3	3804	4	ABK43685	DNA enco
18	6452	32.3	3804	6	ABT07803	Novel hum
19	6452	32.3	3804	6	ABV83885	Human pol
20	6044	31.7	3696	4	AAH75787	Receptor
21	6044	31.7	3706	4	ABN93421	Human gen
22	5485	27.5	3448	6	AB211152	Human pol
23	5012	25.1	2929	4	AAS03887	Human sec
24	4971	24.9	2637	7	ABX34482	Human mdd
25	4930	24.7	3262	6	ABE51807	Human mdd
26	4730	23.7	3128	6	ABK54124	CDNA enco
27	4674	23.4	2575	6	ABQ72635	Human MDD
28	4058	20.3	2437	6	ABK94974	Human nov
29	4045	20.3	2444	6	ABK94928	Human nov
30	4039.5	20.2	2450	6	ABT10760	Human bre
31	4039.5	20.2	2450	9	ADE73131	Human cel
32	4026.5	20.2	2539	3	AACT77331	Human ORF
33	3596	18.0	1952	6	ABA03879	Human POL
34	3580	17.9	1952	7	ABX56475	cDNA enco
35	3547	17.8	1952	6	ABD58962	Human com
36	3133	15.7	2084	9	ABK35664	CDNA sequ
37	3073	15.4	1969	4	AAH16567	Human cDN
38	2892	14.5	1880	4	AAH48345	Human gra
39	2831	14.2	1765	4	AAK94846	Human ful
40	2758	13.8	1493	4	AAS28991	cDNA enco
41	2758	13.8	1493	4	AAS26940	Human cDN
42	2758	13.8	1493	4	ABA06730	Human cDN
43	2758	13.8	1493	4	AAS31645	CDNA enco
44	2758	13.8	1493	6	ABK43966	DNA enco
45	2758	13.8	1493	6	ABT07826	Novel hum
46	2758	13.8	1493	6	ABV84067	Human pol
47	2638	13.2	1652	9	ADC35133	Human bre
48	2622	13.1	1747	2	AZ422234	Human nov
49	2506	12.5	1357	6	ABQ72495	Human MDD
50	2479	12.4	1696	6	ABK54146	CDNA enco
51	2374	11.9	1760	3	AAS294659	Human EGF
52	2305	11.5	1709	6	ABA03878	Human POL
53	2305	11.5	1709	7	ABX56474	cDNA enco
54	2290	11.5	1709	9	AAD58961	Human com
55	2284	11.4	1766	4	ABN93419	Human gen
56	2248	11.3	1377	4	ABN93416	Human gen
57	2247	11.3	1640	2	AAT12162	Partial p
58	2037	10.2	9038	5	AAS64290	DNA enco
59	2032	10.2	7313	4	AAI58380	Human pol
60	2032	10.2	7313	8	ADB48349	Novel hum
61	2032	10.2	7385	7	ABX34686	Human mdd
62	2032	10.2	7821	5	AAS64474	DNA enco
63	2027	10.1	6951	1	AAH91477	CR1 prote
64	2027	10.1	6951	2	AAS38150	Human C3b
65	2027	10.1	6951	6	ABK84738	Human cDN
66	2027	10.1	6951	6	ABA91636	Human C3b
67	2027	10.1	6951	9	ADB85074	Farnesyl
68	2016	10.1	6951	2	AAQ11642	Entire hu
69	2006	10.0	7028	4	ABA09026	Human CR1
70	2006	10.0	7028	4	AAI60166	Human pol
71	1977	9.9	1408	6	ABK35663	cDNA sequ
72	1977	9.9	6951	2	AAQ41867	CR1 codin
73	1852	9.3	12525	6	AAD33319	Rat C3b/C
74	1825.5	9.1	10433	6	AAD33320	Human C3b
75	1825.5	9.1	10673	6	AAD33318	Human C3b
76	1822	9.1	10136	6	ABG64375	Human cub
77	1606.5	8.0	5420	2	AAS38151	Human C3b
78	1606.5	8.0	5420	6	ABL65862	Lung canc
79	1606.5	8.0	5420	6	ABA91637	Human C3b
80	1604.5	8.0	5420	2	AAQ11643	Partial h
81	1498	7.5	1892	4	AAS26857	Human cDN

QY 241 GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaLeu 260
DB 731 GAGCACTGTTACCTGCTACACAGTTTGAAGAAATTTGAGGCTTTAGCTGCCCGGCAATG 790
QY 261 HisGluAspLeuProSerGlySerPheIleGlnAspMetValHisCysSerTyrLeu 280
DB 791 CATGAAGATCTACTTCTGGGAGTTTATTCAAGATGATATGTTCCACTGCTCTTATCTT 850
QY 281 CysAspGluGlyLysAspCysAspArgMetGlySerCysLysCysGlyThrHisThr 300
DB 851 TGTGATGAAGCAAGCACTGCTGTCGACCGAATGGGAAGCTGCAAAATGGGGACACACACA 910
QY 301 GlyHisPheGluCysIleCysGluLysGlyTyrGlyGlySerGlyLeuGlnTyrGluCys 320
DB 911 GGCCATTTTGGTGGCATCTGTGAAAAGGGGTATTACGGGAAGGTCTGCGAGTATGAATGC 970
QY 321 ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys 340
DB 971 ACAGCTTGGCCATCGGGGACATCAAACTTGAGGGCTCACAGAGGGAATCAGCAGTTGC 1030
QY 341 IleProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAspCys 360
DB 1031 ATTCCATGCTCTGATGAATAATCACCTCTCCACCTTGGAGGACATCCCTCTGAAGACTGT 1090
QY 361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
DB 1091 GTCTGCAGAGAGGGATACAGGGCATCTGGCCACAGCTGTGAACTGTGTCCACTGCCCTGCC 1150
QY 381 LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla 400
DB 1151 CTGAAGCTTCCCGAATAATGTTACTTTATTCAAAACACTTGGCAACACCACTTCAATGCA 1210
QY 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuCys 420
DB 1211 GCCTGTGGGGTCCGATGTACCCCTGGATTTGATCTTGTGGGAAGCAGCATCTTATGT 1270
QY 421 LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
DB 1271 CTACCCAAATGGTTGTGTGCTCGGTTCAGAGAGACTCTGCAAGAGTAAGAAATGTCTCAT 1330
QY 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
DB 1331 CTCGGCCAGCCGAAACATGGCCACATCAGCTGTTCTACAAGGGAATGTTATATPAGACA 1390
QY 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
DB 1391 ACATGTTTGGTTCCTGTGATGAAGGTAACAGACTAGAGGCAAGTATAGCTTACTTGT 1450
QY 481 GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr 500
DB 1451 CAAGGAACACGCCAGTGGGATGGGCCAGAACCCCGGTGTGTGGAGCGCCACTGTTCACCC 1510
QY 501 PheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys 520
DB 1511 TTTCAGATGCCCAAGATATCATCATATATCCCCCAACTGTGGCAAGCGCCAGCCCAA 1570
QY 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
DB 1571 TTTGGACGATCTGCTATGTAAGTTCGCGCCCAAGGGTTCATTTTATCTGGAGTCAAGAA 1630
QY 541 MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLys 560
DB 1631 ATGCTGAGATGTACCACTTCTGGAAAATGGAATGTGCGAGTTTCAGGCGAGCTGTGTGAAA 1690
QY 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln 580
DB 1691 GACGTGGAGCTCTCTCAATCAACTGTCTTAAGGACATAGAGGCTAAGACTCTGGGAACAG 1750
QY 581 GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys 600
DB 1751 CAAGATTTCTGCCAATGTCTACCTGGCAGATTTCCAAACAGCTAAAGACAACTCTGTGTGAAAAG 1810

QY 601 ValSerValHisValHisProAlaPheThrProTyrLeuPheProIleGlyAspVal 620
DB 1811 GTGTGAGTCCAGCTTATCCAGCTTTCACCCACCTTACCTTTCCCGAGTTGGAGATGTT 1870
QY 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
DB 1871 GCTATCGTATACACGGCAACTGACCTATCCGGCAACCAAGCCAGCTGCATTTCCATATC 1930
QY 641 LysValIleAspAlaGluProValIleAspTrpCysArgSerProProValGln 660
DB 1931 AAGGTTATTATGTCAGAACCACTGTTCATAGACTGGTGCAGATCTCCACCTCCCGTCAG 1990
QY 661 ValSerGluLysValHisAlaSerTyrAspGluProGlnPheSerAspAsnSerGly 680
DB 1991 GTCTCGGAGAGGTACATGTCGCCAAGCTGGGTGAGCTCAGTTCTCAGACACTCAGGG 2050
QY 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
DB 2051 GCTGAATTTGGTCAATTACCAAGAGTCAACACAGGAGACCTTTTCCCTCAAGGGGAGACT 2110
QY 701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
DB 2111 ATAGTACAGTATACAGCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATT 2170
QY 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
DB 2171 GTCATAAAGGTTCTCCCTGTGAATTTCCATTCACACTGTAAATGGGGATTTTATATGC 2230
QY 741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
DB 2231 ACTCCAGATAATACTGGAGTCAACTGTATACATTAACTTGTGGAGGGCTATGATTTTACA 2290
QY 761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThrTyr 780
DB 2291 GAAGGGTCTACTGACAGTATATTGTGCTTATGAAGATGCGCTGTGGAACCAACATAT 2350
QY 781 ThrThrGlnTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
DB 2351 ACCACTGAATGGCGAGACTGTGCCAAAACGTTTGTCTAACCAAGGGTTCAAGTCTTTT 2410
QY 801 GluMetPheTyrLysAlaLysArgCysAspAspThrAspLeuMetLysLysPheSerGlu 820
DB 2411 GAGATGTTCTACAAAGCAGCTCGTTGTGATGACACAGACTCTGATGAAGAGTTTCTGAA 2470
QY 821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
DB 2471 GCATTTTGAGACGACCTCGGAAAAATGCTCCCATCATTTTGTAGTGTGACAGAGACATT 2530
QY 841 AspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
DB 2531 GACTGCGAGACTGGAGGAGAACCTTGACCAAAAATATTTCCTAGGAATATATATGACTAT 2590
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DB 2591 GAAAAATGGCTTTGCAATTTGGACCAAGCTGGCTGGGTGCAGCTAATAGGCTGATCTCT 2650
QY 881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 900
DB 2651 TACGATGACTTCTCGGACACTGTGCAAGAAACAGCCCAAGCATCGGCAATGCCAAGTCC 2710
QY 901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920
DB 2711 TCACGGAATTAAGAGTGGCCCTTATCTGACTATATAAATTAAGTTAATTTTAAACATC 2770
QY 921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGlnGln 940
DB 2771 ACAGCTAGTGTGCCATTACCCGATGAAGAAATGATACCTTGAATGGAAAAATCAGCAA 2830
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QY 961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuAlaAspSerAsnSerLeuGlu 980

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QY 3301 ThrProLeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArgThrGlyProAsn 3320
DB 9911 ACTCCATTGAATTTCTCAATGGGAAGCTGACATTTGAAACACAGGACGCTGGACCCAC 9970
QY 3321 ValValTyrSerCysAsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThr 3340
DB 9971 GTGCTATATTCTGCAACAGAGGCTACAGTCTTGAAGGGCCATCTGAGGCGACACTGCACA 10030
QY 3341 GluAsnGlyThrTTPSerHisProValProLeuCysLysProAsnProCysProValPro 3360
DB 10031 GAAATGGAACCTGGAGGCCACCCAGTCCCTCTCTGCAAAACAAATCATGCCCTGTCTCT 10090
QY 3361 PheValIleProGluAsnAlaLeuLeuSerGluLysGluPheTyrValAspGlnAsnVal 3380
DB 10091 TTTGTGATTTCCCGAATGCTGCTGCTGCTGAAAGGAGTTTTATGTTCATCAGAAATGTG 10150
QY 3381 SerIleLysCysArgGluGlyPheLeuLeuGlnGlyHisGlyLleIleThrCysAsnPro 3400
DB 10151 TCCATCAAAATGTAGGAAGGTTTTCTGCTGCGAGGGCCACGGCATCATTTACCTGCAACCCC 10210
QY 3401 AspGluThrTTPThrGlnThrSerAlaLysCysGluLysLysIleSerCysGlyProProAla 3420
DB 10211 GACGAGCGTGGACACAGACAGCGCCCAATGTGNAANAATCTCANTGTGTCCACCACTGT 10270
QY 3421 HisValGluAsnAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyr 3440
DB 10271 CACGTAGAAATGCAATTTGCTCGAGGGGTACATTTATCAATATGAGACATGATCACCTAC 10330
QY 3441 SerCysTyrSerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGly 3460
DB 10331 TCATGTTTACAGTGGATACATGTTGAGAGGGTTTCTGAGGAGTGTGTTCTTAGAATAATGGA 10390
QY 3461 ThrTTPThrSerProIleCysArgAlaValCysArgPheProCysGlnAsnGlyGly 3480
DB 10391 ACATGGACATCACTCTCTATTTGACAGAGCTGTCTGTGATTTCAATGTCAGATGGGGCC 10450
QY 3481 IleCysGlnArgProAsnAlaCysSerCysProGluGlyTTPMetGlyArgLeuCysGlu 3500
DB 10451 ATCTGCCAACGCCCAATGCTTGTCTGTCAGAGGGCTGGATGGGGCTCTGTGAA 10510
QY 3501 GluProIleCysIleLeuProCysLeuAsnGlyGlyArgCysValAlaProTyrGlnCys 3520
DB 10511 GAACCAATCTGCATTTCTTCCCTGTCTGTAACGGAGGTCGCTGTGTGGGCCCTTACCACTGT 10570

QY 3521 AspCysProGlyTTPThrGlySerArgCysHisThrAlaValCysGlnSerProCys 3540
DB 10571 GACTGCCCGCTGCTGGACGGGCTCTCGCTGTCATACAGCTGTTTCCAGTCTCCCTGC 10630
QY 3541 LeuAsnGlyGlyLysCysValArgProAsnArgCysHisCysLeuSerSerTTPThrGly 3560
DB 10631 TTAATAGTGTGAAATGCTGAAGACCAACCGATGCTCACTGCTTCTTCTTGTGACGGGA 10690
QY 3561 HisAsnCysSerArgLysArgArgThrGlyPhe 3571
DB 10691 CATAACTGTTCCAGGAAAGAGGACTGGGTTT 10723
RESULT 2
AAD57253
ID AAD57253 standard; CDNA; 11546 BP.
XX
AC AAD57253;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CGDD-33 CDNA.
XX
KW Human; cell growth, differentiation and death protein; CGDD; leukaemia;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
KW transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic;
KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
KW protozoacide; nootropic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 298..11010
FT /*tag= a
FT /product= "Human CGDD-33 protein"
XX
MO2003050253-A2.
XX
PD 19-JUN-2003.
XX
PF 04-DEC-2002; 2002WO-US039133.
XX
PR 07-DEC-2001; 2001US-0340747P.
PR 20-DEC-2001; 2001US-0342761P.
PR 15-JAN-2002; 2002US-0349705P.
PR 06-FEB-2002; 2002US-0354764P.
PR 12-FEB-2002; 2002US-0356216P.
XX
FA (INCY-) INCYTE GENOMICS INC.
XX
PI Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
PI Marquis JP, Baughn MR, Corvad AE, Yue H, Lee BA, Becha SD, Tang YT;
PI Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
PI Sprague WW, Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
PI Burhill JD, Blake JJ, Ho A, Zheng W;
XX
DR WPI; 2003-532903/50.
DR P-PSDB; AAD37944.
XX
FT New CGDD polypeptides, useful for diagnosing, preventing, and treating
FT disorders associated with an abnormal expression or activity of CGDD,
FT e.g. neuromuscular, immunological, cardiovascular disorders, cancer
FT and/or infections.
XX
PS Claim 5; Page 296-299; 299pp; English.
XX
CC The present invention relates to novel cell growth, differentiation and
CC death (CGDD) proteins and polynucleotides encoding them. The sequences of

CC the invention are useful in diagnosing, preventing and treating disorders
 CC associated with an abnormal expression or activity of CGDD such as
 CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
 CC disease), muscular disorders (e.g. myotonic dystrophy, catatonias),
 CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
 CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis),
 CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 CC create humanised animals or transgenic animals to model human diseases.
 CC The invention is also used in gene therapy. The present sequence is human
 CC CGDD-33 cDNA

XX Sequence 11546 BP; 3008 A; 2726 C; 2836 G; 2976 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 11546
 Score: 19905.50 Matches: 3561
 Percent Similarity: 99.80% Conservative: 3
 Best Local Similarity: 99.72% Mismatches: 6
 Query Match: 99.66% Indels: 1
 DB: 8 Gaps: 1

US-09-977-053-4 (1-3571) x AAD57253 (1-11546)

QY	1	MetTProArgLeuAlaPheCysTyrGlyLeuAlaLeuValSerGlyTProAlaThr	20
DB	298	ATGTGGCCCTCGCCCTGGCCCTTTTGTCTGGGGTCTGGCGCTGTTTGGGGTGGGGGACC	357
QY	21	PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro	40
DB	358	TTTCAGCAGATGTCCTCCGTCGGCAATTTTCAGCTTCGGCTCTTCCCGCAGACCTGGGCC	417
QY	41	GlyAlaProGlySerIleProAlaProProAlaProGlyAspGluAlaAlaGlySerArg	60
DB	418	GGGGCCCCGGGAGTATCCCGCGCCCGCTCTCTGGCGAGCGAAGCGGGGAGCAGAGA	477
QY	61	ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu	80
DB	478	GTGGAGCGGCTGGGGCAGCGGTTCGGCGACGGGTGGCGCTGCTGGGGAGCTCAGCGAG	537
QY	81	ArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGluValAlaAsnPheArg	100
DB	538	CGCTTGAGCTTGTCTCTCTGGTGATGATTCGTCCAGCGTGGCGAAGTCAACTTCGCG	597
QY	101	SerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThr	120
DB	598	AGCGAGCTCATGTTCTCGCGCAAGCTGCTTCGACTTCCTCCGTGGTGGCCAGCGCAG	657
QY	121	ArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIle	140
DB	658	CGCGTGGCCATCGTGACCTCTCTCTCCAGAACTACGTGGTGGCGCGCTCGATTACATC	717
QY	141	SerThrArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluIleProAlaIle	160
DB	718	TCCACCCGCGCGCGCGCAGCACAAGTGGCGCTGCTCTCCAGAGATCCCTGCCATC	777
QY	161	SerTyrArgGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeu	180
DB	778	TCTACCGAGGTGGCGGCACCTACACCAAGGGCGCTTCAGCAAGCGCGCAAAATCTT	837
QY	181	LeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn	200
DB	838	CTTCATCGTAGAGAAACTCACAAAGTTGTATTTCTCATCTACTGTGATATTCAT	897
QY	201	GlyGlyAspProArgProIleAlaIleSerLeuArgAspSerGlyValGluIlePheThr	220
DB	898	GGGGGAGACCTTAGACCAATTGCGAGCTTACCTCGAGATTCAGAGTGGAGATCTTCACT	957
QY	221	PheGlyIleTyrGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu	240

DB	958	TTTGGCATATGCAAGGGAAACATTCGAGAGCTGAATGACATGGCTTCCACCCCAAGGAG	1017
QY	241	GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeu	260
DB	1018	GAGCAGCTGTACTGCTACACAGTTTGAAGAATTTAGGCTTTAGCTCGCGGCATTG	1077
QY	261	HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu	280
DB	1078	CATGAAGATCTACTTCTGGGAGTTTATTTCAAGATGATATGCTCCACTGCTCATATCTT	1137
QY	281	CysAspGluGlyAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr	300
DB	1138	TGTGATGAAGGCAAGAGACTGCTGTGACCGAAATGGGAAGCTGCAAAATGTGGGACACACA	1197
QY	301	GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys	320
DB	1198	GGCCATTTTGAATGTCATCTGTGAAAGGGGTATTACGGGAAGGCTCTGCAGTATGAATGC	1257
QY	321	ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys	340
DB	1258	ACAGCTTGGCCATCGGGACATACAAACCTGAAGGCTCACCAGGAGGAATCAGCAGTGC	1317
QY	341	IleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCys	360
DB	1318	ATTCCATGTCCTGATGAATAATCACCTCTCCACCTGGAGACATCCCTCTGAAGACTGT	1377
QY	361	ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla	380
DB	1378	GTCTGCAGAGGGGATACAGGGCATCTGGCCAGACCTGTGAACCTTGTCCACTGCGCTGCC	1437
QY	381	LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla	400
DB	1438	CTGAAGCCTCCCGAAATGGTTACTTTATTCAAACACTTGCACCAACCACTTCAATGCA	1497
QY	401	AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys	420
DB	1498	GGCTGGGGGTCCGATGTCACTTGGATTTGATCTTGTGGAGAGCAGCATCACTTATGT	1557
QY	421	LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis	440
DB	1558	CTACCCAAATGTTTGGTCCGGTTCAGAGAGCTACTGCAGAGTAAGAACATGTCTCAT	1617
QY	441	LeuArgGlnProLysHisGlyIleSerCysSerThrArgGluMetLeuTyrLysThr	460
DB	1618	CTCGCGCAGCCGAAACATGGCCACATCAGCTGTCTCAAGGGAAATGTTATATAAGACA	1677
QY	461	ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys	480
DB	1678	ACATGTTTGGTTCCTGTGTATGAGGGTACAGACTAGAGGCGAGTATAGCTTACTTGT	1737
QY	481	GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr	500
DB	1738	CAAGGAACAGCCAGTGGCATGGCCAGAACCCCGGTGTGTGGAGCGCCACTGTTCACCC	1797
QY	501	PheGluMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLys	520
DB	1798	TTTCAGATGCCAAGATGTTCATCATATCCCCCACAACCTGTGGCAGCAGCAGCCAAA	1857
QY	521	PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu	540
DB	1858	TTTGGACAGTCTGCTATGTAGTTCGCCCAAGGGTTCATTTTATCTGGAGTCAAGAA	1917
QY	541	MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaIleValCysLys	560
DB	1918	ATGCTGAGATGTACCACTTCTGGAAATGGAATGTGGAGTTCAGGCGAGCTGTGTGAAA	1977
QY	561	AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln	580
DB	1978	GAGCTGGAGGCTCTCAAAATCAACTGTCTTCAAGACATAGAGCTTAGACTCTTGGACAG	2037
QY	581	GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys	600
DB	2038	CAAGATTCCTGCCAATGTTTACCTGGCAGATTCCAAACAGCTAAAGACAATCTCTGGTGAAGAAG	2097

Qy 601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620
Db 2098 GTGTCAGTCACAGGTTTCAACAGCTTTTCAACCCACTTACCTTTTCCCAATGGAGATGT 2157
Qy 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
Db 2158 GCTATCGTATACAGCGCAACTGACCTATCCGGCAACAGGCCAGCTGCATTTTCCATATC 2217
Qy 641 LysValIleAspAlaGluProProValIleAspTyrCysArgSerProProProValGln 660
Db 2218 AAGGTTATTGATGACAGAACCACTGTTGATAGACTGGTGCGAGATCTCACCTCCCGTCCAG 2277
Qy 661 ValSerGluLysValHisAlaAlaSerTyrAspGluProGlnPheSerAspAsnSerGly 680
Db 2278 GTCTCGGAGAGGTACATGCGCGAAGCTGGATGAGCTCACTGTTCTCAGACAACTCAGGG 2337
Qy 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
Db 2338 GCTGAATGGTTCATTACAGAGTATACACAGGAGACCTTTTCCCTCAAGGGGAGACT 2397
Qy 701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
Db 2398 ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATT 2457
Qy 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
Db 2458 GTCATAAAGGTTCTCCCTGTGAAATTCATTCACACTGTAAATGGGATTTTATATGC 2517
Qy 741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
Db 2518 ACTCCAGATTAATCTGGAGTCAACTGTATATTAATTCGTTGGAGGGCTATGATTTCCACA 2577
Qy 761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyr 780
Db 2578 GAAGGGTCTACTGACAAATATATTGTGCTTATGAAGATGGCGTCTGGAAACCAACATAT 2637
Qy 781 ThrThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
Db 2638 ACCACTGAATGGCGAGACTGTGCCAANAAGTTTTCANAACCAAGGGTTCAAGTCTCTTT 2697
Qy 801 GluMetPheTyrLysAlaLysArgCysAspThrAspLeuMetLysLysPheSerGlu 820
Db 2698 GAGATGTTCTACAAAGCAGCTCGTTGTGTATGATGACACAGATCTGAAGAAGTTTTCGAA 2757
Qy 821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
Db 2758 GCATTTTGAGACGACCTCGGGAAAAATGGTCCCATCATTTTGTAGTATGACAGGACATT 2817
Qy 841 AspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
Db 2818 GACTGCAAGCTGGAGGAAACCTGACCAANAATTTTGGCTAGATATATATTATGACTAT 2877
Qy 861 GluAsnGlyPheAlaIleGlyProGlyTyrGlyAlaAlaAsnArgLeuAspTyrSer 880
Db 2878 GAAATGGCTTTGCAATTTGACACAGGTGGCTGGGGTGCAGCTAATAGCTGATTACTCT 2937
Qy 881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 900
Db 2938 TACGATGACTTCTCGGACACTGTGCAAGAAACAGCCCAAGGATCGGCAATGCCAAGTCC 2997
Qy 901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920
Db 2998 TCACGGATTAAGAAGTGGCCCAATATCTGACTATTAANAATTAAATTTTAAATC 3057
Qy 921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnGln 940
Db 3058 ACAGTAGTGTGCAATTTACCGATGAAGAAATGATACCTTGAATGGGAAATCAGCAA 3117
Qy 941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
Db 3118 CGACTCCTTCAGACATTGGAAACTATCACAAATAAATGAAGAGGACTCTCAACAAAGAC 3177

Qy 961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGlu 980
Db 3178 CCCATGATTCTCTTTCAGCTTGCATCAGAAATCTATTAGCCGACAGCAATTCATTAGAA 3237
Qy 981 ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal 1000
Db 3238 ACAAAAAGGCTTCCCTCTCTGAGACAGGCTCAGTGTCTGAGAGGGCGTATGTGTGTC 3297
Qy 1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
Db 3298 AATTGCCCTTTGGGAACCTATTATACTGGAACATTTCACTGTGAAGCTCAGTGTAAAACAGGCACC 3357
Qy 1021 GlySerTyrGlnAspGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr 1040
Db 3358 GGATCTTATCAAGATGAAGAAGGGCACTTCAGTGCAGCTTTGCCCTCTCGGATGTAC 3417
Qy 1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr 1060
Db 3418 ACGGAATATATCATTCAAGAAACATCTCTGATTGTAAGCTCAGTGTAAAACAGGCACC 3477
Qy 1061 TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLys 1080
Db 3478 TACTCATACAGTGGACTTGAAGTGTGCACTGGGCACCTTATCAGGCCAAAA 3537
Qy 1081 PheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAla 1100
Db 3538 TTTGGTTCCCGAGCTGCTCTCTGTTCCAGAAACACTCACTGTGAAAAGAGAGGCC 3597
Qy 1101 ValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeu 1120
Db 3598 GTGAACATTTCTGATGCGAGTTCTTGTGTCAGAAAGGAAAAATTCGCGTCTCGGTTA 3657
Qy 1121 MetProCysHisProCysProAspAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
Db 3658 ATGCCCTGTACCCATGCTCTCGTACTATTACCAACCTAATGAGGAGAGGCCCTCTCTGC 3717
Qy 1141 LeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCys 1160
Db 3718 CTGGCCTGTCTCTTTTATGGAACCTACCCCATTCGCTGGTTCCAGATCGCTCACAGATGT 3777
Qy 1161 SerSerPheSerSerThrPheSerAlaAlaGluLysSerValValProProAlaSerLeu 1180
Db 3778 TCAAGTTTATAGTTCACTTTCTCAGCGCAGAGAAAGTGTGGTCCCTCTCTCTCTCT 3837
Qy 1181 GlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn 1200
Db 3838 GGCATATTAAAGAGCGCATGAATTCAGCACTCAGGTTTTCCATGAATGCTCTCTTTAAC 3897
Qy 1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
Db 3898 CTTTGGCCACAATAGTGGAACTGCGCAGCAACTGGGGGTGGTTATGTTGTTCTCTGTCCA 3957
Qy 1221 LeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCys 1240
Db 3958 CTTGGATATACAGGCTTAAAGTGTGAACAGACATCGATGATGTCAGCCCTCTCTCTTC 4017
Qy 1241 LeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGly 1260
Db 4018 CTCACAAATGAGTTTGTAAAGACCTAGTTGGGGAATTCATTTGTGAGTGGCCATCAGT 4077
Qy 1261 TyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsn 1280
Db 4078 TACACAGTTCAGCGTGTGAAGAAATATTAATCAGTGTAGCTCCAGTCTCTGTTTAAAT 4137
Qy 1281 LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal 1300
Db 4138 AAAGGAATCTGTGTGTGATGGTGTGGCTATGCTTGCATCATGTGTGAAAAGGATTTGTA 4197
Qy 1301 GlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAla 1320
Db 4198 GGCCTGATGTTGAAACAGAGATCAATGAATGCCAGTCAAAACCCATGCTTTAATTAATGCA 4257
Qy 1321 ValCysGluAspGlnValGlyPheLeuCysLysCysProProGlyPheLeuGlyThr 1340

Db 4258 GTCTGTGAAGACAGAGTTGGGGATCTTGTGCAATGCCCACCTGGATTTTGGGTACC 4317
QY 1341 ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCys 1360
Db 4318 CGATGTGGAAAGAACGTGATGAGTGTCTCAGTCAGCCATGCAAAATGGAGCTACCTGT 4377
QY 1361 LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys 1380
Db 4378 AAAGACGGTGCCAATAGCTTCAGATGCCCTGTGTGCAGCTGGCTTCACAGGATCACACTGT 4437
QY 1381 GluLeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAsp 1400
Db 4438 GAATTTGACATCAATGAAATGTCATCTAATCCATGAGTAATCAGGCCACCTGTGTGGAT 4497
QY 1401 GluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThr 1420
Db 4498 GAATTAATTCATACAGTTGTAAATGTCAGCCAGGATTTTCAGGCCAAAGGTGTGAACA 4557
QY 1421 GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet 1440
Db 4558 GAACAGTCTACAGGCTTTAAACCTGGATTTTGAAGTTTCTGGCATCTATGGATATGTCATG 4617
QY 1441 LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTyrMetLysSerSer 1460
Db 4618 CTAGATGGCATGCTCCCATCTCTCCATGCTCTTAACCTGTACCTCTGTGGATGAATCCTCT 4677
QY 1461 AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr 1480
Db 4678 GACGACATCAACTATGGAACACCACTCTCTATGCAGTGTGATAACGGCAGCGACATACC 4737
QY 1481 LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThr 1500
Db 4738 TTGCTCTCTGACTGATTAATACCGCTGGGTCTTTATGTGAATGGCGGGAAGATAACA 4797
QY 1501 AsnCysProSerValAsnAspGlyArgTyrHisIleAlaIleThrTyrSerAla 1520
Db 4798 AACTGTCCCTCGTGAAATGATGGCAGATGGCATCATATTGGCATCACTTGGACAGTGCC 4857
QY 1521 AsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer 1540
Db 4858 AATGGCATCTGGAAAGTCTATATCGATGGGAAATATATCTGACGGTGGTGTGCGCTCTCT 4917
QY 1541 ValGlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGluAspLysIys 1560
Db 4918 GTTGGTTTCCCATACCTGGTGGTGGTGTGTAGTTCTGGGGCAAGCAGACAAAGAA 4977
QY 1561 GlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTyr 1580
Db 4978 GGAGAGGGATTCAGCCAGCTGATCTTTTGTGGGCTCCNTAAGCCAGCTCAACCTCTGG 5037
QY 1581 AspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeu 1600
Db 5038 GACTATGTCTGTCTCCACAGCAGGTGAAGTCACTGGCTACCTCTCTGCCCCAGAGAACTC 5097
QY 1601 SerLysGlyAsnValLeuAlaTyrProAspPheLeuSerGlyIleValGlyLysValLys 1620
Db 5098 AGTAAAGGAACCGTGTAGCATGGCTGATTTCTGTCAAGAAATGTGGGAAAGTGAAG 5157
QY 1621 IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis 1640
Db 5158 ATCGATTCTAAGAGCATATTTGTCTGATGCCCACGCTTAGGAGGGTCAGTGCCTCAT 5217
QY 1641 LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro 1660
Db 5218 CTGAGAACTGCATCTCAAGATTTAAAGCCAGGTTCCTCAAAATGCAATCTGTCTGTGATCCA 5277
QY 1661 GlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGln 1680
Db 5278 GGCCTTCAGCTGGTGGGAACCTGTGCGAGTACTGTCTGAATCAGAGCAGGTGGACAA 5337
QY 1681 ProLeuProHisCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPhe 1700

Db 5338 CCACCTTCCTCAGCTGTGAACGCAATTAGCTGTGGGGTGCACCTCTCTTTGGAGAAATGGCTTC 5397
QY 1701 HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr 1720
Db 5398 CATTTCAGCGATGACTTCTATGCTGCAGCACAGTAACCTTACCAAGTGCACAACTATGGCTAC 5457
QY 1721 TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTyrAsnGlyValSer 1740
Db 5458 TATCTATTTGGTGAAGTCTCAAGGATGTTCTGTACAGATTAATGGGAGCTGGAAACGGGTTTCA 5517
QY 1741 ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer 1760
Db 5518 CCATCTCTGCTTGAATGATGATGAGTGTGCAGTTGGATTCAGATTTGTAGTGAGCATGCTTCT 5577
QY 1761 CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGly 1780
Db 5578 TGCCTGAAACGTAGATGATCTTACATATGTTCTATGTTGCCACCGTACACAGAGATGGG 5637
QY 1781 LysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer 1800
Db 5638 AAAAATCTGTGCAGAACCTATTAATGTAAGCTCCAGGAAATCCGGAAATATGGCCACTCC 5697
QY 1801 SerGlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGln 1820
Db 5698 TCAGGTGAGATTTATACAGTAGTGGCGCGCAGTCCACATTTTGTGTCCAGGAAGATACCAG 5757
QY 1821 LeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluThrPheAsnHisLeuIlePro 1840
Db 5758 TTGATGGGAGTAAACCAAAATCACTGTTTGGAGTCTGGAGAAATGGAATTCATCTAATACCA 5817
QY 1841 TyrCysLysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGlu 1860
Db 5818 TATTGTAAAGCTGTTTCATGTGGTAAACCGGCTATTTCAGGAAATATGGTTCATTGAGGAG 5877
QY 1861 LeuAlaPheThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAla 1880
Db 5878 TTAGCATTTACTTTTGGCAGCAAGATGACATATAGTGTAAATAAGGATATCTCTGGCC 5937
QY 1881 GlyAspLysGluSerSerCysLeuAlaAsnSerSerTyrSerHisSerProValCys 1900
Db 5938 GGTEGTAAGAATCATCTCTGTCTTGTAAACAGTCTTGTGAGTCAATTCCTCTCTGTGTGT 5997
QY 1901 GluProValLysCysSerSerProGluAsnIleAsnAsnGlyLysTyrIleLeuSerGly 1920
Db 5998 GAACCGTGCAGTGTCTAGTCCGGAATATTAATAATGGAATAATATATTTTGGTGGG 6057
QY 1921 LeuThrTyrLeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuGlnGlyPro 1940
Db 6058 CTTACCTACCTTTCTACTGCTCATCATATTCTGCGATACAGGATACAGCTTACAGGGCCCT 6117
QY 1941 SerIleIleGluCysThrAlaSerGlyIleTyrAspArgAlaProProAlaCysHisLeu 1960
Db 6118 TCCATTATTGAATGACCGGCTTCTGGCATCTGGGACAGAGCGCCACTCTGCTGTACCTC 6177
QY 1961 ValPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThr 1980
Db 6178 GTCTTCTGTGGAGAACCACTGCGCATCAAGATGCTGTCTATTACGGGGGAATAACTTCACT 6237
QY 1981 PheArgAsnThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThr 2000
Db 6238 TTCAGGAACACCGCTCACTTACACCTTGCAAAAGAGGCTATATCTTGTGTGTCTTTCACCC 6297
QY 2001 IleGluCysLeuAlaAspGlyLysTyrSerArgSerAspGlnGlnCysLeuAlaValSer 2020
Db 6298 ATTGAATGCTGGCCGACCGGCAAGTGGAGTAGAGTAGACCGACGATGCTGTGGTGTCTCC 6357
QY 2021 CysAspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGly 2040
Db 6358 TGTGATGACCCACCACTTGTGGACCAAGCTCTCCAGAGACTGCCCATCGGCTCTTTGGA 6417
QY 2041 AspIleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeu 2060
Db 6418 GACATTGCATTTCTACTACTGCTCTGATGGTTACAGCTTAGCAGCAATATCCCGACTTCTC

QY 3521 AspCysProGlyTyrThrGlySerArgCysHisThrAlaValCysGlnSerProCys 3540
 DB |||||
 DB 10855 GACTGCCCGCTGCTGGAGCGGGTCTCGCTGCTATACAGCTTTTCCAGTCTCCCTGC 10914

QY 3541 LeuAsnGlyLysCysValArgProAsnArgCysHisCysLeuSerSerThrThrGly 3560
 DB |||||
 DB 10915 TTAATGGTGGAAATGTGTAGACCAACCGATGCTCACTGTCTTCTTCTTGGACGGGA 10974

QY 3561 HisAsnCysSerArgLysArgArgThrGlyPhe 3571
 DB |||||
 DB 10975 CATAACTGTTCCAGGAAAGAGGACTGGGTTT 11007

RESULT 3
 ABT08491
 ID ABT08491 standard; cDNA; 11152 BP.
 AC ABT08491;
 XX
 XX 28-NOV-2002 (first entry)
 DT
 XX Human novel protein NOV2b coding sequence SEQ ID NO: 7.
 DE
 XX Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;
 KW antiarteriosclerotic; antidiabetic; antiasthmatic; antiinflammatory;
 KW haemostatic; hypotensive; neuroprotective; anorectic; nootropic;
 KW antiepressant; immunosuppressive; antibacterial; antiparasitic;
 KW virucide; tranquilizer; anticonvulsant; osteopathic; analgesic;
 KW antiparkinsonian; dermatological; antiinfertility; cerebroprotective;
 KW antiaddictive; gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200259315-A2.
 PN
 XX 01-AUG-2002.
 PD
 XX
 XX 19-DEC-2001; 2001WO-US050076.
 XX
 XX 19-DEC-2000; 2000US-0256619P.
 PR
 XX 19-JAN-2001; 2001US-0262959P.
 PR
 XX 28-FEB-2001; 2001US-0272408P.
 PR
 XX 20-APR-2001; 2001US-0285189P.
 PR
 XX 26-JUL-2001; 2001US-0308039P.
 PR
 XX 09-AUG-2001; 2001US-0311266P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimketa RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U;
 PI Shenoy S, Spytek KA, Gangolli B, Miller C, Boldog F, Li L;
 PI Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD;
 PI Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
 PI Rothenberg M;
 XX
 XX WPI; 2002-666903/71.
 DR
 XX P-PSDB; ABJ10590.
 DR
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
 PT or Alzheimer's disease.
 XX
 XX Claim 8; Page 43-45; 363pp; English.
 PS
 XX The present invention provides the protein and coding sequences of
 CC several novel human proteins, designated NOVX. These can be used in the
 CC treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-
 CC Lindau syndrome, Alzheimer's disease, stroke, tuberosus sclerosis,
 CC hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral
 CC palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia
 CC telangiectasia, leukodystrophies, addiction, anxiety, depression, pain,
 CC obesity, Crohn's disease, osteoporosis, inflammatory bowel disease,
 CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,

CC diabetes, pancreatitis, autoimmune disease, asthma, arthritis,
 CC immunodeficiencies, HIV, viral, bacterial or parasitic infections, or
 CC graft-versus-host disease. The present sequence is a coding sequence of
 CC the invention

XX SQ Sequence 11152 BP; 2951 A; 2606 C; 2711 G; 2884 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 11152
 Score: 19616.00 Matches: 3510
 Percent Similarity: 98.82% Conservative: 16
 Best Local Similarity: 98.37% Mismatches: 40
 Query Match: 98.21% Indels: 2
 DB: 6 Gaps: 1

US-09-977-053-4 (1-3571) x ABT08491 (1-11152)

QY 4 ArgLeuAlaPheCysCysTyrGlyLeuAlaLeuValSerGlyTyrAlaThrPheGlnGln 23
 DB |||||
 DB 83 AGAATTTCGCGCGCTTCTGGGGTCTGGCGCTCGTTTCGGGCTGGCGACCTTTTCAGCAG 142

QY 24 MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro 43
 DB |||||
 DB 143 ATGTCCCGCTGGCGCAATTTTCAGCTTCGCGCTCTTCCCGAGACCGCGCGGGGCCCCC 202

QY 44 GlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArgValGluArg 63
 DB |||||
 DB 203 GGGAGTATCCCGCGCGCGCTCTTGGCGACGAGCGCGGGGAGCAGAGTGAGCGG 262

QY 64 LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu 83
 DB |||||
 DB 263 CTGGCCAGGCGTTT-----CGCGTGGCGTGTCTGGCGAGCTCAGCGAGCGCTGGAG 316

QY 84 LeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArgSerGluLeu 103
 DB |||||
 DB 317 CTGTCTTCTCTGGTGGAGATTCGTCCAGCGTGGCGGAAGTCAATTCGCGAGCGAGCTC 376

QY 104 MetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThrArgValAla 123
 DB |||||
 DB 377 ATGTTCTGTCGCAAGCTGCTGTCGAGCTTCCCGTGGTGGCCCGCCAGCGCGTGGCC 436

QY 124 IleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIleSerThrArg 143
 DB |||||
 DB 437 ATCTGACCTTCTCGTCCAGACTAGTGTGGTGGCGGCGTGCATTTACATCTCCACCGC 496

QY 144 ArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnIleProAlaIleSerTyrArg 163
 DB |||||
 DB 497 CGCGCGCGCCAGCACAAGTGGCGCTGCTCTCCAAGAGATCCCTGCGCATCTCTTACCGA 556

QY 164 GlyGlyGlyThrTyrThrLysGlyValAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAla 183
 DB |||||
 DB 557 GGTGGCGGCGACCTACACACAGGGGCGCTTCCAGCAGCGCGGCAAAATTTCTTTCATGCT 616

QY 184 ArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAsp 203
 DB |||||
 DB 617 AGAGAAACTCAACAAAAGTTGTATTTCTCATCTGATGATATTTCCAAATGGGGGAGAG 676

QY 204 ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle 223
 DB |||||
 DB 677 CCTAGACCAATTTGACGCTCATCTCGAGATTCAGAGTGGAGATCTTCACATTTTGGCATA 736

QY 224 TrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCys 243
 DB |||||
 DB 737 TGGCAAGGAAACATTCGAGAGCTGATGACATGGCTTCCACCCCAAGAGGAGCACTGT 796

QY 244 TyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgArgAlaLeuHisGluAsp 263
 DB |||||
 DB 797 TACCTGTACACAGTATTTGAAGAAATTTGAGGCTTTTAGCTCGCGGCGCATTTGCATGAAGT 856

QY 264 LeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeuCysAspGlu 283
 DB |||||
 DB 857 CTACCTCTTGGAGTTTTATTTCAGAGATGATATGTTCCACTGCTCTCAATCTTTGTATGAG 916

QY 284 GlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThrGlyHisPhe 303
DB 917 GGCAGGAGCTGCTGTGACCGAATGGGAAGCTGCAAAATGTGGGACACACACAGGCCATTTT 976
QY 304 GluCysIleCysGluLysGlyTyrGlyLysGlyLeuGlnTyrGluCysThrAlaCys 323
DB 977 GAGTGCATCTGTGAAAGGGGTATACGGGAAGGCTGCGAGTATGAAATGCCACAGCTTGC 1036
QY 324 ProSerGlyThrTyrLysProGluGlySerProGlyGlyLysSerSerCysIleProCys 343
DB 1037 CCATCGGGGACATACAAACCTGAAGCCTCAACAGGAGGAATCAGAGTTGTCATTCCCATGT 1096
QY 344 ProAspGluAsnHisThrSerProGlySerThrSerProGluAspCysValCysArg 363
DB 1097 CCGGATGAAATCACACCTCTCCACCTCGGAAGCACATCCCTCGAAGACTGTGTGTGCGA 1156
QY 364 GluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuLysPro 383
DB 1157 GAGGGATACAGGCATCTGGCCAGACTGTGAACTTGTCCACTGCTCCCTCGAAGCCT 1216
QY 384 ProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAlaIaCysGly 403
DB 1217 CCGGAAATGGTTACTTTATCCAAACACTTGCACCAACCACTTCAATGCAGCCTGTGG 1276
QY 404 ValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeuProAsn 423
DB 1277 GTCCGATGTCAACCTGGATTTGATCTGTGGGAAGCAGCATCATCTTATGTCTACCCAA 1336
QY 424 GlyLeuTyrSerGlySerGluSerTyrCysArgValArgThrCysProHisLeuArgGln 443
DB 1337 GGTGTGTGTCGGTTTCAGAGACTACTGCGAGGTAAAGACATGCTCTCATCTCCGCCAG 1396
QY 444 ProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThrThrCysLeu 463
DB 1397 CCGAAACATGGCCACATCAGCTGTCTACAGGCAAAATGTTATATAAGACAAACATGTTG 1456
QY 464 ValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCysGlnValAsn 483
DB 1457 GTTGCCTGTGATGAAGGGTACAGACTAGAGAGGAGTGTAAGCTTACTTGTCAAGGAAC 1516
QY 484 SerGlnTyrAspGlyProGluProArgCysValGluArgHisCysSerThrPheGlnMet 503
DB 1517 AGCCAGTGGATGGCCAGAACCCCGTGTGTGGAGGCCACTGTGTCCACCTTTCAGATG 1576
QY 504 ProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPheGlyThr 523
DB 1577 CCGAAAGATGTTCATCATATCCCCCACAACCTGTGGCAGCAGCCCAAAATTTGGGACG 1636
QY 524 IleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGluMetLeuArg 543
DB 1637 ATCTGCTATGTAAAGTTGGCCCAAGGGTTCAATTTATCTGGAGTCAAGAAATGCTGAGA 1696
QY 544 CysThrThrSerGlyLysTyrAsnValGlyValGlnAlaValCysLysAspValGlu 563
DB 1697 TGTAACACTTCTGGAAATGGATGTGGAGTTCCAGCAGCTGTGTGTAAAGACGTGGAG 1756
QY 564 AlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGlnGlnAspSer 583
DB 1757 GCTCCTCAAAATCAACTGTCTAAGGACATAGAGGCTAAGACTCTGGAAACAGCAAGATTCT 1816
QY 584 AlaAsnValThrTyrGlnIleProThrAlaLysAspAsnSerGlyGluLysValSerVal 603
DB 1817 GCCAAATGTGTACCTGGCAGATTCCACAGCTTAAGACAACCTCTGGTGAAGGGTGCAGTC 1876
QY 604 HisValHisProAlaPheThrProPctTyrLeuPheProIleGlyAspValAlaIleVal 623
DB 1877 CGGTTTCATCCACTTTCACCCCACTTACCTTTTCCCAATTCGAGATGTTGTATCGTA 1936
QY 624 TyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLysValIle 643
DB 1937 TACACGGCAACTGACCTATCCGGCAACAGGCCAGCTGCATTTTCCATATCAAGGTTATT 1996
QY 644 AspAlaGluProProValIleAspTyrCysArgSerProProValGlnValSerGlu 663

DB 1997 GATGCAGAACCCACTGTCTATAGACTGTGTGCAGATCTCCACTCCCGTCCAGGTTCTCGAG 2056
QY 664 LysValHisAlaAlaSerTyrAspGluProGlnPheSerAspAsnSerGlyAlaGluLeu 683
DB 2057 AAGGTACATGTCGCAAGCTGGGATGAGCTCAGTTCTCAGACAACCTCAGGGGCTGAATTG 2116
QY 684 ValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGln 703
DB 2117 GTCATTTACCAGAGTCTATACACAAGGAGACCTTTTCCCTCAAGGGGAGACTATATAGTACAG 2176
QY 704 TyrThrAlaThrAspProSerGlyAsnAspArgThrCysAspIleHisIleValIleLys 723
DB 2177 TATACAGCCACTCAGCCCTCAGGTAAACAGGATATGTGATATCCATATTGTCTATGAA 2236
QY 724 GlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThrProAsp 743
DB 2237 GGTTCTCCCTGTGNAATTCATTCACACCTGTAAATGGGATTTTATATGCACCTCCAGAT 2296
QY 744 AsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGlySer 763
DB 2297 AATACTGGAGTCAACTGTACATTAACCTTGTCTGGAGGGCTACGATTTTCACAGAAGGGTCT 2356
QY 764 ThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyrThrGlu 783
DB 2357 ACTGACAAAGTATTATTGTGCTTATGAAGATGGGCTCTGGAAACCAACATATACCACTGAA 2416
QY 784 TrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGluMetPhe 803
DB 2417 TGSCCAGACTGTGCCAAAAAAGCTTTTGCAAAACCCAGGTTCAAGTCTCTTGAGATGTTT 2476
QY 804 TyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAlaPheGlu 823
DB 2477 TACAAAGCAGCTCGCTGTGTGATGACTCAGATCTCATGAAGAAGTTTCTCTGAAGCAATTTGAG 2536
QY 824 ThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAspCysArg 843
DB 2537 ACGACCTTGGGAAATATGTTCCCATCATTTTGTAGTATGCAGAGGACATTTGACTGCAGA 2596
QY 844 LeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGly 863
DB 2597 CTGGAGGAGAACCTGACCAAAAAATATATGCTAGAAATATATATATGATATGAAAAATGGC 2656
QY 864 PheAlaIleGlyProGlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAsp 883
DB 2657 TTTGCAATTTGGTCCAGTGGCTGGGGTGCAGCTAAATAGGCTGGATTAATCTCTTACATGAC 2716
QY 884 PheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIle 903
DB 2717 TTCTTGACACTGTGCAAGAAACAGCCCAAGCATCGGCATTCGCAAGTCTCTCAGGATTT 2776
QY 904 LysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIleThrAlaSer 923
DB 2777 AAAAGAAGTGGCCCATTTCTGACTATATAAATTAAGTTAAATTTTAAACATCACAGCTAGT 2836
QY 924 ValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnAlaGluLeu 943
DB 2837 GTCCCATTTACCCATGAAAGAAATGATPACCTTGAATGGGAAATTCAGACACGACTCTCT 2896
QY 944 GlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyr 963
DB 2897 CAGACATTTGGAAACTATCAAAATAAATCGAAAGGACTCTCAACAAAGACCCCATGTAT 2956
QY 964 SerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLys 983
DB 2957 TCCCTTTTCAGCTTCATCAGAAATACTTATATAGCCACAGCAATTCATTTAGAAACAAAAAG 3016
QY 984 AlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsnCysPro 1003
DB 3017 GCTTCCCTCTCTGCAACACAGGCTCAGTGTAGAGGGGCTATGTGTGTCAATGGCCT 3076
QY 1004 LeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyr 1023

Db 3077 TTGGGACCTATTATTAATCTGGACACATTTTCCACTGTGAAAGCTGCCGGATCGGATCCTAT 3136
Qy 1024 GlnAspGluGluGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyr 1043
Db 3137 CAAGATGAAGAGGGCAACTTGAGTCAAGCTTGGCCCTCTGGGATGTACACGGAAATAT 3196
Qy 1044 IleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyr 1063
Db 3197 ATCCATTCAAGAACATCTCTGATTGTAAGCTCAGTGTAAACCAAGGCACCTACTCATAC 3256
Qy 1064 SerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPheGlySer 1083
Db 3257 AGTGGACTTGAGACTTGTGAATCGTCTCCACTGGGCACCTATCAGCCAAAATTTGGTTC 3316
Qy 1084 ArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIle 1103
Db 3317 CGGAGCTGCTCTCGTGTCCAGAAAACACCTCACTGTGAAAGAGAGCGGTGAACATT 3376
Qy 1104 SerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCys 1123
Db 3377 TCTGCATGTGGAGTCTCTTGTCCAGAAAGGAAAATTTCTCGCGTTCTGGGTTAATGCCCTGT 3436
Qy 1124 HisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCys 1143
Db 3437 CACCCATGCTCTCGTGAATATTAACCACTTAATGCGAGGAAGCCCTTCTGCCCTGGCTGT 3496
Qy 1144 ProPheTyrGlyThrProPheAlaGlySerArgSerIleThrGluCysSerSerPhe 1163
Db 3497 CCTTTTATGGAACTACCCCATTCGCTGGTGTCCAGATCCATCAGAAATGTTCAAGTTTT 3556
Qy 1164 SerSerThrPheSerAlaGluGluSerValValProProAlaSerLeuGlyHisIle 1183
Db 3557 AGTTCAACTTTCTCAGCGGCAGAGGAAGTGTGTGCCCCCTCGCTCTCTTGGACATATT 3616
Qy 1184 LysLysArgHisGluLeuSerSerGlnValPheHisGluCysPhePheAsnProCysHis 1203
Db 3617 AAAAAGGCACTGAATACAGCATCAGGCAGTCAATGATGCTTCTTTAACCTTGCCAC 3676
Qy 1204 AsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyr 1223
Db 3677 AATAGTGAACCTGCCAGCACTTGGCGTGGTATGTTGTCTCTGTCCACTTGGATAT 3736
Qy 1224 ThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsn 1243
Db 3737 ACAGGTTAAAGTGTGAAAACAGACATCGATGAGTGCAGCCCTGCTTGCCTCAACAAT 3796
Qy 1244 GlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGly 1263
Db 3797 GGAATTTGTAAAGCTAGTTGGGGAATTCATTTGTGAGTGCCCAACAGGTTACACAGGT 3856
Qy 1264 GlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLysGlyIle 1283
Db 3857 AAGCACTGTGAATTGAACATCAATGAATGTCACTTAATCCATGTAGAAATCAGGCCACC 3916
Qy 1284 CysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGlyLeuHis 1303
Db 3917 TGTGTGATGAATTAATTCATACAGTTGTAAATGTGCAGCCAGGATTTTCAGGCAAAAGG 3976
Qy 1304 CysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCysGlu 1323
Db 3977 TGTGAACAGGATGATATCACTCAGTGTATTATTAATCACTTAATATGATGATCTGTGAA 4036
Qy 1324 AspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCysGly 1343
Db 4037 GACCAGGTTGGGGATTTCTTGTGCAAAATGCCACCTCGATTTTGGGTATCCCGATGTGA 4096
Qy 1344 LysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAspGly 1363
Db 4097 AAGAAGCTCGATGAGTGTCTCAGTGCAGCCATGCAAAAATGGAGCTACTCTGAAGACGGT 4156
Qy 1364 AlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGluLeuAsn 1383
Db 4157 GCCAATAGCTTCAAGTGCCTTGTGTGACAGCTGGCTTTCACAGATCACACTGTGAATTGAC 4216

Qy 1384 IleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGluLeuAsn 1403
Db 4217 ATCAATGAATGTCAAGTCTAATCCATGTAGAAATCAGGCCACCTCTGTGTGGATGAATTAAT 4276
Qy 1404 SerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGluGlnSer 1423
Db 4277 TCATACAGTTGTAAATGTCAAGCAGGATTTTCAGGCCAAAAGGTCTGAAACAGACAGCTCT 4336
Qy 1424 ThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeuAspGly 1443
Db 4337 ACAGGCTTTAACTCGAATTTGAAGTTTTCAGGATCTATGCGATATGTCATCTAGATGGC 4396
Qy 1444 MetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAspAspMet 1463
Db 4397 ATGCTCCCATCTCTCCCATGCTCTAAACCTGTACCTTCTGGATGAATTCCTCTGACGACATG 4456
Qy 1464 AsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeuLeuLeu 1483
Db 4457 AACTATGGAAACACCATCTCTATGCGATTTGATNACGCGCAGCAATACCTTGTCTCTGT 4516
Qy 1484 ThrAspTyrAsnGlyTrpValLeuTyrValAsnGlyArgGluLysIleThrAsnCysPro 1503
Db 4517 ACTGATTATAACGGTGGTTCCTTATGTGATGCGAGSGAAAGATAACAACATGCTCCC 4576
Qy 1504 SerValAsnAspGlyArgTrpHisIleAlaIleThrTrpThrSerAlaAsnGlyIle 1523
Db 4577 TCGGTGAATGATGCGCAGATGCGCATCATATTGCAATCACTTGGACAAGTACTGGTGGAGCC 4636
Qy 1524 TrpLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerValGlyLeu 1543
Db 4637 TGGAGGTCTATTAATAATGGGAATTAATCGACCGTGTACTGGCTCTCCATTGGCAAA 4696
Qy 1544 ProIleProGlyGlyGlyAlaLeuValLeuGlyGlnGluAspLysLysGlyGlyGly 1563
Db 4697 GCCATACCTGCTGGCGGTGCTATTGTTCTGGGCAAGACAGCAACAAAAGGAGAGGG 4756
Qy 1564 PheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrpAspTyrVal 1583
Db 4757 TTCAACCCGGCTGAGTCTTTTGTGGGCTCCATAAGCCAGCTCAACCTCTGGGACTATGTC 4816
Qy 1584 LeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeuSerLysGly 1603
Db 4817 CTGTCTCCACAGCGGTGAAGTCACTGGCTACTCTCTGCCCCAGAGGAACTCAGTAAAGGA 4876
Qy 1604 AsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLysIleAspSer 1623
Db 4877 AACGTGTAGCATGGCTGATTTCTTGTGAGAAATTTGTGGGAAAGTGAAGATCGATTTCT 4936
Qy 1624 LysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHisLeuArgThr 1643
Db 4937 AAGAGCATATTTTGTGATTTGCCACGCTTGGAGGGTTCAGTGGCTCATCTTGAGAACT 4996
Qy 1644 AlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGlyPheGln 1663
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Qy 1664 LeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyInTrpThrGlnProLeuPro 1683
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Qy 1684 HisCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPheHisSerAla 1703
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Qy 1704 AspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeu 1723
Db 5177 GATGACTTCTATGCTGGCAGCAGCAGTAACCTACCAAGTCAACAAATGGCTACTATCTATTG 5236
Qy 1724 GlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSerProSerCys 1743
Db 5237 GGTGACTCAAGGATGTTCTGTACAGATAATGGGAGCTGGAAACGGCGGTTTCCACCATCTGCG 5296

1744 LeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAsn 1763
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1764 ValAspGlySerThrIleCysSerCysValProProThrThrGlyAspGlyLysAsnCys 1783
5357 GTAGATGGATCCTACATATGTTCAATGTGTCACCGGTACACAGAGATGGGAAAACTGT 5416
1784 AlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSerSerGlyGlu 1803
5417 GCAGAACCTATAAATGTAAGGCTCCAGGAATCCGGAATATGCGCAATCTCCTCAGGTGAG 5476
1804 IleThrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyThrGlnLeuMetGly 1823
5477 ATTTATACAGTAGGTGCGGAAGTACATATTTCTGTGTGAGAGATACCAAGTTGATGGGA 5536
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6377 GCTGGCTCAGTGTGAGCTTTAATGATGATGGAAGGCTTTGTACTGAACACCTCAGCAAG 6436
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2144 ValArgCysGlyGluProProSerIleMetAsnGlyTyrlAlaSerGlySerAsnTyrlSer 2163
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6797 GTCTGCCAAAGCAATGCCACTGGCAGTGAATCCCTCTGATGTGTGTCTCTCGAC 6856
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DB 10757 TCAGGAAAAGGAGGACTGGGTTT 10780
 RESULT 4
 ABT08490
 ID ABT08490 standard; cDNA; 11158 BP.
 XX
 AC ABT08490;
 XX
 DT 28-NOV-2002 (first entry)
 XX
 DE Human novel protein NOV2a coding sequence SEQ ID NO: 5.
 XX
 KW Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;
 KW antitumor; anti-HIV; cytostatic; anti-HIV; cytostatic; anti-HIV; cytostatic;
 KW haemostatic; hypotensive; neuroprotective; anorectic; nootropic;
 KW antidepressant; immunosuppressive; antibacterial; antiparasitic;
 KW virucide; tranquilizer; anticonvulsant; osteopathic; analgesic;
 KW antiparkinsonian; dermatological; antinfertility; cerebroprotective;
 KW antiaddictive; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(717,G)
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 FT variation replace(2303,A)
 FT variation /*tag= b
 FT variation replace(7348,T)
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 FT variation replace(7370,C)
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 FT variation /*tag= h
 FT variation replace(9790,T)
 FT variation /*tag= i
 FT variation replace(10025,G)
 FT variation /*tag= j
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 FN WO200259315-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050076.
 XX
 PR 19-DEC-2000; 2000US-0256619P.
 PR 19-JAN-2001; 2001US-0262959P.
 PR 28-FEB-2001; 2001US-0272408P.
 PR 20-APR-2001; 2001US-0285189P.
 PR 26-JUL-2001; 2001US-0308039P.
 PR 09-AUG-2001; 2001US-0311266P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U;
 PI Shenoy S, Szytek KA, Gangolli E, Miller C, Boldog F, Li L;
 PI Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD;
 PI Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
 PI Rothenberg M;
 XX
 DR WPI: 2002-666903/71.
 DR P-PSDB; ABJ10589.
 XX
 PT New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
 PT or Alzheimer's disease.

XX Claim 8; Page 38-41; 363pp; English.

PS The present invention provides the protein and coding sequences of

CC several novel human proteins, designated NOVX. These can be used in the

CC treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-

CC Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis,

CC hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral

CC palsy, epilepsy, Leach-Nyhan syndrome, multiple sclerosis, ataxia,

CC telangiectasia, leukodystrophies, addiction, anxiety, depression, pain,

CC obesity, Crohn's disease, osteoporosis, inflammatory bowel disease,

CC infertility, atherosclerosis, hypertension, scleroderma, haemophilia,

CC diabetes, pancreatitis, autoimmune disease, asthma, arthritis,

CC immunodeficiencies, HIV, viral, bacterial or parasitic infections, or

CC graft-versus-host disease. The present sequence is a coding sequence of

CC the invention

XX SQ Sequence 11158 BP; 2952 A; 2603 C; 2710 G; 2893 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	11158
Score:	19566.00	Matches:	3503
Percent Similarity:	98.57%	Conservative:	16
Best Local Similarity:	98.12%	Mismatches:	47
Query Match:	97.96%	Indels:	4
DB:	6	Gaps:	2

US-09-977-053-4 (1-3571) x ABT08490 (1-11158)

QY 4 ArgLeuAlaPheCysCysTyrPheGluLeuValSerGlyTyrAlaThrPheGlnGln 23

DB 83 AGAATTTCGGCGGCTTCTGGGGTCTGGGCTCGTTCGGGCTGGGCGACCTTTCAGCAG 142

QY 24 MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro 43

DB 143 ATGTCCCGCTCGCGCAATTTTCAGCTTCGGCTTCGGCTTCGGCGAGCGCGCGCGCC 202

QY 44 GlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArgValGluArg 63

DB 203 GGGAGTATCCCGCGCGCGCTTCGGCGAGCGCGCGCGCGCGAGCGAGTGGAGCGG 262

QY 64 LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu 83

DB 263 CTGGCGCAGGGGTTT-----CGCGTGGCGCTGCTGGCGAGCTCAGCGAGCGCTGGAG 316

QY 84 LeuValPheLeuValAspSerSerValGlyGluValAlaAsnPheArgSerGluLeu 103

DB 317 CTGTCTTCTGTGTGATGATTCGTCCAGCGTGGCGCGAAGTCAACTTCCGCGAGCGGCTC 376

QY 104 MetPheValArgLeuLeuSerAspPheProValValProThrAlaThrArgValAla 123

DB 377 ATGTTCGCGCAAGCTGTCTCGACTTCCCGGTGGTCCCGCGCGCGCGCGCGTGGCC 436

QY 124 IleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIleSerThrArg 143

DB 437 ATCGTGACCTTCTGTCCAGAACTACGTGTGGTGGCGCGCGTGGTATCATCTCCACCGC 496

QY 144 ArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluIleProAlaIleSerTyrArg 163

DB 497 CGCGCGCGCGCAGCAAGTGGCGCTGCTCTCCAGAGAGATCCCTGGCATCTCTCCACCGA 556

QY 164 GlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAla 183

DB 557 GGTGGCGCGCCTTACACACAGGGCGCTTCAGCAGAGCGCGCGCGCAATTTCTTCATGCT 616

QY 184 ArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAsp 203

DB 617 AGAGAAACTCAACAAAGTTGTATTTCTCATCATCATGATGATATTCATATGGGGAGAC 676

QY 204 ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle 223

DB 677 CCTAGACCAATTGCGCGCTCACTCGAGATTTCAGGAGTGGAGATCTTCACTTTTGGCAT 736

QY 224 TrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHisCys 243

DB 737 TGGCAGGGAGACATTCGAGAGCTGATGACATGGCTTCCACCCCAAGGAGGAGGACTGT 796

QY 244 TyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArg-----ArgAlaLeuHis 261

DB 797 TACCTGCTACACAGTTTTCAGAAATTTGAGGCTTTAGTCCGCTCTGTCTATATGTTATTT 856

QY 262 GluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeuCys 281

DB 857 GTAGATCTACCTTCTGGGAGTTTATTTCAAGATGATATGTCACCTGCTCATATCTTTGT 916

QY 282 AspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThrGly 301

DB 917 GATGAGCGCAGGACTGCTGTGACCGAATGGAGCTGCAATGTGGGAAACACACAGGC 976

QY 302 HisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCysThr 321

DB 977 CATTTGAGTGCATCTGTCAAAAGGGGTATATACGGGAAAGGCTTCGAGTATGACTGCACA 1036

QY 322 AlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCysIle 341

DB 1037 GTTTCGCCCATCGGGACATACAACTGAAGCTCACCAGGAGGAATCAGCAGTTCGACT 1096

QY 342 ProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCysVal 361

DB 1097 CCAATGCTCTGATGAATATCACTCTCCACTGGAGCAGCATCCCTGAGAGCTGTGTC 1156

QY 362 CysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeu 381

DB 1157 TGCAGAGAGGGATACAGGGCATCTGGCAGACTCTGTGAAGTTGTCCACTGCCCTGCCCTG 1216

QY 382 LysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAlaAla 401

DB 1217 AAGCTCCCGAAATGGTTACTTTATCCAAACACTTGCACACACCTTCATGAGGCC 1276

QY 402 CysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuLeuCysLeu 421

DB 1277 TGTGGGTCGATGTCACCTGGATTGATCTTGTGGGAGCAGCATCATCTTATGCTA 1336

QY 422 ProIleGlyLeuThrSerGlySerGluSerTyrCysArgValArgThrCysProHisLeu 441

DB 1337 CCCAATGTTGTGTGTCGGTTTCAGAGAGCTACTGTCAGAGTAAAGAACATGCTCTCATCTC 1396

QY 442 ArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThrThr 461

DB 1397 CGCCAGCGGAAACATGGCCCATCATCAGCTGTCTCAAGGAAATGTTATATAGACAAACA 1456

QY 462 CysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCysGln 481

DB 1457 TGTGTTGTTGCTGTGATGAAGGTTACAGGCTAGAGGCGAGTATAGCTTACTTGTCAA 1516

QY 482 GlyAsnSerGlnThrAspGlyProGluProArgCysValGluArgHisCysSerThrPhe 501

DB 1517 GGAACACCCAGTGGGATGGGCCAGAACCCCGGTGTGTGGAGCGCCTGTTTCCACTTT 1576

QY 502 GlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPhe 521

DB 1577 CAGATGCCCAAGATGTATCATATATCCCCCAAACTGTGGCAGCAGCAGCAGCAATTT 1636

QY 522 GlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGluMet 541

DB 1637 GGGAGCATCTGTATGTAAGTTGGCCGCAAGGGTTTCAATTTATCTGGAGTCAAGAAATG 1696

QY 542 LeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLysAsp 561

DB 1697 CTGAGATGATACCTTCTGGAAATGGAATGTGCGAGTTTCAGGAGCTGTGTGTAAAGAC 1756

QY 562 ValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGlnGln 581

DB 1757 GTGAGGCTCTCAATCACTGTCTAAGGACATAGAGGCTTAGACTCTGGAACAGCAA 1816

QY 582 AspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLysVal 601

Db 1817 GATTCTGCCAAATGTTACCTGGCAGATTCACACAGCTAAAGACCACTCTGGTGAAGAGGTG 1876
Qy 602 SerValHisValHisProAlaPheThrProTyrLeuPheProIleGlyAspValAla 621
Db 1877 TCAGTCCAGCTTCATCCAGCTTCACCCACCTTACTCTTTTCCAAATGGAGATGTGCT 1936
Qy 622 IleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLys 641
Db 1937 ATCGTATACAGGCAACTGACCTATCCGGCAACAGCCAGCTGCATTTTCCATATCAAG 1996
Qy 642 ValIleAspAlaGluProProValIleAspTyrCysArgSerProProValGlnVal 661
Db 1997 GTTATTGATGCAGACCACTGTCTAGACTGGTGAGATCTCCACCTCCCGTCCAGGTC 2056
Qy 662 SerGluLysValHisAlaLaserTyrAspGluProGlnPheSerAspAsnSerGlyAla 681
Db 2057 TCGAGAGAGTCAATCCCGCAGCTGGATGAGACCTCAGTTCTCAGACCACTCAGGTGCT 2116
Qy 682 GluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIle 701
Db 2117 GAATTCGTCAATACCAAGAGTCATACACAGGAGACCTTTTCCCTCAAGGGGAGACTATA 2176
Qy 702 ValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleVal 721
Db 2177 GTACAGTATACAGCCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATATGTC 2236
Qy 722 IleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThr 741
Db 2237 ATAAAGGTTCTCCCTGTGAAATTCCTATTCACACCTGTAAATGGGATTTTATATGCACT 2296
Qy 742 ProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGlu 761
Db 2297 CCAGATAAATACTGGAGTCAACTGTACATTAATCTGCTTGGAGGCTATGATTTTACAGAA 2356
Qy 762 GlySerThrAspLysTyrCysAlaTyrGluAspGlyValTyrPheLysProThrTyrThr 781
Db 2357 GGGTCTACTGACAAAGTATTTATGCTTATGAGATGGCGCTCTGGAAACCAACATATACC 2416
Qy 782 ThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGlu 801
Db 2417 ACTGAATGGCCAGCTGTGCAGTAAGCTTTGCAAAACCAACCGGTTCAAGTCTTTGAG 2476
Qy 802 MetPheTyrLysAlaLysCysAspThrAspLeuMetLysLysPheSerGluAla 821
Db 2477 ATGTTCTACAAAGCAGCTCGTTGTGATGACACAGATCTCATGAAGAAGTTTCTGAAGCA 2536
Qy 822 PheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAsp 841
Db 2537 TTTGAGACGACCTGGGAAAATGGTCCCATCATTTTGTAGTATGAGAGGACATTTGAC 2596
Qy 842 CysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyrGlu 861
Db 2597 TGCAGACTGGAGGAGAACCTGACCAAAAATATTCCTAGATATATATGACTATGAA 2656
Qy 862 AsnGlyPheAlaIleGlyProGlyGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyr 881
Db 2657 AATGGCTTTGCAATTTGCTCCAGTGGCTGGGTGAGCTAATAGGCTGGATTTACTCTTAC 2716
Qy 882 AspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSerSer 901
Db 2717 GATGACTTCTTGACACTGTGCAAGAAACAGCCCAAGCATCGGCAATGCCAGTCTCTCA 2776
Qy 902 ArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIleThr 921
Db 2777 CGGATTAAGAGAGTGGCCCATTTATCTGACTATAAATAAGTTAATTTTAAACATCACA 2836
Qy 922 AlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnArg 941
Db 2837 GCTAGTGTGCATTTACCCGATGAAGAAATGATACCTTGAATGGGAAAATFCAGAACGA 2896
Qy 942 LeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspPro 961

Db 2897 CTCCTTCAGACATTTGAAACCTATCACAAAATAAACTGAAAAAGGACTCTCAACAAGAGACCCC 2956
Qy 962 MetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThr 981
Db 2957 ATGTATTCTTTTCAGCTTGCATCAGAAATACTATATAGCCGACAGCAATTCATTAGAAACA 3016
Qy 982 LysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsn 1001
Db 3017 AAAAAGGCTTTCCCTCTTCAGACAGGCTCAGTGTGAGAGGGCGGTATGTGTGTCAAT 3076
Qy 1002 CysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGly 1021
Db 3077 TGCCTTTTGGAAACCTATTATAATCTGGAACATTTTACCTGTGAAAGCTGCCGATCGGA 3136
Qy 1022 SerTyrGlnAspGluGluGlnLeuGluCysLysLeuCysProSerGlyMetTyrThr 1041
Db 3137 TCCTATCAAGATCAAGAGGCAACTTGTAGTCAAGCTTTTGGCCCTCTGGGATGTACAG 3196
Qy 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
Db 3197 GAATATATCCATTTCAAGAAACATCTCTGATTGTAAAGCTCAGTGTAAACCAAGGACCTTAC 3256
Qy 1062 SerTyrSerGlyLeuGluThrCysGluSerCysProLeuGluGlyThrTyrGlnProLysPhe 1081
Db 3257 TCATACAGTGGACTTGAGACTTGTGATCTGTCTCCACTGGGCACCTTATCAGCCAAAATTT 3316
Qy 1082 GlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaVal 1101
Db 3317 GGTTCCTGGAGCTGCCTCTCTGTCTCCAGAAAACACCTCAACTGTGAAAAGAGAGGCGCTG 3376
Qy 1102 AsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMet 1121
Db 3377 ACAAATTTCTGCATGTGGAGTTCTTGTCTCCAGAGGAAAATTTCTCGCGTTCTGGGTAAAG 3436
Qy 1122 ProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeu 1141
Db 3437 CCTGTGACCAATGTCCTGTGTGACTATTACCACTTAATCAGGAGAGGCTTCTGCGCTG 3496
Qy 1142 AlaCysProPheTyrGlyThrProPheAlaGlySerArgSerIleThrGluCysSer 1161
Db 3497 GCCTGTCCCTTTTATGGAACCTACCCCATTCGCTGTTCAGATCCATCAGCAAAATGTTCA 3556
Qy 1162 SerPheSerSerThrPheSerAlaAlaGluSerValValProProAlaSerLeuGly 1181
Db 3557 AGTTTATAGTTCAACTTTCTCAGCGCAGAGAAAGTGTGGTGGCCCTCTCTCTTGTGA 3616
Qy 1182 HisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnPro 1201
Db 3617 CATATTAAGAGGCAATGAATCAGCAGTCAGGCAAGTCATGAATGCTTCTTTAACCT 3676
Qy 1202 CysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeu 1221
Db 3677 TGCACAAATAGTGGAACTTCCAGCAACTTGGCGGTGGTTATGTTGTCTCTGTCCACTT 3736
Qy 1222 GlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeu 1241
Db 3737 GGATATACAGTTTAAAGTGTGAACACAGACATCGATGAGTGCAGCCCACTGCTTGTCTC 3796
Qy 1242 AsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyr 1261
Db 3797 AACAAATGGAGTTTGTAAAGACCTAGTTTGGGAAATTCATTTGTGAGTGGCCATCAGGTAC 3856
Qy 1262 ThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsnLys 1281
Db 3857 ACAGGTAAAGCACTGTGAATTTGAACATCAATGAATGTGAGTCTAATCTCAGTAAATCAG 3916
Qy 1282 GlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGly 1301
Db 3917 GCCACCTGTGTGGATGAATTAATTCATAGTTGTAAATGTGAGCCAGGATTTTCAGGC 3976
Qy 1302 LeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaVal 1321
Db 3977 AAAAGGTGTGAACAGGTATGTATCAACTCAGTGTGTTATTAATTAACCTTAATTAATGAGTC 4036

1322 CysGluAspGlnValGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArg 1341
Db TGTGAAGACCAAGGTGGGGGATCTTGTGCAAAATGCCACCTGGATTTTGGGTACCCGA 4096
1342 CysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyValAlaThrCysLys 1361
Db TGTGGAAGAACGTGAGTGTCTCAGTCAGCCATGCCAAATGGAGCTACCTGTAA 4156
1362 AspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGlu 1381
Db GACGCTGCCAATAGCTTCAGGTGCTGTGTGAGCTGGCTTTCACAGGATCACACTGTGAA 4216
1382 LeuAsnIleAsnGlnCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu 1401
Db TTGAACATCAATGAATGTCACTTAATCCATGTGAATAATCAGGCCACCTGTGTGGATGAA 4276
1402 LeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlu 1421
Db TTAATTCATACAGTTTAAATGTTCAGCCAGATTTTCAGGCATAAAGGTGTGAAACAGA 4336
1422 GlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeu 1441
Db CAGTCTACAGGCTTTAACTCGAATTTTGAAGTTTCTGGCATCTATGGATATGTCAATGCTA 4396
1442 AspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAsp 1461
Db GATGGCATGTCTCCCATCTCTCAATCTTAACCTGTATCTTCTGGATGAATCTCTCTGAC 4456
1462 AspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeu 1481
Db GACATGAACATATGNAACCAATCTCTATGCATGTGATTAAGCGCAGCGACACATACCTTG 4516
1482 LeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGluLysIleThrAsn 1501
Db CTCCTCACTGATTAATAACGGGTGGGTCTTTATGTGAATGGCAGGAAAGATAACAAC 4576
1502 CysProSerValAsnAspGlyArgTrpHisIleAlaIleThrTyrSerAlaAsn 1521
Db TGTCCCTCGGTGAATGAGGAGATGGCATCATATTTGCATCCTTGGCAAGTACTGGT 4636
1522 GlyIleTrpLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSerVal 1541
Db GGACCTGGAGGTCTATATAATGGGAATTAATCTGACGGTGGTACTGGCTCTCCAT 4696
1542 GlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGlnAspLysLysGly 1561
Db GGCAAAAGCCATACCTGGTGGCGGTGCATTAATTTCTGGGCAAGAGCAAGACAAAAAGGA 4756
1562 GluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrpAsp 1581
Db GAGGGGTTCAACCCCGCTGAGTCTTTGTGGGCTCCATAAGCCAGCTCAACCTCTGGGAC 4816
1582 TyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluGluLeuSer 1601
Db TATGTCTGTCTCCACAGCAGGTGAAGTCACTGGCTACTCTCTGCCAGAGAACTCAGT 4876
1602 LysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLysIle 1621
Db AAAGAAACCGTGTAGCATGCCCTGAATTTCTGTTCAGGAATGTGGGGAAAGTGAAGATC 4936
1622 AspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHisLeu 1641
Db GATTCTAAGAGCATATTTGTCTTCATATGCCACGCTTGGAGGGGTCAAGTCCCTCATCTG 4996
1642 ArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGly 1661
Db AGAACTGCATCTGAAGATTTAAACACAGGTTCAAAGTCAATCTGTCTGTGAACACGCG 5056
1662 PheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTrpThrGlnPro 1681
Db TTCAGCTGGTGGGAACCCCTGTGTGACGTACTGTCTGAATCAAGGACAGTGGACACAACA 5116

1682 LeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPheHis 1701
Db CTCCTCCCACTGTGAACGATTCGCTGTGGGGTGGCCACCTCTCTTGGAGAAATGGCTTCCAT 5176
1702 SerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyr 1721
Db TCAGCCGATGACTTCTATGCTGGCAGCAGTAACCTACACAGTGCACAACTGGCTACTAT 5236
1722 LeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSerPro 1741
Db CTATTTGGGTGACTCAAGGATGTTCTGTACAGATAATGGAGCTGGAAACGGCGTTTCACCA 5296
1742 SerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCys 1761
Db TCCTGCTTAGATGTCAGATGAGTGCAGTTCAGATTCAGATTTAGTGAGGATGCTTCTTGC 5356
1762 LeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyLys 1781
Db CTGAACGTAGATGATCTCTACATATGTTCTGATGTTCCACCGTACACAGGAGATGGGAA 5416
1782 AsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSerSer 1801
Db AACTGTGCAGAACCTTATAAATGTAAAGCTCCAGGAAATCCGGAAATGGCCACTCTCA 5476
1802 GlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeu 1821
Db GGTGAGATTTATACAGTAGGTCCGAGTCACTTTTCTGTTCAGGAGGATACAGTTG 5536
1822 MetGlyValThrLysIleThrCysLeuGluSerGlyGluTrpAsnHisLeuIleProTyr 1841
Db ATGGAGTAACCAATCACATGTTTGGAGTCTGCAGAAATGGAATCATCTAATACCATAT 5596
1842 CysLysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGluLeu 1861
Db TGTAAAGCTGTTTCATGTGGTAAACCGGTATTTCAGAAATATGGTTCATTTAGGAGTTA 5556
1862 AlaPheThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAlaGly 1881
Db GCATTTACTTTTGGCAGCAGTGCATATAGTGTATTAAGGATATATCTCTGGCGGT 5716
1882 AspLysGluSerSerCysLeuAlaAsnSerTrpSerHisSerProProValCysGlu 1901
Db GATAAAGAAATCATCTGTCTGTAAACAGTCTTGGAGTCAATTCCTCTCTGTGTGAA 5776
1902 ProValLysCysSerSerProGluAsnIleAsnAsnGlyLysTyrIleLeuSerGlyLeu 1921
Db CCAGTGAAGTGTCTAGTCCCGGAAATATAATAATAGGAAATATATTTTGTAGTGGCTT 5836
1922 ThrTyrLeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuGlnGlyProSer 1941
Db ACCTACCTTTCTACTGTCATCATATTCATGCCGATACAGGATACAGCTTACAGGGCCCTTC 5896
1942 IleIleGluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeuVal 1961
Db ATTATTTGAATGACAGGCTTCTGGCATCTGGGACAGAGCGCCACCTGCTCTCACTCTGTC 5956
1962 PheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThrPhe 1981
Db TTCTGTGGAGAACCAACCTGCCATCAAGATGCTCATTAACGGGAAATTAACCTTCACTTTC 6016
1982 ArgAsnThrValThrTyrThrCysLysGlyTyrThrLeuAlaGlyLeuAspThrIle 2001
Db AGGAACACCGTCACTTACATTCGAAAGAGGCTATCTCTTGTGCTTCTTGACACCAT 6076
2002 GluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnGlnCysLeuAlaValSerCys 2021
Db GAATGCTCTGGCGAGCGCAAGTGGAGTAGAGTACCAGCAGTGGCTGCTGCTCTCTGT 6136
2022 AspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGlyAsp 2041
Db GATGAGCCACCATTTGTGGACCAACCTCTCAGAGACTGGCCATCGGCTCTTTGGAGAC 6196
2042 IleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeuCys 2061

Db	6197	ATTGCAATTCCTACTACTGCTCTGATGGTTACAGCTTAGCAGCAAAATCCAGAGCTTCTGCG	6256
Qy	2062	AsnAlaGlnGlyLysTrpValProGluGlyGlnAspMetProArgCysIleAlaHis	2081
Db	6257	AATGCCAGGGCAGTGGGTACCCCAAGAGGTCAAGACATGCCCGTGTATAGTCAAT	6316
Qy	2082	PheCysGluLysProProSerValSerTrpSerIleLeuGluSerValSerIysAlaLys	2101
Db	6317	TTCTGTGAAAAACCTCCATCGGTTTCTATAGCATCTTGGAACTCTGTGAGCAAGCAAAA	6376
Qy	2102	PheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThrSer	2121
Db	6377	TTTGCAGCTGGCTCAGTTGTGAGCTTTAAATGCAATGGAAGGCTTTGTACTGAACACCTCA	6436
Qy	2122	AlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGlnCys	2141
Db	6437	GCAAGATTGAAATGATGAGAGTGGGAGTGGAGACCTTCCCCATGTCATCCAGTGC	6496
Qy	2142	IleProValArgCysGlyGluProProSerIleMetAsnGlyTrpAlaSerGlySerAsn	2161
Db	6497	ATCCCTGTGGGTGTGGAGAGCCACCAAGCATCATGAATGGCTATGCAAGTGGATCAAC	6556
Qy	2162	TyrSerPheGlyAlaMetValAlaTrpSerCysAsnLysGlyPheTrpIleLysGlyGlu	2181
Db	6557	TACAGTTTGGAGCCATGGTGGCTTACAGCTGCACAAGGGGTTCACATCAAGGGGAA	6616
Qy	2182	LysLysSerThrCysGluAlaThrGlyGlnTrpSerSerProIleProThrCysHisPro	2201
Db	6617	AAGAAGACACCTGCGAGCCACAGCGAGTGGAGTAGTCTATACCGAGCTGCCACCG	6676
Qy	2202	ValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrGlyArg	2221
Db	6677	GTATCTGTGGTGAACACCACTAAGTTGAGATGGCTTTCTGAGGACATACAACTGGCAGG	6736
Qy	2222	IlePheGluSerGluValArgTrpGlnCysAsnProGlyTrpLysSerValGlySerPro	2241
Db	6737	ATCTTTGAGAGTGAAGTGAAGTATCAGTGTAAACCCGGGCTATGAAGTCAGTCGGAATGCT	6796
Qy	2242	ValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysValPro	2261
Db	6797	GTATTTGTCTGCCAAGCCATCGCCATCGCCACAGTGAATCCCTCTCTGATGTGTTCT	6856
Qy	2262	LeuAspCysGlyLysProProProIleGlnAsnGlyPheMetLysGlyGluAsnPheGlu	2281
Db	6857	CTCGACTGTGAAAAACCTCCCGGATCCAGATGGCTTCATGAAAGGAGAGAAACTTTGAA	6916
Qy	2282	ValGlySerLysValGlnPhePheCysAsnGluGlyTrpGluLeuValGlyAspSerSer	2301
Db	6917	GTAGGGTCCAAGGTTCAAGTTTCTGTAAATGAGGGTTATGAGCTTGTGTGACAGTTCT	6976
Qy	2302	TrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAla	2321
Db	6977	TGGACATGTCAGAAATCTGCCAAATGGAATAAGAGTCAAAATCCAAAGTGCATGCCCTGCC	7036
Qy	2322	LysCysProGluProProLeuLeuGluAsnGlnLeuValLeuLysGluLeuThrGlu	2341
Db	7037	AAGTGCCAGAGCGCGCCCTCTTGGAAAAACAGCTAGTATTAAAGAGGTTGACACCGAG	7096
Qy	2342	ValGlyValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerValLeu	2361
Db	7097	GTAGGAGTTGTGACATTTTCTGTAAATGAGGGTATGAGCTTGTGTGACAGTTCT	7156
Qy	2362	LysCysLeuProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeuCys	2381
Db	7157	AAATGCTTCCCATCCAGCAATGGAATGACTCTTCCCTGTTTGTAAAGATTGTCTTTGT	7216
Qy	2382	ThrProProLeuIleSerPheGlyValProIleProSerSerAlaLeuHisPheGly	2401
Db	7217	ACCCACCTCCCTTAATTTCTTTTGGTGTGCCCATTCCTTCTGCTCTCTCAATTTTGA	7276
Qy	2402	SerThrValIleTrpSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrLeu	2421

Db	7277	AGTACTGTCAAGTATTTCTTGTAGTGGGTTTTTCTTAAGAGAAATTTCTACCACTC	7336
Qy	2422	CysGlnProAspGlyThrTrpSerSerProLeuProGluCysValProValGluCysPro	2441
Db	7337	TGCCAACCTGATGGCACCTTGGAGCTCTCCACTGCCAGAAATGTGTCTCCAGTAGAATGTCCC	7396
Qy	2442	GlnProGluGluIleProAsnGlyIleIleAspValGlnGlyLeuAlaTrpLeuSerThr	2461
Db	7397	CAACCTGAGGAATATCCCAATGGAATCATTTGATGTGCAAGGCTTGCCTATCTCAGACA	7456
Qy	2462	AlaLeuTrpThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCysGly	2481
Db	7457	GCTCTCTATACCTGCAAGCCAGGCTTTGAATGTGTGGAAATTACTACCACTTGTGGA	7516
Qy	2482	GluAsnGlyHisTrpLeuGlyLysProThrCysLysAlaIleGluCysLeuLysPro	2501
Db	7517	GAATAATGCTCACTGGCTTGGAGGAAACCAACATGTAAGCCATTTGAGTGCCTGAAACCC	7576
Qy	2502	LysGluIleLeuAsnGlyLysPheSerTrpThrAspLeuHisTrpGlyGlnThrValThr	2521
Db	7577	AAGGAGATTTTGAATGGCAAAATTTCTTTACACGAGCTTACATATGGACAGACCGTTACC	7636
Qy	2522	TyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThr	2541
Db	7637	TACTCTTGCACCGAGGCTTTTGGCTGCAAGTCCCACTGAGTGCCTTGAATTTAGAGACA	7696
Qy	2542	GlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGlnPro	2561
Db	7697	GGTGAATGGATGTAGATGCCCATCTTGCATATGCCATCCATCTGTGATTCGCCCAACCC	7756
Qy	2562	IleGluAsnGlyPheValGluGlyAlaAspTrpSerTrpGlyAlaIleIleIleTrpSer	2581
Db	7757	ATTGAAATATGGTTTGTAGAGGTGCAGATTACAGCTATGGTGCATTAATCATCTACAGT	7816
Qy	2582	CysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrp	2601
Db	7817	TGCTTCCCTGGGTTTCAAGTGGCTGGTCATGCCATGCAGACCTGTGGAAGAGTCAGGATGG	7876
Qy	2602	SerSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAspPhe	2621
Db	7877	TCAAGTTCCATCCCAACATGTATGCAATAGACATGTGGGCTCCCTCTCTCATATAGATTTT	7936
Qy	2622	GlyAspCysThrLysLeuLysAspAspGlnGlyTrpPheGluGlnGluAspAspMetMet	2641
Db	7937	GGAGACTGTACTAAACTCAAAAGATGACAGGATATTTTGGAGCAAGAGACGACATATG	7996
Qy	2642	GluValProTrpValThrProHisProProTrpHisLeuGlyAlaValAlaLysThrTrp	2661
Db	7997	GAAGTTCCATATGTGACTCTCCACCTCTTATCATTTTGGAGCAGTGGCTTAAACCTGG	8056
Qy	2662	GluAsnThrLysGluSerProAlaThrHisSerSerAsnPheLeuTrpGlyThrMetVal	2681
Db	8057	GAATAATCAAGAGAGTCTCTGCTACACATTCATCAAACTTTCTGTATGTGTACCATGGTT	8116
Qy	2682	SerTrpThrCysAsnProGlyTrpGluLeuLeuGlyAsnProValLeuLysCysGlnGlu	2701
Db	8117	TCATACCTGTATTCAGGATATGAATCTCTGGGAGACCTCTGTGCTGATCTGCCAGGA	8176
Qy	2702	AspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuProThr	2721
Db	8177	GATGAACCTTGGATGCGAGTCACCATCTCTGCATTTCAATTTGAATGTGACTTGCCTACT	8236
Qy	2722	AlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGlnTrp	2741
Db	8237	GCTCTGAAAAATGGCTTTTGGCTTTTACAGAGACTAGCATGGGAATGTCTGTGCAGTAT	8296
Qy	2742	SerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArg	2761
Db	8297	AGCTGTAAACCTGACACATCTTAGCAGGCTCTGACTTAAGGCTTCTCTAGAGATAGA	8356
Qy	2762	LysTrpSerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProAsnProVal	2781
Db	8357	AAGTGAGTGGTGGCTCCCCACCGCTGTGAGGCAATTTTCAATGCAAAAGCCAAATCCAGTC	8416

QY 2782 MetAsnGlySerIleIysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGluCys 2801
DB 8417 ATGAATGGATCCATCAAGAGGAGCAACTACATACCTCAGACAGCTGTACTATGAGTGT 8476
QY 2802 AspProGlyTyrValIleuAsnGlyThrGluArgArgThrCysGlnAspAspLysAsnTrp 2821
DB 8477 GACCCCGGATATGTCTGAATGGCACTGAGAGAGAGAAACATGCCAGGATGACAAAACTGG 8536
QY 2822 AspGluAspGluProIleCysIleProValAspCysSerSerProProValSerAlaAsn 2841
DB 8537 GATGAGGATGAGCCCATTTGCCATTTCTGTGGACTGCGAGTTTCACTCCCGCAGTCTCAGGCCAAT 8596
QY 2842 GlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIleGluTyrThrCysAsnGlu 2861
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QY 2862 GlyPheLeuLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTrpSerGly 2881
DB 8657 GGGTTCTTCTGTCAGGAGCCAGGAGTCTGGTTTGTCTTGGCCAATGGAAAGTTGGAGTGA 8716
QY 2882 AlaThrProAspCysValProValArgCysAlaThrProProGlnIleuAlaAsnGlyVal 2901
DB 8717 GCCACTCCCGACTGTCTGTCTGTAGATGTGCCACCCCGCCACAACTGGCCCAATGGGGTG 8776
QY 2902 ThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGluGlyTyr 2921
DB 8777 ACGGAAGGCTGGACTATGTGCTTCATGAAGGAAGTAACATTTCCACTGTACAGAGGGCTAC 8836
QY 2922 IleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAlaGluIle 2941
DB 8837 AACTTGCACGGTGTCTCAAAACTCCTGTCTCAGTCAGATGGCAACTGGGATGCAGAGATT 8896
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DB 8897 CCTCTCTGTAACCACTCAACTGTGGACCTCTCTCAATGGCTCTCTGAGTGGCAGCTCACCTTCC 8956
QY 2962 GlyPheSerPheIleHisGlyIleGlnTyrGlnCysPheProGlyTyrLysLeu 2981
DB 8957 GGTFTTTTCTTTATCATGGGGGCCATATACAGTATCAGTGTCTTCTGGTTTATAAGCTC 9016
QY 2982 HisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerProSer 3001
DB 9017 CATGGAAATTCATCAAGAGGTGCTCTCTCAATGGCTCTCTGAGTGGCAGCTCACCTTCC 9076
QY 3002 CysLeuProCysArgCysSerThrProValIleGluTyrGlyThrValAsnGlyThrAsp 3021
DB 9077 TGCCTGCTTGCAGATGTTCCACACCACTAATTTGAATATGAACTGTCTCAATGGGACAGAT 9136
QY 3022 PheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGlyPheLysLeuLeu 3041
DB 9137 TTTGACTGTGGAAAGCAGCCCGGATTCAGTGTCTCAAGGGCTTCAAGCTCTCAGGACTT 9196
QY 3042 SerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGlyPheProHisCysGluHis 3061
DB 9197 TCTGAATATCACTGTGAGCCGATGAGGAGTGGAGCTCTGGGTTCCTCCCACTGTGAACAC 9256
QY 3062 ThrSerCysGlySerLeuProMetIleProAsnAlaPheIleSerGluThrSerSerTrp 3081
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QY 3082 LysGluAsnValIleThrTyrSerCysArgSerGlyTyrValIleGlnGlySerSerAsp 3101
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QY 3102 LeuIleCysThrGluLysGlyValTrpSerGlnProTrpProValCysGluProLeuSer 3121
DB 9377 CTGATTTGTACAGAGAAAGGGGTATGGAGCCAGCTTATTCAGTCTGTGAGCCCTTGTCC 9436
QY 3122 CysGlySerProProSerValAlaAsnAlaValAlaThrGlyGluAlaHisThrTyrGlu 3141
DB 9437 TGTGGGTGCCACCGCTGTCTGTGGCCAAATGTCAGTGGCACTGGAGGGGCACACACTATGAA 9496

QY 3142 SerGluValLysLeuArgCysLeuGluGlyTyrThrMetAspThrAspThrAspThrPhe 3161
DB 9497 AGTGAAGTGAACCTCAGATGTCTGGAAGGTTATACGATGATACAGATACAGATACATTC 9556
QY 3162 ThrCysGlnLysAspGlyArgTrpPheProGluArgIleSerCysSerProLysLysCys 3181
DB 9557 ACCTGTCCAGAAAGATGGTGGTCTGCTCCCTGAGAGAAATCTCTCTGACGTCTTAAATAATGT 9616
QY 3182 ProLeuProGluAsnIleThrHisIleLeuValHisGlyAspAspPheSerValAsnArg 3201
DB 9617 CCTCTCCGGAAACATAACATATATCTTGTATCGGGACGATTTCAAGTGTGAATAGG 9676
QY 3202 GlnValSerValSerCysAlaGluGlyTyrThrPheGluGlyValAsnIleSerValCys 3221
DB 9677 CRAGTTTCTGTGTGTCATGTGCAAGAGGATATACCTTTGAGGGAGTTTACATATCAGTATGT 9736
QY 3222 GlnLeuAspGlyThrTrpGluProProPheSerAspGluSerCysSerProValSerCys 3241
DB 9737 CAGCTTGATGGAACCTGGGAGCCACCAATTTCTCCGATGAATCTTGCAGTCCAGTTTCTTGT 9796
QY 3242 GlyLysProGluSerProGluHisGlyPheValValGlySerLysTyrThrPheGluSer 3261
DB 9797 GGGAAACCTGAAAGTCCGAAACATGGAATTTGTGTGGCAGTAAATACACCTTTGAAAGC 9856
QY 3262 ThrIleIleTyrGlnCysGluProGlyTyrGluLeuGluGlyAsnArgGluArgValCys 3281
DB 9857 ACAATTTATTCAGTGTGAGCTTGGCTATGAACTAGAGGGGACAGGGAAGTGTCTGC 9916
QY 3282 GlnGluAsnArgGlnTrpSerGlyValAlaIleCysLysGluThrArgCysGluThr 3301
DB 9917 CAGGAGAACACAGACAGTGGAGTGGAGGGTGGCAATATGCAAGAGAGCCAGGTGTGAAACT 9976
QY 3302 ProLeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArgThrThrGlyProAsnVal 3321
DB 9977 CCACTTGAATTTCTCAATGGGAAAGCTGACATTTGAAACAGGACGACTGGAGCCCAACGTG 10036
QY 3322 ValTyrSerCysAsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThrGlu 3341
DB 10037 GTATATTTCTGCAACAGAGGCTACAGTCTTGAAGGGCCATCTGAGGGCACACTGCACAGAA 10096
QY 3342 AsnGlyThrTrpSerHisProValProLeuCysLysProAsnProCysProValProPhe 3361
DB 10097 AATGGAACCTGGAGCCACCCAGTCCCTCTCTGCAACCAATCCATGCCCTGTCTCTTTT 10156
QY 3362 ValIleProGluAsnAlaLeuSerGluLysGluPheTyrValAspGlnAsnValSer 3381
DB 10157 GTGATTTCCGAGAAATGCTCTGCTGTCTGAAAGAGGATTTTATGTGATCAGAAATGTGTCC 10216
QY 3382 IleLysCysArgGluGlyPheLeuGlnGlyHisGlyIleIleThrCysAsnProAsp 3401
DB 10217 ATCAATGTAGGAGGAGTTTCTGCTGAGGGGCCACGGCATCATTTACCTGCAACCCCGAC 10276
QY 3402 GluThrTrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProProAlaHis 3421
DB 10277 GAGACGTGGACACACAGACGCGCAATGTGAAATAATCTCATGTGTGTCACCGACTCAC 10336
QY 3422 ValGluAsnAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyrSer 3441
DB 10337 GTAGAAATGCAATTTGCTCGAGGGCTATCATTAATGAGAGCATGATCACCTACTACA 10396
QY 3442 CysTyrSerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGlyThr 3461
DB 10397 TGTACAGTGGATACATTTGGAGGGTTTCTGAGGAGTGTGTGTGTAGAAATAGNACA 10456
QY 3462 TrpThrSerProProIleCysArgAlaValCysArgPheProCysGlnAsnGlyGlyIle 3481
DB 10457 TGGACATCACTCTCTATTTGCAGAGCTGTCTGTCCATTTCCATGTCCAGATGGGGGCATC 10516
QY 3482 CysGlnArgProAsnAlaCysSerCysProGluGlyTyrMetGlyArgLeuCysGluGlu 3501
DB 10517 TGCACACGCCCAATGCTGTCTCTGTCACAGAGGGCTGATGGGGCGGCTCTCTGTGAAGAA 10576
QY 3502 ProIleCysIleLeuProCysLeuAsnGlyGlyArgCysValAlaProTyrGlnCysAsp 3521

10577	CCAATCGCAATCTTCCCTGCTCTGAACGGAGGTGCGTGTGTGGCCCTTACCAGTGTGAC	10636
Qy	CysProProGlyTTPThrGlySerArgCysHisThrAlaValCysGlnSerProCysLeu	3541
10637	TGCCCGCGCTGGCTGGACGGGGTCTCGCTGTGCATACAGCTGTTTGCAGCTCCCTCGCTTA	10696
Qy	AsnGlyGlyCysCysValArgProAsnArgCysHisCysLeuSerSerTTPThrGlyHis	3561
10697	AATGSGTGGAAAATGTGTAAACCAACCAAGTGTCACTGTCTTCTTCTTGGACGGGACAT	10756
Qy	AsnCysSerArgLysArgThrGlyPhe	3571
10757	AACGTGTTCCAGGAAAAGGAGCACTGGGTTT	10786

RESULT 5
AAD32026
ID AAD32026 standard; cDNA; 11230 BP.

Mouse; C3b/C4b complement receptor-like protein; CR-like; diabetes;
 immune system disorder; rheumatoid arthritis; psoriatic arthritis;
 inflammatory arthritis; osteoarthritis; inflammatory joint disease;
 autoimmune disease; multiple sclerosis; inflammatory bowel disease;
 transplant rejection; graft versus host disease; atherosclerosis; lupus;
 stroke; Alzheimer's disease; ischaemic condition; neutropic; restenosis;
 myocardial infarction; ischaemia; metabolic disorder; obesity;
 reproductive disorder; infertility; nervous system disorder;
 gene therapy; immunomodulatory; antipsoriatic; antiinflammatory;
 neuroprotective; vasodilator; cardiatic; anorectic; gene; ss.

XX
 XX
 OS Mus musculus.

Key	Location/Qualifiers
CDS	95..110879
aa	/*tag= a
FT	/product= "Mouse C3b/C4b CR-like protein"
FT	/transl_except= (pos:5363..5365, aa:Xaa)
FT	/note= "Xaa corresponds to an unknown amino acid; CDS
FT	does not include start codon"
FT	/partial

PN WO200210388-A2.

XX
PD 07-FEB-2002.

24-JUL-2001: 2001WO-US023548.

XX
PR 01-AUG-2000: 2000US-0222438P.

XX PA (AMGE-) AMGEN INC.

XX PI Welcher AA. Elliot GS:

XX
DR WPI: 2002-257381/30.

DR P-PSDB; AAE20147.
YY

XX Nucleic acid encoding a novel C3b/C4b Complement Receptor (CR)-like
PT nucleic acid molecule, useful for treating, preventing and diagnosing
PT rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, and
PT multiple sclerosis

XX
PS
Claim 1: Fig 2A-2H: 201pp: English:

xx The invention relates to C3b/C4b complement receptor (CR)-like protein
cc and its corresponding nucleic acid sequence. The C3b/C4b CR-like
cc polypeptide and nucleic acid molecules may be used to treat, prevent,
cc ameliorate, diagnose and/or detect diseases such as immune system

disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory
arthritis, osteoarthritis, inflammatory joint disease, autoimmune
disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
transplant rejection, graft versus host disease, nervous system disorders
(e.g. stroke, Alzheimer's disease), ischaemic conditions (e.g.
atherosclerosis, restenosis, myocardial infarction, and ischaemia),
metabolic disorders (e.g. obesity and diabetes); and reproductive
disorders and infertility. The C3b/C4b CR-like nucleic acid molecules are
used in gene therapy. The present sequence is mouse C3b/C4b CR-like cDNA
Sequence 11230 BP; 2714 A; 2981 C; 2886 G; 2648 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	0	Length:	11230
Score:	16707.00	Matches:	2915
Percent Similarity:	89.72%	Conservative:	289
Best Local Similarity:	81.63%	Mismatches:	361
Query Match:	83.65%	Indels:	5
DB:	6	Gaps:	6

US-09-977-053-4 (1-3571) x AAD32026 (1-11230)

Qy		1	MetTrpProArgLeuAlaPheCysCysTrpGlyLeuAlaLeuValSerGlyTrpAlaThr	20
Db		176	ATGTGGTCGGCCCTGGCCCTTTTGTGTCTGGGCTCTGGCACATGGTGTCGGGCCTGGACCAAC	235
Qy		21	PheGlnGlnMetSerProSerArgAsnPheserPheArgLeuPheProGluThrAlaPro	40
Db		236	TTCAGGCCCGTGGCCCCCTTCGCTCAACTTCAGCTTCGCGCTGTTCGCCGAGGCCTCTCCG	295
Qy		41	GlyAlaProGlySerIleProAlaProProAlaProGly---AspGluAlaAlaGlySer	59
Db		296	GGGACTCTGGGCAGACTGGCGGTACTTCCCGGTCCAGTGAGGAGGAGGCGCAGCGGAGC	355
Qy		60	ArgValGluArgLeuGlyGlnAlaPheArgArgValArgValArgLeuArgGluLeuSer	79
Db		356	AAAGTGGAGCCCTGGGCGCGCGTTCGCGAGCCGCGTGGCGGAGCTGCGGGAGCTCAGC	415
Qy		80	GluArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGluValAsnPhe	99
Db		416	GGCAGCCTGGAGCTCGCTTCTGTGTGACGAGTGTCCAGGTGGCGGCCNAACCAACTTTC	475
Qy		100	ArgSerGluLeuMetPheValArglysLeuLeuSerAspPheProValValProThrAla	119
Db		476	CTCAACGAGCTCAAGTTGCTGGCCAAGCTGTGTCCGACTTCCCCTGGTGTCTCCAGCGC	535
Qy		120	ThrArgValAlaLalleValThrPheSerserIylsAsnTyrValValProArgValAspTyr	139
Db		536	ACGCGTGTGGCATCGTCACCCTTCTCATCCAAGAACAACGTGTGTGGCGCGCGTGGATTAC	595
Qy		140	IleSerThrArgArgAlaArgGlnHisIylsCysAlaLeuLeuGlnGluIleProAla	159
Db		596	ATCTCCACAGCCGCGCGCCACCAACANGTGGCGCTGTCTCAGCGCGAGATCCCGGCC	655
Qy		160	IleSerTyArgGlyGlyGlyThyTrThrIysGlyAlaPheGlnGlnAlaAlaGlnIle	179
Db		656	ATCACCTACCGCGTGTGGCACCTATACCAAGGCGCCTTCCAGCNAGCCCGCCAAATC	715
Qy		180	LeuLeuHisAlaArgGluAsnSerThrIylsValValPheLeuIleThrAspGlyTyrSer	199
Db		716	CTTCGTCACTCTAGAGAAAACTCACCAAGTCAATAATTTCATCACCGACGGCTATTCC	775
Qy		200	AsnGlyGlyAspProArgProIleAlaAserLeuArgAspSerGlyValGluIlePhe	219
Db		776	AATGGCGGAGCCCCAGACCTATTTCAGCAATCGCTTCGGGATTTCCGAGTGGAGATCTTC	835
Qy		220	ThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetalSerThrProIyls	239
Db		836	ACGTTTCGGGATTTTCGAGGGGAATATCCGGGAACTGAATGACATGGCTTCCACCCCGAAG	895
Qy		240	GluGlnHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgArgAla	259
Db		896	GAAGAACATTGTACCTGCTCCACAGTTTTCAAGAAATTGAGGCTTAGCGAGGGCG	955

QY 260 LeuHisGluAspLeuProSerGlySerPheIleGlnAspMetValHisCysSerTyr 279
DB 956 TTGCATGAAGTCTACCTCTCGGAGTTTATCCAGAGATATGCGCCACTGCTCTAT 1015
QY 280 LeuCysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHis 299
DB 1016 CTCTGTGAGCTGGGAAGACTGCTGTGACAGAAATGGCCAGCTGCAAAATGTGGACACAC 1075
QY 300 ThrGlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGlu 319
DB 1076 ACGGGTCAATTTGAATGTCATCTGTGGAAGGGCTATTACGGGAAGGTCTGCGACATGAG 1135
QY 320 CysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSer 339
DB 1136 TGCACAGCTTGGCCATCAGGACATATACCGGAGCTTCTCAGGAGGAATCAGCC 1195
QY 340 CysIleProCysProAspGluAenHisThrSerProGlySerThrSerProGluAsp 359
DB 1196 TGCATCCCATGCTCTGAGGTAAAGCCACACCTCCCACTTGGAGCCTTCCCTGAGAC 1255
QY 360 CysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysPro 379
DB 1256 TGGGTGTGCGAGAGGATACAGAGATCTGGCCAGACCTGTGAGGTGTGCCACTGTCT 1315
QY 380 AlaLeuLysProProGluAenGlyTyrPheIleGlnAenThrCysAenAenHisPheAen 399
DB 1316 GCCCTGAGGCTCTGAAATGTTTTTTTATACAAACACTTGCAAAACACTTCTTCAT 1375
QY 400 AlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeu 419
DB 1376 GCGCGCTGTGGGTCCGATGTCGCCCGGGCTTGGACCTTGTGGNAGCAGATCCATTG 1435
QY 420 CysLeuProAenGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysPro 439
DB 1436 TGTCAACCCCAATGGTTGTGCTGTGGACAGAAAGCTTCTGCAGAGTGAAGACGTGCC 1495
QY 440 HisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLys 459
DB 1496 CACCTCCGACAGCCCAACACGCGCCACATCAGCTGTCTCCACTCGGGAATGTCTCTAC 1555
QY 460 ThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThr 479
DB 1556 ACCCTGTGTTGTTGCTACCTGCAATGAAGGATACAGATTAGAGGCAGCAGCTAGCTTACC 1615
QY 480 CysGlnGlyAenSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSer 499
DB 1616 TGTCAAGGAAATGCCAGTGGGATGGCCAGAGCCCGGTGTGTAGAACGCCATTTGTGCC 1675
QY 500 ThrPheGlnMetProLysAspValIleIleSerProHisAenCysGlyLysGlnProAla 519
DB 1676 ACCTCCAGAGCCCAAGCGGTCATCATTTCTCCACCCAGCTGGCGAAGCAGCCGCC 1735
QY 520 LysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLys 539
DB 1736 AGGCTGGGATGACCTGTACGTGAAGTGGCGCGCAGGGATACATTTTATCGGGGTGAGA 1795
QY 540 GluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCys 559
DB 1796 GAA--GTGAGATGTGCCATCTGGGAAGTGGAGTGCCAAAGTTTCAGACAGCTGTGTGC 1852
QY 560 LysAspValGluAlaProGlnIleAenCysProLysAspIleGluAlaLysThrLeuGlu 579
DB 1853 AAGATGTGGAGCTCCACAAATCAGCTGTCCAAATGACATGAGGCAAGATCTGGGAG 1912
QY 580 GlnGlnAspSerAlaAenValThrTrpGlnIleProThrAlaLysAspAenSerGlyGlu 599
DB 1913 CAGCAGACTCTGCTAATGCCACTGCGAAGTCCCAAGTCCCAAGTCCCAAGTCCCAAGT 1972
QY 600 LysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp 619
DB 1973 AAGGTGTAGTCCAGCTCCACCCAGCTTTACCCCACTTACCTCTTCCCAATTTGGAGAC 2032

QY 620 ValAlaIleValTyrThrAlaThrAspLeuSerGlyAenGlnAlaSerCysIlePheHis 639
DB 2033 GTGGCATCACCTACACGGCAACCGACTCATCCGTTAACCAAGCCAGCTGCATTTCTAC 2092
QY 640 IleLysValIleAspAlaGluProProValIleAspTrpCysArgSerProProVal 659
DB 2093 ATTAAAGTCAATTGATGTGGAACCGCTGTATAGATTGGTCCGATCTCCACTCCAATC 2152
QY 660 GlnValSerGluLysValHisAlaAspTrpAspGluProGlnPheSerAspAenSer 679
DB 2153 CAGTCTGATAGAGAGGACCCCTGCAAGCTGGATGAGCTCAGTCTTCAGACACTCC 2212
QY 680 GlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGlu 699
DB 2213 GGGGTGAATTGGTCAATTACAGCAGTACACACAGGCGACATGTTTCTCATGGGAA 2272
QY 700 ThrIleValGlnTyrThrAlaThrAspProSerGlyAenAenArgThrCysAspIleHis 719
DB 2273 ACGTGTGTGTGTACACAGCCACTGACCCCTCAGGCAACACAGGACCTGTGACATCCAC 2332
QY 720 IleValIleLysGlySerProCysGluIleProPheThrProValAenGlyAspPheIle 739
DB 2333 ATTGTCAATAAAGGTCTCCCTGTGAGGTCCCTTCAACCTGTAAACGGGACTTTATC 2392
QY 740 CysThrProAspAenThrGlyValAenCysThrLeuThrCysLeuGluGlyTyrAspPhe 759
DB 2393 TGTGCCCAGATAGTGTGGAGTTAACTGTAGCTGAGCTGCAAGAGGGCTATGATTTC 2452
QY 760 ThrGluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThr 779
DB 2453 ACAGAAGGTCACTGAGAAGTACTCTGTGCTTTTGAAGATGTGTATCTGGAGACCA 2512
QY 780 TyrThrThrGluTrpProAspCysAlaLysLysArgPheAlaAenHisGlyPheLysSer 799
DB 2513 TACTTACAGAATGGCCAGACTGTGCTGTATAAAGCTTTGCAACCATGGTTTCAAGTCC 2572
QY 800 PheGluMetPheTyrLysAlaAlaAargCysAspAspThrAspLeuMetLysLysPheSer 819
DB 2573 TTTGAAATGCTATACAAACCACTCGCTGTGTGATGACATGCTGTTTAAAGATTTTCT 2632
QY 820 GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
DB 2633 GCAGCATTTTCAGACTACCTGGGGAACATGTCCTCCGCTCTTTGTAACGATGCTGATAC 2692
QY 840 IleAspCysArgLeuGluAenLeuThrLysLysTyrCysLeuGluTyrAsnTyrAsp 859
DB 2693 ATTGACTGCAGACTGGAGGAC---CTGACCAAAAATACTGCATCGAGTATATATTACAA 2749
QY 860 TyrGluAenGlyPheAlaIleGlyProGlyTyrTrpGlyAlaAlaAenArgLeuAspTyr 879
DB 2750 TATGAAATGGCTTTGCAATTTGACCCAGGAGGCTGGGGTGCAGGCAACAGGCTGATAT 2809
QY 880 SerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLys 899
DB 2810 TCCTACGATCACTTCTCGATGTTGTACAGAAACACCCAGCATGTGGGCAAGGCCAGA 2869
QY 900 SerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAen 919
DB 2870 TCTGTACGGAATTAAGAACTGTCCCATTTGTGACCCCAAAATTCAGTAAATTTTAAAC 2929
QY 920 IleThrAlaSerValProLeuProAspGluArgAenAspThrLeuGluTrpGluAenGln 939
DB 2930 ATCAGCTAGCTGTGCACCTCCAGAGGAAGAAACGATACCTTTGAATTGGAGAAATCAG 2989
QY 940 GlnArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLysArgThrLeuAenLys 959
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Qy 1680 GlnProLeuProHisCysGluArgIleSerCysGlyValProProLeuGluAsnGly 1699
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Db 10721 TGTGACTGCCCCCAACAGCTGAGCTGGGTCCCGCTGTCTATACAGCTACTTGTGAGTCCCCC 10780

Qy 3540 CysLeuAsnGlyGlyLysCysValArgProAsnArgCysHisCysLeuSerSerTrpThr 3559
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Qy 3560 GlyHisAsnCysSerArgLysArgArgThrGly 3570
Db 10841 GGACATGATGTTTCCAGGAAAGAGAGCGCGG 10873
RESULT 6
AAK94920
ID AAK94920 standard; cDNA; 5421 BP.
XX AC AAK94920;
XX 06-NOV-2001 (first entry)
XX Human full-length cDNA, SEQ ID NO: 4152.
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX Homo sapiens.
XX EP1130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000EP-00114089.
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
XX 02-MAY-2000; 2000JP-00183765.
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI: 2001-524255/58.
XX P-PSDB; AAM93954.
XX 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX Claim 8; SEQ ID NO 4152; 1380pp + Sequence Listing; English.
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have
XX been determined. Primers for synthesizing the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a full length human cDNA of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in CD-ROM format directly
XX from EPO
XX SQ Sequence 5421 BP; 1398 A; 1275 C; 1318 G; 1430 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 5421
Score: 9400.00 Matches: 1676
Percent Similarity: 97.56% Conservative: 4
Best Local Similarity: 97.33% Mismatches: 11
Query Match: 47.06% Indels: 32
DB: 4 Gaps: 1
US-09-977-053-4 (1-3571) x AAK94920 (1-5421)
Qy 1881 GlyAspLysGluSerSerCysLeuAlaAsnSerSerTrpSerHisSerProProValCys 1900
Db 3 GGTGATAAAGAAATCATCTCTGCTTGTAAACAGATTCTTGGAGTCATTCCTCCCTCTGTGTGT 62

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Db 2222 GGTCTGTCATGCGACAGACCTGTGAAGAGTCAGGATGGTCAAGTTCCATCCCAACATGTATG 2281
Qy 2610 ProIleAspCysGlyLeuProHisIleAspPheGlyAspCysThrIysLeuIysAsp 2629
Db 2282 CCAATAGACTGTGGCTCCCTCTCATATAGATTTTGGAGACTGTACTAAACTCAAGAT 2341
Qy 2630 AspGlnGlyTrpPheGlnGlnGluAspAspMetMetGluValProIleHis 2649
Db 2342 GACCAGGATATTTTCAGCAAGAGAGACATCATGGAAGTTCCATATGTGACTCTCTCAC 2401
Qy 2650 ProProIleHisLeuGlyAlaValAlaIysThrTrpGluAsnThrIysGluSerProAla 2669
Db 2402 CCTCTTATCATTTGGGAGCAGTGGCTAAACCTGGCAAAATACAAAGGAGTCTCTGCT 2461
Qy 2670 ThrHisSerSerAsnPheLeuTrpGlyThrMetValSerTrpCysAsnProGlyTrp 2689
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Qy 2710 ProSerCysIleSerIleGluCysAspLeuProThrAlaProGluAsnGlyPheLeuArg 2729
Db 2582 CCATCTCTGATTCATTAATGATGTGACTTGGCTTACTGCTCTCTGAAATGGCTTTTGGGT 2641
Qy 2730 PheThrGluThrSerMetGlySerAlaValGlnTrpSerCysIysProGlyHisIleLeu 2749
Db 2642 TTTACAGAGACTAGCATGGGAGTGTGTGACATATAGCTGTAAACCTGGACACATTTCTA 2701
Qy 2750 AlaGlySerAspLeuArgLeuCysLeuGluAsnArgIleTrpSerGlyAlaSerProArg 2769
Db 2702 GTGGGCTCTGGCTTAAGGCTTTGTCTAGAGATAGAAAGTGGAGTGGTGGCTCCCAAGC 2761
Qy 2770 CysGluAlaIleSerCysIysIysProAsnProValMetAsnGlySerIleIysGlySer 2789
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Qy 2790 AsnTrpThrIleuSerThrIleuTrpGlyLeuGluCysAspProGlyTrpValLeuAsnGly 2809
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Qy 2810 ThrGluArgArgThrCysGlnAspAspIysAsnTrpAspGluAspProIleCysIle 2829
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Qy 2910 MetIysGluValThrPheHisCysHisGluGlyTrpIleLeuHisGlyAlaProIysLeu 2929
Db 3182 ATGAAGGAAGTAACATTCCTGTCACGAGGGGTACATCTTGCACCGGTGCTCCAAACTC 3241
Qy 2930 ThrCysGlnSerAspGlyAsnTrpAspAlaGluIleProLeuCysIysProValAsnCys 2949
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Qy 2950 GlyProProGluAspLeuAlaHisGlyPheProAsnGlyPheSerPheIleHisGlyGly 2969
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Db 3302 GGACCTCTCTGAAGATCTTGCCCATGGTTTCCCTAAATGGTTTCTTTATTTATTCATGGGGGC 3361
Qy 2970 HisIleGlnTrpGlnCysPheProGlyTrpLysLeuHisGlyAsnSerSerArgArgCys 2989
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Qy 3230 ProPheSerAspGluSerCysSerProValSerCysGlyIysProGluSerProGluHis 3249
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 DB 4562 TCTGAAGAGGAGTTTATGTTGATCAGATGTCATCAATGTAGGGAAGTTTCTG 4621
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 DB 4622 CTGACGGGCCACCGCATCATTAACCTACACCCGCGACGACGTCGACACAGACGCGC 4681
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 QY 3430 ValHisTyrGlnTyrGlyAspMetIleThrTyrSerCysTyrSerGlyTyrMetLeuGlu 3449
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 QY 3450 GlyPheLeuArgSerValCysLeuGluAsnGlyThrTrpThrSerProPheCysArg 3469
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 DB 4862 GCTGTCTGTCGATTTCCATGTGAGAAATGGGGCATCTGCACAGCCCAATGCTTGTTC 4921
 QY 3490 CysProGluGlyTyrMetGlyArgLeuGluGluProIleCysIleLeuProCysLeu 3509
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 QY 3510 AsnGlyGlyArgCysValAlaProTyrGlnCysAspCysProGlyTyrThrGlySer 3529
 DB 4982 AACGGAGGTGCTGTGTGGCCCTTACAGTGTGACTGCGCGCTGGTGGAGGGGCT 5041
 QY 3530 ArgCysHisThrAlaValCysGlnSerProCysLeuAsnGlyGlyLysCysValArgPro 3549
 DB 5042 CGCTGTCTACAGCTGTTGGCCAGTCTCTCTGCTTAAATGGTGAATAATGTATAGACCA 5101
 QY 3550 AsnArgCysHisCysLeuSerTrpThrGlyHisAsnCysSerArgLysArgThr 3569
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 QY 3570 GlyPhe 3571
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RESULT 7
 ABA03880
 ID ABA03880 standard; cDNA; 6153 BP.

AC ABA03880;
 DT 14-FEB-2002 (first entry)
 XX Human POLY11 nucleotide sequence SEQ ID NO:21.
 DE Human; POLYX; gamma aminobutyric acid receptor; GABA receptor;
 KW epidermal growth factor; EGF; complement receptor; HSPC; syntaxin;
 KW haematopoietic stem and progenitor cell; sulphotransferase; prohibitin;
 KW antidepressant; neuroleptic; antiparkinsonian; neurotropic; relaxant;
 KW anticonvulsant; neuroleptic; neuroprotective; antialcoholic; cardiant;
 KW tranquilliser; antiarrhythmic; psychiatric; medical; depression; anxiety;
 KW Parkinson's disease; Huntington's disease; Tourette's syndrome; stroke;
 KW amyotrophic lateral sclerosis; head trauma; Alzheimer's disease;
 KW alcoholism; vigilance; muscle tension; epileptogenic; memory function;
 KW cardiomyopathy; arrhythmogenic right ventricular dysplasia; 88.

XX OS Homo sapiens.
 XX Key
 FH CDS
 FT 1. 6153
 FT /tag= a "POLY11"
 FT /product= (pos:1099..1101,aa:Xaa)
 FT /transl_except= (pos:1099..1101,aa:Xaa)
 FT /note= "Xaa is unknown"
 XX WO200179294-A2.
 XX 25-OCT-2001.
 XX 19-APR-2001; 2001WO-US012854.
 XX 19-APR-2000; 2000US-0198293P.
 XX 20-APR-2000; 2000US-0198645P.
 XX 25-APR-2000; 2000US-0199476P.
 XX 26-APR-2000; 2000US-0199880P.
 XX 26-APR-2000; 2000US-0200024P.
 XX 26-APR-2000; 2000US-0200025P.
 XX 09-JUN-2000; 2000US-0210809P.
 XX 17-JUL-2000; 2000US-0218591P.
 XX 11-AUG-2000; 2000US-0224610P.
 XX 09-FEB-2001; 2001US-0267673P.
 XX 27-FEB-2001; 2001US-0271814P.
 XX (CURA-) CURAGEN CORP.
 XX Taupier RJ, Vernet CAM, Fernandes E, Shinkets RA, Majumder K;
 PI Padigaru M, Colman SD, Zerhusen BD, Spytek KA, Burgess CE, Liu X;
 XX WPI; 2002-017601/02.
 XX P-PSDB; AAG68264.
 XX New isolated polypeptides for treating a broad range of pathological
 PT states, e.g., depression, stroke, Parkinson's disease, Huntington's
 PT disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma,
 PT and Alzheimer's.
 XX Claim 9; Page 43-45; 155pp; English.
 XX The present invention describes polypeptides (I), designated POLYX
 CC polypeptides (e.g. POLY1, POLY2, etc.), and the polynucleotide sequences
 CC (II) encoding them. POLY1-4 are members of the gamma aminobutyric acid
 CC (GABA) receptor family; POLY5-8 are members of the epidermal growth
 CC factor (EGF) family; POLY9-11 are members of the complement receptor
 CC family; POLY12 is a member of the haematopoietic stem and progenitor cell
 CC (HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14
 CC -16 are members of the syntaxin family; and POLY17 is a member of the
 CC prohibitin family. (I) and (II) can have antidepressant,
 CC neuroprotective, antiparkinsonian, neurotropic, relaxant, anticonvulsant,
 CC neuroleptic, neuroprotective, antialcoholic, cardiant, tranquiliser and
 CC antiarrhythmic activities. (I) and (II) can be used for treating or
 CC preventing a POLYX-associated disorder in humans as a therapeutic in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease selected from a POLYX-associated disorder, for treating a
 CC pathological state in a mammal, especially patients suffering from, e.g.,
 CC psychiatric and medical conditions, depression, stroke, Parkinson's
 CC disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral
 CC sclerosis, head trauma, Alzheimer's disease, alcoholism, vigilance,
 CC anxiety, muscle tension, epileptogenic activity and memory functions,
 CC cardiomyopathy and arrhythmogenic right ventricular dysplasia. The
 CC present sequence encodes POLY11
 XX SQ Sequence 6153 BP; 1610 A; 1482 C; 1563 G; 1497 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 0 Length: 6153
 Score: 8427.00 Matches: 1535
 Percent Similarity: 78.65% Conservative: 1
 Best Local Similarity: 78.60% Mismatches: 5

Query Match: 42.19% Indels: 412
DB: 6 Gaps: 3
US-09-977-053-4 (1-3571) x ABA03880 (1-6153)

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193 TATACTCTTGGTCTTGACACCATTTGAATGCTGGCCGACGCGCAAGTGGAGTAGAGT 252
2013 AspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAlaAspHisAlaSerPro 2032
253 GACACAGAGTGGCTGGCTCTCTCTGATGAGCCACCCATTTGTGACCAAGCGCTCTCCA 312
2033 GluThrAlaHisArgLeuPheGlyAspIleAlaPheTyrTyrCysSerAspGlyTyrSer 2052
313 GAGACTGCCCATGGCTCTTTGGAGACATTTGCATTTACTACTGCTCTGATGTTTACAGC 372
2053 LeuAlaAspAsnSerGlnLeuLeuCysAsnAlaGlnGlyLysTrpValProProGluGly 2072
373 CTAGCAGACATTTCCAGCTTCTCTGCAATGCCAGGSCAAGTGGGTACCCCCAGAGGT 432
2073 GlnAspMetProArgCysIleAlaHisPheCysGluLysProProSerValSerTyrSer 2092
433 CAAGACATGCCCGTGTGTATAGCTCATTTCTGTGAAAAACCTCCATCGGTTTCTATAGC 492
2093 IleLeuGluSerValSerLysAlaLysPheAlaAlaGlySerValValSerPheLysCys 2112
493 ATCTTGGAACTGTGAGCAAGCAAAATTTGCAAGCTGGCTCAGTTGTGAGCTTTAAATGC 552
2113 MetGluGlyPheValLeuAsnThrSerAlaLysIleGluCysMetArgGlyGlyGlnTrp 2132
553 ATGGAAGGCTTTGTACTGAACACCTCAGCAAGATTTGAATGATGAGAGTGGCGAGTGG 612
2133 AsnProSerProMetSerIleGlnCysIleProValArgCysGlyGluProProSerIle 2152
613 AACCCCTTCCCATGATGCCATCCATCCCTGTGCGGTGTGGAGAGCCACCAAGCATC 672
2153 MetAsnGlyTyrAlaSerGlySerAsnTyrSerPheGlyAlaMetValAlaTyrSerCys 2172
673 ATGAATGGCTATGCAAGTGGATCAACTACAGTTTGTGAGCCATGTTGGCTTACAGCTGC 732
2173 AsnLysGlyPheTyrIleLysGlyLysLysSerThrCysGluAlaThrGlyGlnTrp 2192
733 AACAGGGGTTCTACATCAAGGGGAAAAAGAGAGACACCTGCGAAGCCACAGGGCAGTGG 792
2193 SerSerProIleProThrCysHisProValSerCysGlyGluProProLysValGluAsn 2212
793 AGTAGTCTTATACCGAGCTGCCACCCGGTATCTTGTGTGAACCACTAAGGTTGAGAAT 852
2213 GlyPheLeuGluHisThrThrGlyArgIlePheGluSerGluValArgTyrGlnCysAsn 2232
853 GGCTTTCTGGAGTACAACTGGCAGATCTTTGAGAGTGAAGTGAAGTATCAGTGTAAAC 912
2233 ProGlyTyrLysSerValGlySerProValPheValCysGlnAlaAsnArgHisTrpHis 2252
913 CCGGGCTATAAGTCAGTGGAGTCTCTGTATTTGTCTGCCAAGCCATCGCCACTGGCAC 972
2253 SerGluSerProLeuMetCysValProLeuAspCysGlyLysProProProIleGlnAsn 2272
973 AGTGAATCCCTCTGATGTGTGTCTCTCTCGATGTGGAAAAACCTCCCGGATCCAGAAT 1032
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2352 GlyHisValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnGlnTrpAsnAsp 2371
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2372 SerPheProValCysLysIleValLeuCysThrProProProLeuIleSerPheGlyVal 2391
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2392 ProIleProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGlyGly 2411
1393 CCATTTCTTCTTCTCTCTCTTCAATTTTGGAGTACTGTCAAGTATTTCTGTGAGGTGG 1452
2412 PhePheLeuArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerPro 2431
1453 TTTTCTCTAAGAGGAAATTTCTACACCTCTGCCCACTGATGGCAGCTGGAGCTCTCCA 1512
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1513 CTGCCAGAAATGTTCCAGTAGAATGTCCCAACCTGAGGAAATCCCAATGGAATCAAT 1572
2452 AspValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGlu 2471
1573 GATGTGCAAGGCTTGGCTATCTCAGCACAGCTCTCTATACCTGCAAGCCAGGCTTGA 1632
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2572 TyrSerTyrGlyAlaIleIleTyrSerCysPheProGlyPheGlnValAlaGlyHis 2591
1933 TACAGCTATGGTGGCAATATCATCTACAGTTGCTTCCCTGGGTTTCAGGTGGCTGCAT 1992
2592 AlaMetGlnThrCysGluGluSerGlyTrpSerSerSerIleProThrCysMetProIle 2611
1993 GCCATGCAGACCTGTGAAGAGTCCAGATGTTCCATTCACCATGTATGCCAATA 2052
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2632 GlyTyrPheGluGlnGluAspAspMetMetGluValProTyrValThrProHisProPro 2651
2113 GGATATTTTGGACAGAGACGACATGATGGAAGTTCCATATGTGACTCTCTCACCCCTCT 2172
2652 TyrHisLeuGlyAlaValAlaLysThrTrpGluAsnThrLysGluSerProAlaThrHis 2671
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2672 SerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProGlyTyrGluLeu 2691
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2752 SerAspLeuArgLeuCysLeuGluAsnArgIleTyrSerGluValAspProArgCysGlu 2771
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2892 AlaThrProProGlnLeuAlaAsnGlyValThrGluGlyLeuAspTyrGlyPheMetLys 2911
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2972 GlnTyrGlnCysPheProGlyTyrIleLeuHisGlyAsnSerSerArgArgCysLeuSer 2991
3133 CAGTATCAGTGTCTTCTGCTGTTATAAGTCCATGGAAATTCATCAAGAAGGTGCTCTCC 3192
2992 AsnGlySerTrpSerGlySerProSerCysLeuProCysArgCysSerThrProVal 3011
3193 AATGGCTCTGGAGTGGCAGCTCACCTTCTGCTGCTGTGAGATGTTCCACACCACTA 3252
3012 IleGluTyrGlyThrValAsnGlyThrAspPheAspCysGlyIleValAlaArgIleGln 3031
3253 ATTGAATATGGAATCTGCAATGGACAGATTTTGTGCTGGAAAGCAGCCCGGATTCAG 3312
3032 CysPheIleGlyPheIleLeuGlyLeuSerGluIleThrCysGluAlaAspGlyGln 3051
3313 TGCTTCAAGGGCTCAAGCTCTTAGGACTTTCTGAAATATCACTGTGAAGCCGATGGCCAG 3372
3052 TrpSerSerGlyPheProHisCysGluHisThrSerCysGlySerLeuProMetIlePro 3071

3373 TGGAGCTCTGGGTTCCCCCACTGTGAACACACTTCTCTTGTGGTTCTCTTCCAAATGATACCA 3432
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3433 AATGCGTTTCATCAGTGCAGACCACTCTTGGAGGAAAAATGTGATAACTTACAGCTGCAGG 3492
3092 SerGlyTyrValIleGlnGlySerSerAspLeuIleCysThrGluLysGlyValTrpSer 3111
3493 TCTGGAATATGTATACAGGCAGTTCAGATCTGATTTGTATACAGAGAAAGGGGTATGGAGC 3552
3112 GlnProTyrProValCysGluProLeuSerCysGlySerProProSerValAlaAsnAla 3131
3553 CAGCCTTATCAGTCTGTGAGCCCTTGTCTGTGGGTCCCACTGCTGTGCGCAATGCA 3612
3132 ValAlaThrGlyGluAlaHisThrTyrGluSerGluValLysLeuArgCysLeuGluGly 3151
3613 GTGGCAACTGGAGAGGACACACCTATGAAAGTGAAGTGAAGTCAAGATCTCAGATCTCTGGAAGGT 3672
3152 TyrThrMetAspThrAspThrPheThrCysGlnLysGlyValArgTrpPhePro 3171
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3172 GluArgIleSerCysSerProLysLysCysProLeuProGluAsnIleThrHisIleLeu 3191
3733 GAGAGAAATCTCTGAGTCTTAAATAATGTCTCTCCGGAANAACATAACACATATACTT 3752
3192 ValHisGlyAspAspPheSerValAsnArgGlnValSerValSerCysAlaGluGlyTyr 3211
3793 GTACATGGGAGCGATTTTCAGTGTGAATAGCAAGTTCGTGTCACTGTGCAGAGGGGTAT 3852
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4213 CCTCTGGAAGTTTGTCTCAGAGGAATACCCGGCCATGTGAGGTGTGAGTCCGCCCTTAC 4272
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4393 GAAAAACAGGACGACTGGAACCAAGCTGTATATTTCTGCAACAGAGGCTACAGCTCTTGA 4452
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QY 3441 SerCysTyrSerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGly 3460
DB 5773 TCATGTTACAGTGATCATGATGTGAGGGTTCTCGAGAGAGTGTGTTTAAATAATGGA 5832
QY 3461 ThrTrpThrSerProPro1Leu1CysArgAlaValCysAspPheProCysGluAsnGlyGly 3480
DB 5833 ACATGACATCACTCTCATTTTGCAGACCTGTCTGCATTTCCATGTCAGAAATGAGGAC 5892
QY 3481 IleCysGlnArgProAsnAlaCysSerCysProGluGlyTyrMetGlyArgLeuCysGlu 3500
DB 5893 ATTCGCCAAGCCCAATGCTTGTCTCTGTCAGAGGGCTGATGGGGGCTCTGTGA 5952
QY 3501 GluProIleCysValLeuProCysLeuAsnGlyGlyArgCysValAlaProTyrGlnCys 3520
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DB 6013 GACTGCCCTGGCTGAGAGGGGTCTGCTGTCTATACA 6051

RESULT 8
ID ABX56476
ABX56476 standard; cDNA; 6152 BP.
AC ABX56476;
XX
DT 17-FEB-2003 (first entry)
DE
XX cDNA encoding novel human complement receptor-like protein #3.
XX
XX Gamma-aminobutyric acid receptor-like protein; depression; stroke;
XX GABA receptor-like protein; Parkinson's disease; Huntington's disease;
XX Tourette's syndrome; amyotrophic lateral sclerosis; head trauma;
XX Alzheimer's disease; alcoholism; vigilance; anxiety; muscle tension;
XX epileptogenic activity; memory; cardiomyopathy; cancer; angiogenesis;
XX arrhythmogenic right ventricular dysplasia; renal disease; diabetes;
XX epidermal growth factor like protein; leukaemia; lupus; anaemia; ulcer;
XX haematopoietic stem and progenitor cell like protein; cirrhosis;
XX sulfoxotransferase-like protein; cholangitis; hepatitis; hyperthyroidism;
XX developmental disorder; Syntaxin-like protein; myxoid liposarcoma;
XX asthma; Lambert-Raiton myasthenic syndrome; acute myeloid leukaemia;
XX transgenic animal; gene; SS.
XX
XX Homo sapiens.
XX OS
XX US2002123612-A1.
XX
XX
XX 05-SEP-2002.
XX
XX 03-JUL-2001; 2001US-00898570.
XX
XX
XX 19-APR-2000; 2000US-0198293P.
XX 20-APR-2000; 2000US-0198645P.
XX 25-APR-2000; 2000US-0199476P.
XX 26-APR-2000; 2000US-0199898P.
XX 26-APR-2000; 2000US-0200024P.
XX 26-APR-2000; 2000US-0200025P.
XX 09-JUN-2000; 2000US-0210809P.
XX 03-JUL-2000; 2000US-0215855P.
XX 17-JUL-2000; 2000US-0218591P.
XX 11-AUG-2000; 2000US-0224610P.

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PR 27-FEB-2001; 2001US-0271814P.
 XX (GERL/) GERLACH V L.
 PA (EILE/) EILBERMAN K. R.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 PI Gerlach VL, Eilberman K, Macdougall JR, Smithson G,
 XX MPI: 2003-066815/06.
 DR P-PSDB; AB012097.
 XX
 PT Novel polypeptides and nucleic acids which are members of epidermal
 PT growth factor, complement receptor families for diagnosing and treating
 PT psychiatric conditions, depression, stroke, Alzheimer's and Parkinson's
 PT disease.
 XX
 XX Claim 9; Page 28-31; 91pp; English.
 PS
 XX The invention describes an isolated POLYX (POLYX-17) polypeptide and its
 CC variant. POLYX polypeptides (especially POLY5, POLY6 and POLY7), the
 CC polynucleotides encoding them (I) and an anti-POLYX-antibody (III) are
 CC useful for treating or preventing a pathology associated with POLYX
 CC polypeptide in humans and for treating a syndrome associated with human
 CC disease. POLYX polypeptide is also useful for identifying an agent that
 CC binds to POLYX and a cell expressing POLYX is useful for identifying a
 CC therapeutic agent for use in treatment of a pathology related to aberrant
 CC expression or physiological interactions of the polypeptide. (III) is
 CC useful for treating a pathological state in a mammal and for determining
 CC the presence or amount of POLYX in a sample. POLYX-4 (GABA receptor-like
 CC proteins) are useful for the treatment of psychiatric and medical
 CC conditions, depression, stroke, Parkinson's disease, Huntington's
 CC disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma,
 CC Alzheimer's disease, alcoholism, vigilance, anxiety, muscle tension,
 CC epileptogenic activity and memory functions, cardiomyopathy and
 CC arrhythmogenic right ventricular dysplasia. POLY5-8 (Epidermal growth
 CC factor like proteins) may be useful for treating cancer, aberrant
 CC angiogenesis, renal disease and diabetes. POLY12 (hematopoietic stem and
 CC progenitor cell like protein) may be useful for treatment of leukemia,
 CC lupus and anaemia. POLY13 (nucleotransferase-like protein) may be useful
 CC for treating cirrhosis, cholangitis, hepatitis, ulcers, hyperthyroidism
 CC and developmental disorders. POLY14-16 (Syntaxin-like proteins) may be
 CC useful in treatment of Lambert-Eaton myasthenic syndrome, asthma, myxoid
 CC liposarcoma and acute myeloid leukemia, and POLY 18 may be useful in
 CC treatment of cancers. Cells comprising (I) are useful for producing non-
 CC human transgenic animals which are useful for studying the function
 CC and/or activity of POLYX protein and for identifying and/or evaluating
 CC modulators of POLYX protein activity. This sequence encodes a novel human
 CC protein
 CC
 SQ Sequence 6152 BP; 1609 A; 1483 C; 1562 G; 1497 T; 0 U; 1 Other:
 Alignment Scores:
 Pred. No.: 0 Length: 6152
 Score: 8400.50 Matches: 1534
 Percent Similarity: 78.55% Conservative: 0
 Best Local Similarity: 78.55% Mismatches: 7
 Query Match: 42.06% Indels: 413
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 QY 2013 AspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAspHisAlaSerPro 2032
 DB GACCAACAGAGGCTGGCTGCTCTCTGATGAGCAACCATTTGAGCAACGCTCTCCA 312
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 RESULT 9
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 ID AAD58963 standard; DNA; 6153 BP.
 AC AAD58963;
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 DT 18-DEC-2003 (first entry)
 XX
 DB Human complement receptor-like DNA (POLY11).
 XX
 KW Human; tumour; inflammatory disorder; vaccine; gene therapy; cytostatic;
 complement receptor-like protein; POLY11; gene; ds.
 OS Homo sapiens.
 XX
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 FT /tag= a
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 FT /note= "This CDS has translational exceptions"
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 US2003050232-A1.
 PN
 PD 13-MAR-2003.
 PE 19-APR-2001; 2001US-00839446.
 XX
 PR 19-APR-2000; 2000US-0198293P.
 PR 20-APR-2000; 2000US-0198645P.
 PR 25-APR-2000; 2000US-0199476P.
 PR 26-APR-2000; 2000US-0199880P.
 PR 26-APR-2000; 2000US-0200024P.
 PR 26-APR-2000; 2000US-0200025P.
 PR 09-JUN-2000; 2000US-0210809P.
 PR 17-JUL-2000; 2000US-0218591P.
 PR 11-AUG-2000; 2000US-0224610P.
 PR 27-FEB-2001; 2001US-0271814P.
 XX
 PA (TAUP/) TAUPIER R. J.
 PA (PADI/) PADIGARU M.
 PA (SPYT/) SPYTEK K. A.
 PA (BURG/) BURGESS C. B.
 PA (VERNET/) VERNET C. A. M.
 PA (FERN/) FERNANDES E. R.
 PA (SHIM/) SHIMKETS R. A.
 PA (LITX/) LIT X.
 PA (MAJU/) MAJUMDER K.
 PA (COLM/) COLMAN S. D.
 PA (ZERH/) ZERHUSEN B. D.
 PI Taupier RJ, Padigaru M, Spytek KA, Burgess CB, Vernet CM,
 PI Fernandez ER, Shimkets RA, Liu X, Majumder K, Colman SD;
 PI Zernusen BD;
 DR WPI: 2003-605764/57.
 DR P-PSDB; AAB38812.
 XX

PT New POLYX nucleic acid, useful for preparing a composition for treating
 PT or preventing e.g., tumor or inflammatory disorder.
 XX
 PS Claim 8; Page 28-31; 75pp; English.
 XX
 CC The invention relates to new POLYX nucleic acid useful for preparing a
 CC composition for treating or preventing tumor or inflammatory disorder.
 CC The invention is useful as vaccine and in gene therapy. The nucleic acid
 CC is useful for preparing a composition for treating or preventing e.g.,
 CC tumour or inflammatory disorder. The present sequence is human complement
 CC receptor-like DNA (POLY11)
 XX
 SQ Sequence 6153 BP; 1610 A; 1486 C; 1559 G; 1497 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 6153
 Score: 8391.00 Matches: 1530
 Percent Similarity: 78.39% Conservative: 1
 Best Local Similarity: 78.34% Mismatches: 10
 Query Match: 42.01% Indels: 412
 DB: 9 Gaps: 3
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 DB 193 TATACCTTCTGCTGTCTGACCATTTGAATGCTGACGAGCAAGTGAAGAAGT 252
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 QY 2013 AspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAlaPheIleAlaSerPro 2032
 |||||
 DB 253 GACCAAGATCCCTGCTGCTCTCTGTGATGAGCACCCATTGTGACACGCCCTCTTCA 312
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 QY 2033 GluThrAlaHisArgLeuPheGlyAspIleAlaPheTyTrpCysSerArgGlyTyTrpSer 2052
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 DB 313 GAGACTGCCCATGGCTCTTGTGAGACATTGCATTCTACTCTGATGAGTTACAGC 372
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 QY 2053 LeuAlaAspAsnSerGlnLeuLeuGluCysAsnAlaGlnGlyTyTrpValProProGlnGly 2072
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 DB 373 CTAGCAGACAAATTCACAGCTTCTCTGCAATGCCAGGCAAGTGTACCCCGAAGGT 432
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 QY 2073 GluAspMetProArgCysIleAlaHisPheCysGluValProProSerValSerTyTrpSer 2092
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 DB 433 CAGACATGCCCTGCTGTATAGCTCATTTCTGTGAAACCTCATGCTTCTTATAGC 492
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 DB 493 ATCTTGGAATCTGTGAGCAAGCAAAATTTGACGCTGCTCAGTTGTGAGCTTTAAATGC 552
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 QY 2133 AsnProSerProMetSerIleGlnCysIleProValArgCysGlyGluProProSerIle 2152
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 DB 613 AACCTTCCCCCATGTCATCCAGTGCATCTCTGTGGGTGTGAGAGCCACCAAGATC 672
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 QY 2153 MetAsnGlyTyTrpAlaSerGlySerAsnTyTrpSerPheGlyAlaMetValAlaTyTrpSerCys 2172
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 DB 733 AACCAAGGGGTTTCAACATCAAGGAGAAAGAGAGCACTTCAGAGCCAGGCAAGTG 792
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 QY 2193 SerSerProIleProThrCysHisProValSerCysGlyGluProProValGluValAsn 2212
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 DB 793 AGTAGTCTTATACGAGCTGCCACCCGATATCTTGTGTGAACACCACTAAGGTTGAAGAT 852
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 QY 2213 GlyPheLeuGlnIleThrThrGlyArgGlyPheGlnSerGluValAlaGlyTyrgInCysAsn 2232
 |||||
 DB 853 GGCTTCTTGAGAGCATCACTGAGCAGGATCTTTGAGAGTCAAGTATCAGTGTATAC 912
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 QY 2233 ProGlyTyTrpIleSerValGlySerProValPheValCysGlnIleAlaAsnArgHisTrpHis 2252


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Db 973 AGGAAATCCCTCCCTGATGTGTGTTCTCTCGACGTGTGAAACCTCCCGCATCCAAAT 1032
Oy 2273 GlyPheMetLysGlyLysAsnPheGluValGlySerLysValGlnPhePheCysAsnGlu 2292
Db 1033 GGGCTCAATGAAGAGAAACCTTGAACTAGGTCCAAAGGTCAGTCTTTCTGTAAAGAA 1092
Oy 2293 Gly---TyrGluLeuValGlyAspSerSerTyrThrCysGlnLysSerGlyLysTyrAsn 2311
Db 1093 GGGTTATNAGAGCTTGTGTGGGAGACGTTCTTGACATGTGAGAAATCTGGCAATGGAAT 1152
Oy 2312 LysLysSerAsnProLysCysMetProAlaLysCysProGluProProLeuLysGln 2331
Db 1153 AAGAAATCAATCCAAAGTGCATGCTGCCAAGTGCACAGCCGCCCTCTTGAAAC 1212
Oy 2332 GlnLeuValLeuLysGluLeuThrThrGluValGlyValValThrPheSerCysLysGlu 2351
Db 1213 CAGCTAATATTAAAGAGTGAACCAAGAGTGAAGTGTGAATTTCTGTAAAGAA 1272
Oy 2352 GlyHISValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnIntTyrAsnAsp 2371
Db 1273 AGGCATGCTCTGCAAGGCCCTCTGTCTGAAATGCTTGACATCCAGCAATGGAATGAC 1332
Oy 2372 SerPheProValCysLysLleValLeuCysThrProProProLeuLleSerPheGlyVal 2391
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Db 1453 TTTTTCCTTAAGAGAAATTCACACCCCTGCAACCTGATGGACCTGAGCTCTCA 1512
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Oy 2592 AlaMetGlnThrCysGluGluSerGlyTyrPheSerSerLleProThrCysMetProLle 2611
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Oy 2652 TyrHISLeuGlyAlaValAlaLysThrThrGluAsnThrLysGluSerProAlaThrHIS 2671
Db 2173 TATCATTTGGAGAGAGTGGCTTAAACCTGGGAAATACAAAGAGTCTCTGCTACAT 2232
Oy 2672 SerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProGlyTyrGluLeu 2691
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 DB 482 ACATCCCTGACAGCTGTCTGACAGAGGATACAGGGCATCTGGCAGACCTGGAA 541
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 QY 795 HisGlyPheLysSerPheGluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeu 814
 DB 1802 CACGGGTTCAAGTCTTTGAGATGTTCTTACAAAGACGCTCGTGTGATGACACATCTG 1861
 QY 815 MetLysLysPheSerGlyAlaPheGluThrThrLeuGlyLysMetValProSerPheCys 834
 DB 1862 ATGAAGAAAGTTTCTGAAGCACTTGACAGACCCCTGGGAAAATGCTCCCATCTTGT 1921
 QY 835 SerAspAlaGluAspIleAspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeu 854
 DB 1922 AGTATGACAGAGACATTTGACTGAGCTGAGAGGAACTGACCAAAAATATATGCTTA 1981
 QY 855 GluTyrAsnTyrAspTyrGluAsnGlyPheAlaIleGlyProGlyGlyTyrPglValAla 874
 DB 1982 GAATATATATATATGCTATGAATAATGGCTTTCATATGACAGGCTGGGGTCCAGCT 2041
 QY 875 AsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSer 894
 DB 2042 AATAGGCTGATTACTCTTATGATGACTTCTGACACTGTGCAAGAAACAGCCCAAGC 2101
 QY 895 IleGlyAsnAlaLysSerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIle 914
 DB 2102 ATCGCAATGCCAAGTCTCTCAGAGTTTAAAGAGTGGCCCATTTATCTGACTATTAATT 2161
 QY 915 LysLeuIlePheAsnIleThrAlaSerValProLeuProAspGluAsnAspThrLeu 934
 DB 2162 AAGTTAATTTTAAATCATCAGCTAGTGTGCCATTACCCGATGAAGAAATGATACCTT 2221
 QY 935 GluTyrPglLysGlnGlnArgLeuLeuGlnThrLeuGlnThrIleThrAsnLysLeuLys 954
 DB 2222 GAATGGGAAAATCGACAAACGACTCTTCAGCAATTTGAAACATATCAAAATTAACGTAAA 2281
 QY 955 ArgThrLeuAsnLysAspProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAla 974
 DB 2282 AGGACTCTCAACAAAGACCCCATATATCTTTCACTTGTGATCGAATGAATCTTATACC 2341
 QY 975 AspSerAsnSerLeuGlnThrLysLysAlaSerProPheCysArgProGlySerValLeu 994
 DB 2342 GACAGCAATTCATAGGAACAAAAAGGCTTCCCTCTGACAGCCAGGCTCAGTGTGG 2401
 QY 995 ArgGlyArgMetCysValAsnCysProLeuGlyThrTyrTyrAsnLeuGlnHisPheThr 1014
 DB 2402 AGAGGGGTATGTGTCAATTTGCTTGGAACTTATTAATCTGAAATTTTCAAC 2461
 QY 1015 CysGluSerCysArgIleGlySerTyrGlnAspGluGluGluGluCysLysLeu 1034

Db	2462	TGTGAAGACTCCGGATGCGATGTCATCAAGATGTAAGAAAGGCAACTTGAGTGCAGCTT	2521
Qy	1035	CysProSerGlyMetTyrThrGluTyrIleHisSerArgAsnIleSerAspCysValAla	1054
Db	2522	TGCCCTCTCGGATATGTACACGGAAATATATCCATTTCMAAACAATCTCGATTGTAAAGCT	2581
Qy	1055	GlnCysIysGlnGlyThrTyrSerTyrSerGlyLeuGlnTlnCysGlnSerCysProLeu	1074
Db	2582	CAGTGTAAACAAAGGACCTTACTCATGCGAGTGAAGCTTGTGAATCGTGTCCACTG	2641
Qy	1075	GlyThrTyrGlnProIlyPheGlySerIlySerCysIleuSerCysProGlyAsnThrSer	1094
Db	2642	GGCACTTATCAGCCAAAAATTGTTGGTCCCGAGACTCCTCTCGTGTCCAGAAACACTCA	2701
Qy	1095	ThrValIlyPheArgGlyAlaAlaAsnIleSerAlaCysGlyValProCysProGlnGlyIys	1114
Db	2702	ACTGTGAAGAAAGGAGCGGTGAACATTTCTGATGTGAGATTCTTGTGCCAGAAAGAAA	2761
Qy	1115	PheSerArgSerGlyLeuMetProCysHisProCysProArgAspTyrTyrGlnProAsn	1134
Db	2762	TTCTCGCTTCTGGGTATATGCTTCAACCAATCTCTCGAGATTATACCAACTTAT	2821
Qy	1135	AlaGlyIlyValAlaPheCysLeuAlaCysProPheTyrGlyThrProPheAlaGlySer	1154
Db	2822	GCAGGGAAGGCTTCTGCTGCTGGCCCTGTCCCTTATGAGAACTACCCCAATGCTGTGCC	2881
Qy	1155	ArgSerIleThrGlnCysSerSerPheSerSerThrPheSerAlaAlaGlnIlySerVal	1174
Db	2882	AGATCATCAACGAATGTTCAAAGTTTATGTTCAACTTCTCAAGCGCAGAGGAAGTGTG	2941
Qy	1175	ValProProAlaSerLeuGlyHisIleIlyIysIyAlaGlnIleSerSerGlnValPhe	1194
Db	2942	GTGCCCCCTGCCTCTCTTGAGCATATTTAAAGAGGACATGAATCAGCAGTCAAGTTTTC	3001
Qy	1195	HisGlnCysPhePheAsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyValArgIly	1214
Db	3002	CATGAATGCTCTTTTAACTTGTGCCACAATATGTGAACCTGCACACAACTTGTGGGCTGT	3061
Qy	1215	TyrValCysIleuCysProLeuGlyTyrTyrThrGlyLeuIlyCysGlnThrAspIleAspGln	1234
Db	3062	TATGTTTGTCTGTGTCCACTTGGAATATACAGGCTTAAATGTGAAACAGACATGATGAG	3121
Qy	1235	CysSerProLeuProCysIleuAsnAsnGlyValAlaGlyIysAspLeuValGlyIlyPheIle	1254
Db	3122	TGCACCCCACTGCCCTTGCCTCAACAATGAGATTTGTAAAGACTGTGTGGGAAATTCACTT	3181
Qy	1255	CysGlnCysProSerGlyTyrTyrThrGlyGlnArgCysGlnGlnAsnIleAsnGlnCysSer	1274
Db	3182	TGTGATGTCCATCAAGGTTCACAGGTCAAGCGGTGTGAAGAAATATTAATACGTATAC	3241
Qy	1275	SerSerProCysIleuAsnIlyIleCysValAspGlyValAlaGlyTyrArgCysThr	1294
Db	3242	TTCAGTCCCTGTTTAAATAAAGGAATCTGTGTGATGTGGTGGCTGAGTATCGTTGCACA	3301
Qy	1295	CysValIlyPheGlyPheValGlyIleuHisCysGlnTlnGlnValAsnGlnCysGlnSerAsn	1314
Db	3302	TGTGTGAAGAGATTTGTGTGGCCCTGTGATGTGTGAACAGAAATCAATGAATGCCAGTCAAC	3361
Qy	1315	ProCysIleuAsnAsnAlaValCysGlnAspGlnValGlyGlyPheIleuCysIlyCysPro	1334
Db	3362	CCATGCTTAAATTAATGCACTGTGTGAAGACCAAGTTTGGGGGAATCTTGTGGCAAAATGCCA	3421
Qy	1335	ProGlyPheIleuGlyThrArgCysGlyIlyIysAsnValAspGlnCysIleuSerGlnProCys	1354
Db	3422	CTGTGAATTTTGGGTAAACCGAATGTGAAGAACGTGCATGATGTCTCAGTCAAGCAAGC	3481
Qy	1355	IysAsnGlyAlaThrCysIlyAspGlyAlaAsnSerPheArgCysIleuCysAlaAlaGly	1374
Db	3482	AAAAATGAGCTACTCTGTAAACACGTGTCAATACCTTCAGATGCTGTGTGACACTGCGC	3541
Qy	1375	PheThrGlySerHisCysGlnIleuAsnIleAsnGlnCysGlnIlySerAsnProCysArgAsn	1394
Db	3542	TTCAACAGATCACTGTGAATTTGAACATCATATGATGTCAAGTCTTAATCCATGTAGAAAT	3601

QY	1395	GLIAlaThrCysValaLapGluLeuAsnSerTyrSerCysAlvsCysGlnProGlyPheSer	1414
QY	1395	GLIAlaThrCysValaLapGluLeuAsnSerTyrSerCysAlvsCysGlnProGlyPheSer	1414
Db	3602	CAGGCAACCTGTGTGAGAAATTAATTAATCAAGGTGTAAATGTCAAGCCAGATTTC	3661
QY	1415	GIYGIlnaGrcysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluValaSerGly	1434
Db	3662	GGCAAAAGGTGTGAAACGAAACAAGCTTACAGGGCTTTAACCGATTTTGAAGTTTCGGC	3721
QY	1435	IIeTyrGlyTyrValMetLeuAspGlyMetLeuProSerIleuHisAlaLeuThrCysThr	1454
Db	3722	ATCTATGAGATATGTCANCTAGTGGCATGTCTCCATCTCCCAATGCTTAACCTGTAA	3781
QY	1455	PheTrpMetLysSerSerSerAspAspMetAsnTrpGlyThrProIleSerTyrAlaValaAsp	1474
Db	3782	TTCTGAGTGAATCTCTGACACATGAACTATGAAACCAACATCTCTATGCACTTAT	3841
QY	1475	AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValaLeuTyrValaAsn	1494
Db	3842	AAACGACACGACAAATACCTTGCTCTGTGATCATTAATAACGCTGGGTTCTTTATGTGAT	3901
QY	1495	GIYATGlyIuLysIIeThrAsnCyPProSerValaIasnAspGlyAgtTrpHisIleAla	1514
Db	3902	GGCAGGGAGAAAGATACAACTACGTCCCTCGGTGATGATGACATGCAATTAATGCA	3961
QY	1515	IIeThrTrpThrSerAlaAsnGlyIIeThrLysValTyrIIeAspGlyLysLeuSerAsp	1534
Db	3962	ATCATTTGACAGTGGCCAAATGGCATTCGTGGAAAGCTATATACATGGAGAAATTATCTAC	4021
QY	1535	GIYGIYAlaGlyLeuSerValGlyLeuProIleProGly	1547
Db	4022	GGTGGTGTGGCTCTCTGTGGTTTGGCCATTAACCTGAT	4060
RESULT 11			
ABK13101			
ID	ABK13101	standard; DNA; 3991 BP.	
AC	ABK13101;		
XX	23-APR-2002	(first entry)	
XX			
DE	Human RBPTR 12 cDNA sequence.		
XX			
KM	REPR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral;		
KM	anti-HIV; antitharctic; anticonvulsant; nootropic; neuroprotective;		
KM	antiallergic; antidiody; immunogen; endometriosis;		
KM	gastronintestinal disorder; gastritis; oesophageal carcinoma;		
KM	Crohn's disease; irritable bowel syndrome; ulcerative colitis;		
KM	endocrine disorder; hypothyroidism disorder; Kallman's disease;		
KM	autoimmune disease; inflammatory disease; infertility; receptor;		
KM	acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy;		
KM	osteoarthritis; diabetes mellitus; multiple sclerosis;		
KM	systemic lupus erythematosus; cell proliferative disorder; cancer;		
KM	developmental disorder; Duchenne muscular dystrophy;		
KM	Becker muscular dystrophy; neurological disorder; epilepsy;		
KM	Alzheimer's disease; Huntington's disease; reproductive disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	161..3916	
FT		/*tag= a	
FT		/product= "RBPTR12 protein"	
XX			
FM	WO200198354-A2.		
XX			
PD	27-DEC-2001.		
XX			
PF	21-JUN-2001; 2001WO-US019942.		
XX			
PR	21-JUN-2000; 2000US-0214027P.		
PR	25-AUG-2000; 2000US-0228045P.		
PR	12-DEC-2000; 2000US-0255104P.		

XX (INCY-) INCYTE GENOMICS INC.

XX Griffen JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
XX Lal P, Policky JI, Azinzei Y, Lu DM, Graul R, Yao MG, Burford N;
XX Hafalia AM, Baughn KR, Bandman O, Patterson C, Yang J,
XX Ganthi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BW, Lu Y;
XX WPI: 2002-090432/12.
XX P-PsDB: AAU74829.

XX Twelve human receptors (referred to as RBPTR-1 to RBPTR-12), useful in
XX the diagnosis, treatment and prevention of gastrointestinal (e.g.
XX gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell
XX proliferative (e.g. cancer) disorders.

PS Claim 68: Page 155-157; 157pp; English.

XX This invention relates to twelve human receptors cDNA sequences referred
XX to as RBPTR-1 to RBPTR-12), and the proteins encoded thereby. The
XX proteins of the invention may have anti-inflammatory, cyostatic,
XX immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active
XX general, anticonvulsant, nociceptive, neuroprotective, antiallergic
XX activities. The sequences of the invention may be used to produce RBPTR
XX agonists or antagonists, and the protein sequences may be used to raise
XX anti-RBPTR antibodies. These molecules and the RBPTR polynucleotides and
XX polypeptides of the invention are useful in the diagnosis, treatment and
XX prevention of gastrointestinal (e.g. gastritis, esophageal carcinoma,
XX Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine
XX (e.g. hypothyroidism disorder, Kallman's disease), autoimmune, inflammatory
XX (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,
XX allergic, osteoarthritis, diabetes mellitus, multiple sclerosis,
XX systemic lupus erythematosus), cell proliferative (e.g. cancer),
XX developmental (e.g. Duchenne and Becker muscular dystrophy), neurological
XX (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and
XX reproductive (e.g. infertility, endometriosis) disorders. Numerous other
XX examples of each disorder are given in the specification. The present
XX sequence represents the human RBPTR12 cDNA sequence of the invention

XX Sequence 3991 BP; 1041 A; 931 C; 992 G; 1027 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3991
Score: 7471.00 Matches: 1327
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 3
Query Match: 37.41% Indels: 2
DB: 6 Gaps: 0

US-09-977-053-4 (1-3571) x ABK13101 (1-3991)

QY 2205 GYGLUPROBROLYSVALGIUANGLYPHELEUGLUISTHRTNRGLIYARGI1EPHEGLU 2224
DB 1 GGTGAACCACTTAAGTGTGAAGATGCGCTTCTGAGCATACATCGCAGATCTTTGAG 60
QY 2225 SERGLIUALIRGTGTGTYGVAENPROGLIYTRISERVALGIYSERPROVALPHEVAL 2244
DB 61 AGTGAAGTGAATCATCGTAAACCCGGGCTATTAAGTCAAGTCGAGTCCGTATTTGTC 120
QY 2245 CYGGLN-ALIAASNAHISTHPISSERGLIUSERPROLEUMECYVALIPIOLEUAAPCY 2264
DB 121 TGCAGAGCCCAATGCGACATGCGACAGTGAATCCCTCTGATGTGTGTTCTCTCGACTG 180
QY 2264 SGILYSPROBROPROLIEGLIANGLYPHEMETLYGELYGLIUBANPHEGLIUALIYSE 2284
DB 181 TGGAAAACCTCCCGCATCCAGATGCTTCATGAAAGGAAAACCTTGAAGTAAAGGCTC 240
QY 2284 RLYVALIQLNPHEPHECYABANGIUGLYTYRGILUENVALIYAPSERSERTPTHTCY 2304
DB 241 CAAGGTTCAAGTTTCTTGATATGAGGCTTATGAGCTTGTGTGACAGTCTTGGACATG 300
QY 2304 SGILYSPERGLIYETTRPANSILYLSERASNPOLYSCYMETPROIALYSCYSPR 2324

DB 301 TCAGAAATCTGCAAAATGCAATTAAGAAATCAAAATGCAATGCTGCCAAGTCCC 360
QY 2324 OGILUPROBROLYSVALGIUANGLYPHELEUGLUISTHRTNRGLIYARGI1EPHEGLU 2344
DB 361 AGAGCCGCCCTCTGTAAGAAAACAGAGTATTAAGAGAGTTCACACCGAGTAGAGT 420
QY 2344 IVALTHPHESECYALYSGIUGLYVALIYSEVALLEUNGILYPROSERVALLEULYSCYLE 2364
DB 421 TGTGACATTTTCTGTGAAGAGGCAATGTCACAGGCCCTCTGTCTGAAATGCTT 480
QY 2364 UPROSERGLIULTRPANSAPSERPHEPROVALCYALYELIYVALLEUCYSTRPROPR 2384
DB 481 GCCATCCAGAGATGAGATGATCTTTCCTGTTGTGAAGTATTTCTGTATCCACC 540
QY 2384 OPROLEULIUSERPHEGLIYVALPROIUSERSERVALLEULIYSPHEGLYSETRTHVA 2404
DB 541 TCCCTTAATTTCTGTGTGTCGCCCATTCCTCTGTGCTCTCATTTTGAAGTACTGT 600
QY 2404 ILYRTYSECYVALIGLYPHEPHELEUAHGLYASNSERTHTRILEUCYSEGLINP 2424
DB 601 CAAGTATTTCTGTGTAGAGTGGGTTTTCTTAAGAGAAATTTACACCCCTCTGCAAC 660
QY 2424 OASPGLYTHTRISERSEPROLEUPROGLUCYVALIYVALIYGLUCYSPROGLINPROGI 2444
DB 661 TGATGCACTCGAGCTCTCCACTGCGAATGATGTTCCATGAAATGTCCTCAACTGA 720
QY 2444 UGLIULIYPROBANGIYLIYIYASPVALLIYGLIYVALIYIYSESERTHALALEUY 2464
DB 721 GGAATATCCCAATGGAATCATGATGTCAGAGGCTTGCTATCTACAGACAGCTCTCTA 780
QY 2464 RTHCYALYSPROGLYPHEGLIULEUVALIGLYASNSERTHTRILEUCYSEGLIYUANGI 2484
DB 781 TACCTGCAAGCGAGCTTTGAAATGTTGGGAAATTAACAACCTTGTGTGAGAAATG 840
QY 2484 YHISTPHEUGLYGLIYSPROTHRGLYVALIIGLIUCYSEULYSPROLYSGIULI 2504
DB 841 TCACGTGCTTGAGAGAAACCAACATGTAAGCATTAAGTGTCTGAACCAAGAGAT 900
QY 2504 ELEUANGIYLSBHESERTYTHRAAPLEULIYRGLIYGLINTHVALIYTHRTYSECY 2524
DB 901 TTTGAATGGCAAAATTTCTTACACGACCTACATGACAGACCGTTACTACTCTTG 960
QY 2524 SAASATGILYPHEARGLEUGIYIPROSERVALALEUTHCYBLEUGIUTHTNGIYASPT 2544
DB 961 CAACCGAGGCTTGTGCTCGAAGGTCCAGGCTTGAACCTGTTAGAGACAGGAGATTG 1020
QY 2544 PASPVALIAPALAPROSECYASANAIAIYHISCYABSPSERPROGLINPROILEGLIUS 2564
DB 1021 GGAATGATGCCCATCTTGCAATGCCATTCATCTGATTTCCCAACCATTTGAAA 1080
QY 2564 NGIYPHEVALIGLIYALAPPTYSERTYRGLIYALALEIYIYSECYAPHEPR 2584
DB 1081 TGGTTTGTGAAGTGAAGATTAAGCTATGATGAGCCATATCATCTCACTTGCTTCC 1140
QY 2584 OGILYPHEGLIUALIAGLYHISAIAMERGLINTHCYEGILUGIUSERGLYTPSERSESE 2604
DB 1141 TGGATTTCAAGTGTGCTGTATGTCATGACAGACCTGTGAAGATGCTCAAGTTC 1200
QY 2604 RILEPROTHRYSMETPROILEAPCYSGIYLEUPROBROHISILEAPPHEGLIYASPCY 2624
DB 1201 CATCCCAAGATGATGCAATGACATGAGCTGCTCTCTCATATAGATTTTGGAGACTG 1260
QY 2624 STHLYLEULIYASAPANGIYLYRPHGILUGIUGIUBAPHEMETMETGLIUALIPR 2644
DB 1261 TACTTAACTCAAAATATGACAGGATATTTTGAACAAGAACACATGAGAGATGCC 1320
QY 2644 OTYRVALIYTHPROHISPROPTOYTHIYSEUGIYVALIYALYIYSTHTRTPGIUASNT 2664
DB 1321 ATACGTATCTCTACCTCTCTATCATTTTGGAGCATGTGCTTAACCTGGAAAATAC 1380
QY 2664 RLYGLIUSERPROIALTHRISERSEASNPHEULYRGLIYTHMETVALISERTYTH 2684
DB 1381 AAAGAGTCTCTCTACATTCATCAACTTTCTGTATGATACAGGTTTCAATAC 1440

2684 rCysaenProglYrYrGluLeuLeuGlYaaenProValLeuLeuLeuGlnGluuAspGluYTh 2704
Db 1441 CCGTATCCAGGATATGAACTTCGGGGAACCTGTGCTGATCTGCACAGGAATGGAAC 1500
QY 2704 rTTPaenGlySerAlaProSerCyAlIeSerIleGluCyAaenLeuProThrAlaProGlu 2724
Db 1501 TTGGAAATGGACAGGACCAATCCGACATTCMAATGGAATGACCTTCCTCTCTGA 1560
QY 2724 uAaenGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValAlGlnTySerCyAlu 2744
Db 1561 AAATGGCTTTTCCGCTTTTACAGAGCTACATGGAAAGCTGTGACAGTATAGCTTAA 1620
QY 2744 aProGlyAlIeLeuAlaGlySerAaenLeuCyAaenGluuAaenGlyTyPse 2764
Db 1621 ACCTGGACACATTCATGACAGGCTCTGACCTTAAGCTTTGTCTAGAGAAATGGAAGTGAAG 1680
QY 2764 rGlyAlaSerProArgCyGluAlaAlIeSerCyAluGlyPProAaenProValMetAaenGlu 2784
Db 1681 TGTGTCTCTCCCAACGCTGGAAGCCATTCATGCAAAAGCCAAATCCAGTCAATGATGG 1740
QY 2784 ySerIleGlySerAaenTyThrTyThrLeuSerThrLeuTyThrGluCyAaenProGlu 2804
Db 1741 ATCCATCAAGGAAGACACTACACATACCTGAGCACTTGTACTATGAGTGAACCCCG 1800
QY 2804 rTyThrValLeuAaenGlyThrGluArgArgThrCySglAaenAspGlyAaenTTPaenGluuAs 2824
Db 1801 ATATGTGCTGAATGACACTGAGAGGAGAAACATGCAAGATGACAAAACCTGGATGAGGA 1860
QY 2824 rGluProIleCyAlIeProValaAaenCyAaenSerSerProProValaSerAlaAaenGluYTh 2844
Db 1861 TGAGGCCATTTGATGATTCCTGTGTGACGTGCAACCCCACTCTGAGCCCAATGGCCAGGT 1920
QY 2844 lArgGlyAaenGluTyThrPheGlnuGlyGluTyThrCyAaenGluGlyPheLeu 2864
Db 1921 GAGAGAGAGCAAGTACATTCCTCAAAAGAGATTAATACCTTGCAATGAAGGTTCTT 1980
QY 2864 uLeuGluGlyAlaArgSerArgValCyAaenAlaAaenGlySerTyPseGluYAlaThrPr 2884
Db 1981 CCTTGAAGGAGCCAGAGATCGGGTTGTCTTCCCAATGGAAGTGAAGTGAAGCACTCC 2040
QY 2884 aAaenCyAluProValaArgCyAlaAlaThrProProGlnuLeuAlaAaenGlyValThrGluGlu 2904
Db 2041 CCACTGTGTGCTGTGACATGTGCAACCCCAACCACTGGCCCAATGGGGTGAAGGAAG 2100
QY 2904 yLeuAaenTyThrGlyPheMetGlyGluYAlaThrPheHisCyAaenGluGlyTyThrIleuHis 2924
Db 2101 CCTGACATATGGCTTCAAGAAAGATTAACATTCCTGTCAAGAGGGCTACATCTTGCA 2160
QY 2924 sGlyAlaProGlyLeuTyThrCySglAaenAspGlyAaenTTPaenAlaGluIleProLeuCy 2944
Db 2161 CCGTGTCTCCAAACCTCACTGTGACATGAGGCACTGGAGATGACAGAGATTCCTCTCTG 2220
QY 2944 uTyPseProValaAaenCySglYProProGluAaenAlaHisGlyPheProAaenGlyPheSe 2964
Db 2221 TAAACCAAGTCAACTGTGCACTCTGAAGATCTTGGCCATGTGTTCCCTTAATGGSTTTTTC 2280
QY 2964 rPheIleHisGlyGlyAlaHisIleGlnTyThrGlnCyAaenPheProGluYThrTyLeuHisGlyAa 2984
Db 2281 CTTTATTCATGGGGGCCATATACATGATCAAGTCTTCTCGGTATTAAGCTCAATGGAA 2340
QY 2984 nSerSerArgArgCyAaenSerAaenGlySerTyPseGlySerSerProSerCyAaenPr 3004
Db 2341 TTCATCAAGAGGTGCTCTCCCAATGGCTCTGGAATGGGACGCTTCTCCGCTGCTGCC 2400
QY 3004 oCyAaenGlySerSerThrProValIleGluTyThrValAaenGlyThrAaenPheAaenPr 3024
Db 2401 TTGCAGATGTTCACACCAAGTAATGAATGAACGTGCAATGGGACAGATTTTACATG 2460
QY 3024 sGlyTyAlaAlaArgGluGlnCyAaenPheGlyPheTyLeuLeuGluYLeuSerGluI 3044
Db 2461 TCGAAAGGACGCCGAGATTCAGTGTCTCAAGGCTTCAAGCTCTTGAAGCTTTCTGAAT 2520

QY 3044 eThrCySgluAlaAaenGlyGlnTyThrSerSerGlyPheProHisCySgluHisThrSerCy 3064
Db 2521 CACCTGTGAAGCCGATGCGACGTGAGCTCTGGGTTCCCACTGTGAACACATCTCTTG 2580
QY 3064 sGlySerLeuProMetIleProAaenAlaPheIleSerGluThrSerSerTyPseGluuAs 3084
Db 2581 TGGTCTCTTCAATATATCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 2640
QY 3084 nValIleThrTySerCyAaenSerGlyTyThrValIleGlnGlySerSerAaenLeuIleCy 3104
Db 2641 TGTGATACCTTAAGGTGACAGGTCTGATATGTCAATGAAGGACAGTTCAGATCTGATTTG 2700
QY 3104 sThrGluTyGlyValTyPseGlnuProTyProValCySgluProLeuSerCySglYse 3124
Db 2701 TACAGAGAAAGGGGTATGAGCCAGCTTATCCAGTGTGAGCCCTTGTCTCTGTGGTCC 2760
QY 3124 rProProSerValAlaAaenAlaValAlaThrGluGlyAlaHisGlnTyThrGlnuGlu 3144
Db 2761 CCAACGCTGTGCGCAATGCAAGTGGCACTGAGAGGACCCCACTATGAAGTGAAGT 2820
QY 3144 lTyLeuAaenGlyCyAaenGluGlyTyThrThrMetAaenThrAspThrPheThrCySgl 3164
Db 2821 GAATCTCAGATGCTGGAAGTTATAGATGATACAGATACAGATACATTCACCTGTCA 2880
QY 3164 nTyAaenGlyAaenTyThrPheProGluuArgIleSerCySglProGlyTyCySglProLeuPr 3184
Db 2881 GAAGAGATGTGCTGTGCTCTGAGAGAAATCTCTGACAGTCTTAAATAATGCTCTCTCC 2940
QY 3184 oGluAaenIleThrHisIleLeuValHisGlyAaenAspPheSerValAaenArgGlnValSe 3204
Db 2941 GGAATCATTAACATATACCTGTGTCAATGGGAGATTCAGTGTGATAGGCAAGTTTC 3000
QY 3204 rValSerCyAlaGluGlyTyThrPheGlnuGlyValAaenIleSerValCySgluLeuAs 3224
Db 3001 TGTGTATGTGAGAGAGGATATACCTTTGAGGAGTTATACATTCAGTATGTGAGCTTGA 3060
QY 3224 rGlyTyThrTyPseGluProProPheSerAaenGlySerCySglProValaSerGlyTyPr 3244
Db 3061 TGGAACTGGAGCCCACTATTCCTGATGAAATCTTCAAGTCAAGTCAAGTCAAGTCAAGTCA 3120
QY 3244 oGluSerProGluHisGlyPheValValGlySerTyThrPheGlnuSerThrIleI 3264
Db 3121 TGAAGTCCAGAACATGATTTGTGTGCTGAGTAAATACATTCCTTGAAGCAATAT 3180
QY 3264 eTyThrGlnCySgluProGlyTyThrGluLeuGlnuGlyAaenArgGluYAlaCySgluGluAs 3284
Db 3181 TTATCAGTGTGAGCTGTGCTATGACATGAGGGGAAACAGGGAAGTGTGCGCAGGAGAA 3240
QY 3284 nArgGlnTyPseGlyGlyValAlaAlaIleCySglYTyThrArgCySgluThrProLeuGlu 3304
Db 3241 CAGACAGTGAAGTGAAGGGGTGCAATATGCAAAAGAACCAAGGTGTGAACCTCACTGA 3300
QY 3304 uPheLeuAaenGlyTyAlaAaenIleGluAaenArgThrThrGlyProAaenValValTyPse 3324
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RESULT 13

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DT 21-NOV-2001 (first entry)
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DB cDNA encoding for human uterine motility-associated polypeptide #33.
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KM Human; uterine motility-association disorder; uterus; pregnancy; labour;
KM menstrual cycle; gene therapy; ss.
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XX Homo sapiens.
XX OS
XX PN MO200155201-Al.
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PF 17-JAN-2001; 2001MO-US001317.
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QY	2776	LYsIyProAsnProValMetAsnGIySerIIeYsGIySerAsnTYrThrTYrLeuSer	2795
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QY	2816	GIuAspAspIyAsnThrPaspGluAspGIuProlIeCYeIIeProValAspCYeSerSer	2835
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QY	2836	ProProValSerAlaAsnGIyGluValArgGIyAspGIuTYrThrPheGluIySGluIle	2855
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Db	1271	GAATACACTTGCAAATGAAGGGTTCTTGTGAGGAGCCAGAGTGGGTTGTCTTGCC	1330
QY	2876	AsnGIySerThrPProSerGIyAlaThrProAspCYeValProValArgCYeAlaThrProPro	2895
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QY	2896	GluLeuAlaAsnGIyValThrGIuGIyLeuAspTYrGIyPheMetIySGluValThrPhe	2915
Db	1391	CACCTGGCCAAATGGGTATCCGAGAGGCTTGACATATGGCTTCAATGAAGAGTAACTTC	1450
QY	2916	HisCYeHisGIuGIyTYrIleLeuHisGIyAlaProIyLeuThrCYeGInSerAspGIy	2935
Db	1451	CACCTGTACAGAGGGCTACATCTTGCACGGTCTCCAAAACCTCACTGCATCAGATGGC	1510
QY	2936	AsnThrPaspAlaGluIleProLeuCYeSylsPProValAsnCYeGIyProProGIuAspLeu	2955
Db	1511	AACTGGAGATGCAGAAATCTCTCTGTAAACACATGCATCTGTGACCTCTGAAAGACTT	1570
QY	2956	AlaHisGIyPheProAsnGIyPheSerPheIleHisGIyGIyHisIIeGInTYrGIuCYs	2975
Db	1571	GCCATAGGTTTCCCTATATGTTTTCCTTTATTCATGGGGCCATATACATACATGATGC	1630
QY	2976	PheProGIyTYrIyLeuHisGIyAsnSerSerArgArgCYeLeuSerAsnGIySerThrP	2995
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QY	2996	SerGIySerSerProSerCYeLeuPProCYeArgCYeSerThrProValIIeGluTYrGIy	3015
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QY	3016	ThrValaAsnGIyThrAspPheAspCYeGIyIyValaAlaCIIeGInCYePheIySGIy	3035
Db	1751	ACTGTCAATGGAGACGAATTTTGAACGTGTGAAGAGCAGCCCGAATTCATGCTCTCAAGGC	1810
QY	3036	PheIyLeuLeuGIyLeuSerGIuIleThrCYeGIuAlaAspGIyGInThrPProSerSerGIy	3055

Db	1811	TTCAAGCTCCAGGACCTTCTGAATATCACTGTGAGCCAGTGGACCTCTGGG	1870
Qy	3056	PheProHisCysGluHisThrSerCysGlySerLeuProMetIleProAsnAlaPheIle	3075
Db	1871	TTCCCCACCTGTGAACACACTCTTGTGGTGTCTCTTCCATGATGATCAAAATGCGTTATC	1930
Qy	3076	SerGluThrSerSerTTPDySGluAsnValIleThrTyrSerCysArgSerGlyTyrVal	3095
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Qy	3096	ILegGluYSerSerAspLeuIleCysThrGluYsglyValTPSerGlnProTyrPro	3115
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Qy	3116	ValCysGluProLeuSerCysGlySerProProSerValAlaAsnAlaValAlaThrGly	3135
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Db	2711	GAGCACAACCTGCACAGAAATGGAACCTGAGACCAACCACTCCCTCTGCAAAACCAAT	2770
Qy	3356	ProCysProValProPheValIleProGluAsnAlaLeuLeuSerGluYsgluPheTyr	3375
Db	2771	CCATGCGCTGTCTCTTTGTGATTTCCCGAGAAATGCTCTGCTGTCTGAAAAGAGATTAT	2830
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DB 3191 GGGCGCTCTGTGAAGAACCAATCTGCTTCTCCGTGTGAACGAGAGTCTGTGTG 3250
QY 3516 AlaProTyrGlnCysArgProProGlyTyrThrGlySerArgCysHisThrAlaVal 3535
DB 3251 GCCCTTACAGTGTAAGTGCCTGCGCTGAGCGGGGTCTGCTGTCAACAGCTGTT 3310
QY 3536 CysGlnSerProCysLeuAmaGlyGlyValCysValArgProAmaArgCysHisCysLeu 3555
DB 3311 TGCACATCTCCCTGCTAAATGTGTGAAATGTGTAAACCAACCATGTCACTGTCTT 3370
QY 3556 SerSerTyrThrGlyHisAmaCysSerArgLyArgArgThrGlyPhe 3571
DB 3371 TCTTCTGACGGGACATTACTTCTCCAGAAAAGAGAGACTGGTTT 3418

RESULT 14
AAS26868
ID AAS26868 standard; cDNA; 3804 BP.
XX
XX AAS26868:
AC 07-NOV-2001 (first entry)
XX
XX
XX Human cDNA encoding a novel secreted protein, SEQ ID 60.
DB
XX
XX
XX Human: immunosuppressive; antiarthritic; aa: antirheumatic; cytostatic;
KM cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KM antibacterial; virucide; fungicide; ophthalmological; vulnary;
KM secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KM cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KM cerebral ischaemia; angiogenesis; nervous system disorder;
KM Alzheimer's disease; infection; ocular disorder; corneal infection;
KM wound healing; epithelial cell proliferation; skin ageing; food additive;
KM preservative; antiproliferative.
XX
XX Homo sapiens.
OS
XX
XX MO200155441-A2.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001MO-US001320.
PF
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI; 2001-476222/51.
 XX P-PSDB; AAU16963.
 XX
 PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
 PT diagnose diseases or disorders associated with aberrant expression or
 PT activity of polypeptides, for treating blood clotting disorder,
 PT hemophilia.
 XX
 PS Claim 1; SEQ ID NO 60; 601pp; English.
 XX
 CC The invention relates to isolated nucleic acid molecules and their
 CC encoded secreted proteins. The nucleic acids and proteins are used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Antibodies to the proteins can also be used in

[illegible]

Db	671	GAAGTGGCTTAAACCTGGGAAATATCAAGAGCTCTCTGCTACATCATCAAACTTT	1751	ACTGTCAATGGAGACAGATTGTACTGTGAAAGCAGCCCGGATTCTAGTCTTCAAAAGC	1810	
Qy	2676	LeuTYRGIYThmMetValSerTYRThrCysAsnProGlyTYRGIYLeuLeuGlyAsnPro	Qy	3036	PheLYLeuLeuGlyLYLeuSerGluIleThrCysGluValAspGlyGlnTrpSerSerGly	3055
Db	731	CTGTATGGTACCAATGGTTTCTATACCTCTGTAATCCAGATATGAACCTTCTGGGGAACCT	Db	1811	TTCAAGCTCTTACAGACTTTCTTGAATTCACCTGTGAAGCCGATGGCCAGTGGAGCTTGGG	1870
Qy	2696	ValLeuIleCYseGlnGluAsnProGlyTYRTrpAsnGlySerAlaProSerCysIleSerIle	Qy	3056	PheProHicCYseGluHicThrSerCYseGlySerLeuProMetIleProAsnAlaPheIle	3075
Db	791	GGCTGATCTGGCAGAGAAATGGAACTTGGAAATGGCAGTGCACATCTTCAATTCAATT	Db	1871	TTCCCCCACTGTGTAACACACTTCTGTGGTCTCTTCCAAATGATACCAATGCGCTTCATC	1930
Qy	2716	GluCYAsnProLeuProThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMet	Qy	3076	SerGluThrSerSerTrpIleGluAsnValIleThrTYSerCysAsnSerGlyTYRVal	3095
Db	851	GAATGTGACTTGGCTTACTGCTCTCGTGAATGCGCTTTTGGCTTTTACAGAGACTACGATG	Db	1931	AGTGAACAGCTCTTGAAGGAAATGATATTAACCTACAGCTGACAGCTGAGTATGATGTC	1990
Qy	2736	GlySerAlaValGlnTYSerCysLYsProGlyHicIleLeuValAspGlySerAspLeuArg	Qy	3096	IleGlnGlySerSerAspLeuIleCYThrGluLYseGlyValTrpSerGlnProTYPro	3115
Db	911	GGAAAGCTGCTGACGATATAGCTGTAAACCTGGACACATTTCTACAGGCTCTGACTTAAAG	Db	1991	ATACAGGACAGTTCAATCTGATTTGTGACAGAAAGGGGTATGAGCCAGCTTATCCA	2050
Qy	2756	LeuCYLeuGluAsnArgLYSTPserGlyAlaSerProArgCYseGluAlaIleSerCys	Qy	3116	ValCYseGluProLeuSerCYseGlySerProProSerValAlaAsnAlaValAlaThrGly	3135
Db	971	CTTTGTCTAGAGATATGAAGAATGGAGTGGTGGCTCCCAAGCGTGTGAAGCCATTTCAATG	Db	2051	GTCGTGAAGCCCTTGTCCTGTGGGGTCCCAACGCTGTGCGCAATGCGATGCGAACTGGA	2110
Qy	2776	LYseLYsProAsnProValMetAsnGlySerIleLYseGlySerAsnTYRThrLYLeuSer	Qy	3136	GluAlaHicThrTYRGIYserGluValLYseLeuArgCYseLeuGluGlyTYRThmMetAsp	3155
Db	1031	AAAAAGCCAAATCCAGTCAATGATGATCATCAAGAAAGAACTACATACATACCTGAGC	Db	2111	GAGGCACACCTATGAAAGGTGAAGTGAACCTAGATGTCGTGAAGGTATATACATGAT	2170
Qy	2796	ThrLeuTYRGIYLeuCYAsnProGlyTYRValLeuAsnGlyTYRGIYLeuArgTYRThrCys	Qy	3156	ThrAspThrAspThrPheThrCYseGlnLYAspGlyValGrtTrpPheProGluArgIleSer	3175
Db	1091	ACCTGTACTATAGAGTGAACCCGGATATGTCTAAATGGCACTGAAGGAAACATATGC	Db	2171	ACGATATCAATATCAATTCACCTGTGAAAGATGGTGTGCTGCTGCTGAGAGAAATCTCC	2230
Qy	2816	GlnAspAspLYsAsnTrpAsnProGluAsnProIleCYseIleProValAspCysSerSer	Qy	3176	CYseSerProLYseCYsProLeuProGluAsnIleThrHicIleLeuValHicGlyAsp	3195
Db	1151	CAGGATGACAAAACCTGGGATGAGATGAGCCATTGGCATTCCTGTGACTGCACTCACTTCA	Db	2231	TGCAGTCTTAAATATGTCTCTCCCGAATAATPAACATATTACTTGATACATGGGAC	2290
Qy	2836	ProProValSerAlaAsnGlyGlnValArgGlyAspGluTYRThrPheGlnLYseGluIle	Qy	3196	AspPheSerValAsnArgGlnValSerValSerCYseAlaGlnLYseTYRThrPheGlnGly	3215
Db	1211	CCCCGAGTCAAGCCAAATGCGCCAGGTGAGAGAGACAGATACACATTTCCAAAAGAGATT	Db	2291	GATTTAGTGTGAATAGGCAAGTTTCTGTCTATGTGCAGAAAGAGTATACCTTTGAGGGA	2350
Qy	2856	GluTYRThrCysAsnGluGlyPheLeuLeuGluGlyValaAspSerArgValCYseLeuAla	Qy	3216	ValAsnIleSerValCYseGlnLeuAspGlyTYRTrpGluProProPheSerAspGluSer	3235
Db	1271	GAATACACTTGCATATAGAGGTTCTGTGAGGAGCCAGAGTGGGTTTGTCTTGCC	Db	2351	GTTACATATCAATATGCTAGCTTGAATGAACTGGAGGCCACATTTCTCGATGATCT	2410
Qy	2876	AsnGlySerTrpSerGlyAlaThrProAspCYsValProValArgCysAlaThrProPro	Qy	3236	CYseSerProValSerCYseGlyLYsProGluSerProGluHicGlyPheValValGlySer	3255
Db	1331	AATGGAAAGTTGGAGTGAAGCCACTCCGACTGTGCTGTCAAGATGTGCACCCGCCA	Db	2411	TGCAGTCAAGTTCTTGTGGGAAACCTGAAGTCCAGAAATGATGATTTGTGTGGCAGT	2470
Qy	2896	GlnLeuAlaAsnGlyValaThrGluGlyLeuAspTYRGIYPheMetLYseGluValaThrPhe	Qy	3256	LYseTYRThrPheGluSerThrIleTYRGIYLeuGluProGluTYRGIYLeuLeuGluGly	3275
Db	1391	CAACTGGCAATGGGGTGAACGGAAAGCCCTGCACTATGGCTTCATGAAGGAATACATTC	Db	2471	AATATACACTTTGAAAGCAATATATTTATCAGTGTGAGCTGTGCTATGAACTGAGAGGG	2530
Qy	2916	HicCYHicGluGlyTYRTrIleLeuHicGlyValaProLYLeuThrCYseGlnSerArgGly	Qy	3276	AsnArgGluArgValCYseGlnGluAsnArgGlnTrpSerGlyGlyValaIleCYsLYs	3295
Db	1451	CACGTGCAGAGGGCTACATCTTGCACGGTGTCCAAAATCTCACTGTCTCAGATGGAG	Db	2531	AACAGGAAAGCTGTCTGCCAGAGAAACAGACAGTGAAGTGAAGGGGTGGCAATATGCAA	2590
Qy	2936	AsnTrpAspAlaGluIleProLeuCYsLYsProValaAsnCYseGlyProProGluAspLeu	Qy	3296	GluThrArgCYseGluThrProLeuGluPheLeuAsnGlyLYsAlaAspIleGluAsnArg	3315
Db	1511	AACCTGGAGTCAAGATTTCTCTCTTAAACAGTCAACGTGGAACCTCTGAAAGATCTT	Db	2591	GAGACCAAGGTGTAACTCACTTGAAATTTCTCAATGGGAAACCTGACATTTGAAACAGG	2650
Qy	2956	AlaHicGlyPheProAsnGlyPheSerPheIleHicGlyGlyHicIleGlnTYRGIYLeu	Qy	3316	ThrThyGlyProAsnValaIleTYSerCYsAsnArgGlyTYRserLeuGluGlyProSer	3335
Db	1571	GGCCATGCTTCCCTTAATGGTTTCTTTATTCATGGGGGCCAATATACAGTTCAGTGC	Db	2651	ACGACTGAACCCCAAGCTGTATATCTCTGCACAGAGGCTGACAGTCTGAAAGGCAATCT	2710
Qy	2976	PheProGlyTYRLYLeuHicGlyAsnSerSerArgArgCYseLeuSerAsnGlySerTrp	Qy	3336	GluAlaHicCYeThrGluAsnGlyTYRTrpSerHicProValProLeuCYsLYsProAsn	3355
Db	1631	TTTCTGGTATTAAGTCCATGGAATTAATCAAGAAAGGCTCTTCCATAGCTCTCTGG	Db	2711	GAGGCACACTGCACAAAATGGAACCTGAGCCACCCAGTCCCTCTGCAAAACCAAT	2770
Qy	2996	SerGlySerSerProSerCYsLeuProCYsArgCYseThrProValIleGluTYRGIY	Qy	3356	ProCYsProValProPheValIleProGluAsnAlaLeuLeuSerGluLYseGluPheTYR	3375
Db	1691	AGTGGAGCTCACTTCTCGCTGCTTCCAGATGTTTCCACACAGATTAATGAATGGA	Db	2771	CCATGCTGCTTCTTGTGATTTCCGAGAAAGCTCTGTGCTGTAAGAAAGGTTTAT	2830
Qy	3016	ThrValAsnGlyTYRAspPheAspCYseGlyLYsValaIleArgIleGlnCYsPheLYseGly	Qy	3376	ValAspGluAsnValSerIleLYsCYsArgGluGlyPheLeuLeuGlnGlyHicGlyIle	3395
			Db	2831	GTTGATCAAAATGTGTTCATCAATATGAGGAAGTTTCTGTGCAAGGCCACGCGATC	2890

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QY 3416 CysGlyProProAlaHisValGluAsnAlaIleAlaArgIleValHisGlyTrpGly 3435
DB 2951 TGTGGTCCACGACGACGACGTAAGAAATGCAATGCTGAGCGCTGACATTAATCAATATGA 3010
QY 3436 AspMetIleThrLysSerCysLysSerGlyLysMetLeuGluGlyPheLeuArgSerVal 3455
DB 3011 GACATATATACCTGATCATCTTACAGTGATCATGTTGAGGGTTCTTGAGGAGTGT 3070
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DB 3071 TGTTTGAAAAATGAAACATGACATCACTCTCTTTGACAGGCTGTCTGATTTCCA 3130
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DB 3131 TGTCAAAATGGGGGCACTGCGCAAGCCCAATGCTGTGTTCTGTCCAGAGGCTGAGT 3190
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DB 3371 TCTTCTTGACGGGACATTACTGTTCCAGAAAAAGGAGCTGGTTT 3418

RESULT 15
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XX 10-JAN-2002 (first entry)
DT
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XX Human cDNA SEQ ID NO: 214.
DE
XX
XX Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; inflammation; ss.
XX
XX Homo sapiens.
OS
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XX W0200154474-A2.
PN
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PR 20-OCT-2000; 2000US-0241809P.

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PR	05-JAN-2001;	2001US-0259678P.
XX	(HUMA-)	HUMAN GENOME SCI INC.
PA		
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX	WPI, 2001-476161/51.	
DR	P-PSDB; ABB10326.	
XX		
PT	Isolated nucleic acid molecule encoding an inflammation-associated	
PT	polypeptide is used in preventing, treating or ameliorating a medical	
PT	condition.	
XX		
PS	Claim 1; SEQ ID NO 214; 859pp + Sequence Listing; English.	
XX		
CC	The present invention provides human cDNAs, proteins and related genomic	
CC	cDNAs. These can be used in the treatment of neural, immune system,	
CC	muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,	
CC	renal and proliferative disorders and inflammation. The present sequence	
CC	is a cDNA of the invention	
XX		
XX	Sequence 3804 BP; 1025 A; 858 C; 915 G; 1006 T; 0 U; 0 Other;	

DB 3131 TGTCAATGAGGGGACATCTGCCACCCCAATGCTTGTCTCCAGAGGGCTGAGTC 3190
QY 3496 GATAGTleuCYseGluGluProIleCYsIleuProCYseleuAnGIpGIYAGCYsVal 3515
DB 3191 GGGCGCTCTGTGAAACCAATCTGCATCTTCCCTGTGACGAGGTGCTGTG 3250
QY 3516 AAlaProTYGlnCYsAspCYsProProGlyTTPThrGlySerArgCYsHisThrAlaVal 3535
DB 3251 GGGCTTACAGTGTACTGCCCGCTGCTGACGGGGGTCTGCTGTATACAGCTGTT 3310
QY 3536 CYseGlnSerProCYseleuAnGIYGIYleCYsValArgProAsnArgCYsIleu 3555
DB 3311 TCCCACTCTCCCTGCTTAATGTGTGAAATGTGTAAAGACCAACGATGTCACTGCTT 3370
QY 3556 SerSerTTPThrGlyHisAsnCYsSerArgIleArgArgThrGlyPhe 3571
DB 3371 TCTTCTGACGGGACATACCTGTCTCAGGAAAGAGACTGGGTTT 3418
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ID AAS31587 standard; cDNA; 3804 BP.
AC AAS31587;
XX
DT 04-DEC-2001 (first entry)
XX
DE cDNA encoding novel human calcium-binding protein #11.
XX
KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antithrombotic; cytostatic; vasotropic; antibacterial; nootropic;
KW vincide; ss.
XX
OS Homo sapiens.
XX
PN WO20015304-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001302.
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Qy	2796	ThrLeuTyrTyrGluCysAspProGlyTyrValLeuAsnGlyTyrGluIuArgTyrThrCys	2815
Dd	1091	ACGTTGTACTATGAGTGTGACCCCGAGATATATGTCGTAATGGCACTGAAGAGGAACATGC	1150
Qy	2816	GlnAspAspIlyValAsnTTPAspGlnAspGluProIleCysIleProValAspCysSerSer	2835
Dd	1151	CAGGATGACAAAAATCTGGAGATGAGATAGCCCATTTTCATCTCTGATGACATGCAGTTCA	1210
Qy	2836	ProProValSerIleAsnGlyGlnValArgGlyAspAspIlyTyrThrPheGlnIlyGluIle	2855
Dd	1211	CCCCCAGCTCTCAGCCCAATGCGCGAGGTGAGAGAGAGACGAGTACATTTCCAAAAGAGATT	1270
Qy	2856	GluTyrTyrCysAsnGluGlyPheLeuLeuGluGluIlyIleArgSerArgValCysLeuVala	2875
Dd	1271	GAAATACACTTGCAATGAAGAGGTTCTTGCTTGAGGGAGCAAGAGATGCGGTTGTCTTGCC	1330
Qy	2876	AsnGlySerTTPSerGlyValIleThrProAspCysValProValArgCysAlaThrProPro	2895
Dd	1331	AATGGAAGTTGGAGTGGAGCCACTCCCACTGTGTGCTGTGCAGATGTGGCAACCCCGCA	1390
Qy	2896	GlnLeuAlaAsnGlyValIleThrGluGlyLeuAspTyrGlyPheMetLysGluValIleThrPhe	2915
Dd	1391	CAACTGGCCAAATGGGGGTGACGGAAGGCTGGACATATGGCTTCATGAAAGAAATTAATTTC	1450
Qy	2916	HisCysHisGluGlyTyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGly	2935
Dd	1451	CACCTGTCAAGAGGGCTTACATCTGTGACGGTGTCCAAAATCACTGTGCATTCAGATGGC	1510
Qy	2936	AsnTTPAspAlaGluIleProLeuCysLysProValAsnCysGlyProProGlnAspLeu	2955
Dd	1511	AACTGGAGTGCAGAGATTCTCTCTGTAAACACAGTCAACTGTGGACCTCTCGAAGATCTT	1570
Qy	2956	AlaHisGlyPhePheProAsnGlyPheSerPheIleHisGlyGlyHisIleGlnTyrGlnCys	2975
Dd	1571	GCCCAATGGTTCCCTTAATGGTTTTTCCTTTATCAATGGAGGACAAATACATATCACAGGC	1630
Qy	2976	PheProGlyTyrTyrLysLeuHisGlyValAsnSerSerArgArgCysLeuSerAsnGlySerTyr	2995
Dd	1631	TTTCTCGTTATTAAGCTTCATGGAATTCATCAAGAAAGTGTCTCTCAATGGCTCTCGG	1690
Qy	2996	SerGlySerSerProSerCysLeuProCysArgCysSerThrProValIleGluTyrGly	3015
Dd	1691	AGTGGCAGCTCACTTCTTCGCTCGCTTGCAGAGATTTCCACACACAGTATTAATATAGGA	1750
Qy	3016	ThrValaAsnGlyThrAspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGly	3035
Dd	1751	ACTGTCAATGGGACAGATTTTGACTGTGAAAGGAGCCCGGATTCAGTGTCTTAAGGC	1810
Qy	3036	PheLysLeuLeuGlyLeuSerGluIleThrCysGlnIleAspGlyGlnTTPSerSerGly	3055
Dd	1811	TTTCAGCTCTCCAGACTTCTTGAAATCACTGTGAAGCCGATGGCCAGTGAAGCTCTGGG	1870
Qy	3056	PheProHisCysGluHisIleThrSerCysGlySerLeuProMetIleProAsnAlaPheIle	3075
Dd	1871	TTCCCCCACTGTGAACACACTTCTTGTTGATCTCTTCCAAATGATCCAAATGGCTTATTC	1930
Qy	3076	SerGluThrSerSerTTPLysGlnAsnValIleThrTyrSerCysArgSerGlyTyrVal	3095
Dd	1931	AGTGAAGACAGCTCTGTGAAGGAATATGATTAACCTTACACTGTGAGGTCTGGAATATGTC	1990
Qy	3096	IleGlnGlySerSerAspLeuIleCysThrGluLysGlyValIleTTPSerGluProTyrPro	3115
Dd	1991	ATACAGAGCACTTCAGATCTGATTTGTACAGAGAAAGGGGTATGAGCCACTTATTCGA	2050
Qy	3116	ValCysGluProLeuSerCysGlySerProProSerValAlaAsnAlaValAlaThrGly	3135
Dd	2051	GTCGTGAGCCCTTGTCTCTGTGGAGTCCCAACGCTGTGTGCGCAATGAGTGGCAACTGGA	2110
Qy	3136	GluAlaHisIleThrTyrGluSerGluValLysLeuArgCysLeuGluGlyTyrThrMetAsp	3155
Dd	2111	GAGGACACACCTATGAAGAAGTGAAGTGAACCTCAATATCTGTGAAGGTTATACAGATGAT	2170

QY	3156	ThrAspThrAspThrPheThrCysGlnLysAspGlyArgTrpPheProGluLysGlnLeuSer	3175
Db	2171	AcGAGTAAcAGTAAcATcATcCAcCTGcACAGAAATGcGTcGTcGTcCTcCGAAGAAATcCTcC	2230
QY	3176	CysSerProLysLysCysProLeuProGluAsnLLeThrHisLeuValHisGlyAsp	3195
Db	2231	TGCAGTcCTTAAAAATGcTcCTcCTcCGGAAAAcATTAcCAcATATAcCTGTATcATAcGGGAc	2290
QY	3196	AspPheSerValAsnAspGlnValSerValSerCysAlaGluGlyTrpThrPheGluGly	3215
Db	2291	GATTTCAGTcGTGAATAGcCAAGTTCGTGTGTcCAAGTcGACAGAGGcGTATAcCTTTGAAGGA	2350
QY	3216	ValAsnLLeSerValCysGlnLeuAspGlyThrTrpGluProProPheSerAspGluSer	3235
Db	2351	GTTAAcATATAcAGTATGTcGAcCTGTATGAAcCTcGGAGcCAcCATTTcCGAGATcCT	2410
QY	3236	CysSerProValSerCysGlyLysProGluSerProGluHisGlyPheValValGlySer	3255
Db	2411	TGCAGTcCAgTTTCTGTGTGGAAAcCTGAAGTcCAAGAcATGATATTGTGTGGcAGT	2470
QY	3256	LysTrpThrPheGluSerThrHisLeuGlnCysGluProGlyTrpGluLeuGluGly	3275
Db	2471	AAATACAcCTTTGAAAGAcCAATATTATcTAcGTGAcCTGTcATGAAcCTAGAGGG	2530
QY	3276	AsnArgGluArgValCysGlnGluAsnArgGlnTrpSerGlyGlyValAlaLeCysLys	3295
Db	2531	AAcAGGAAcCTGTcCTcCGAGAAAcCAcAGAcAGTcGAGGGcGTGcCAATTcGCAA	2590
QY	3296	GluThrArgCysGluThrProLeuGluPheLeuAsnGlyLysAlaAspLLeGluAsnArg	3315
Db	2591	GAGAcCAcAGTcGTGAACcCTcCAcTGTGAATTcCTcAATGGGAAAcGTGAcATTGAAACAG	2650
QY	3316	ThrThrGlyProAsnValValTrpSerCysAsnArgGlyTrpSerLeuGluGlyProSer	3335
Db	2651	AcGAcGTGAcCCAcAGcGTATATcCTcGcCAcAGAcGTcATcCAcGTcCTTGAAGcCAcCT	2710
QY	3336	GluAlaHisCysThrGluAsnGlyTrpThrSerHisProValProLeuCysLysProAsn	3355
Db	2711	GAGcCAcAcTcCAcAGAAATAGAAAcCTcGAGcCAcCAcGAcCTcCTcCTcGAAAcCAAT	2770
QY	3356	ProCysProValProPheValLeProGluAsnAlaLeuLeuSerGluLysGluPheTrp	3375
Db	2771	CCATGcCTcGTcCTTTGTGTATcCTcCGAGATcCTcGTcGTcTGAAGAcGATTTAT	2830
QY	3376	ValAspGluAsnValSerLeuLysCysArgGluGlyPheLeuLeuGlnGlyHisGlyLe	3395
Db	2831	GTTATcATcGATATGTcCTcATcCAATATGATGGAGAcGTTTCTcGTcGAcAGGGcCAcGGAcATc	2890
QY	3396	LeuThrCysAsnProAspGluThrTrpThrGlnHisSerAlaLysCysGluLysHisLeuSer	3415
Db	2891	ATTAcCTGTcCAcCCcCGAcAGAcGTGAcCAcAGcCAAGcCGcCAATATGAAAAATcCA	2950
QY	3416	CysGlyProProAlaHisValGluAsnAlaLeuAlaArgGlyValHisTrpGlnTrpGly	3435
Db	2951	TGTGTcCAcCAcAGcCTcCAcGTATGAAATGTcCATcCTcGAcGGcGTATcATATAGGA	3010
QY	3436	AspMetLeuThrTrpSerCysTrpSerGlyTrpMetLeuGluGlyPheLeuArgSerVal	3455
Db	3011	GAcATGTAcCAcCTTAcCTcATcTTATcCAGTcGATAcATcTGTGAcGGcGTTCcTGAAGAcAGcGT	3070
QY	3456	CysLeuGluAsnGlyThrTrpThrSerProProLLeCysArgAlaValCysArgPhePro	3475
Db	3071	TGTTTAGAAATGTAAcATGTGAcATcATcCTcCTATTTGcAGAcGTcGTcGTcCATTTCCA	3130
QY	3476	CysGlnAsnGlyLysLeCysGlnArgProAsnAlaCysSerCysProGluGlyTrpMet	3495
Db	3131	TGTcCAATGTGGGGAcATcCTcGcCAAcGCCcCAATcCTcTTcCTGTcCAcAGGGcGTGATG	3190
QY	3496	GluArgLeuCysGluGluProLLeCysHisLeuProCysLeuAsnGlyLysArgCysVal	3515
Db	3191	GGGGcCTcCTGTGAAGAcCAATcGTcATcTTcCTcGTcTGAAGcGAGcGTcGTGTGTG	3250

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 PR 05-JAN-2001; 2001US-0255678P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX MPI; 2001-581633/65.

DR P-PSDB; AAU87355.

PT New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

XX Claim 1; SEQ ID NO 275; 837bp; English.

CC The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (II) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Alignment Scores:

Pred. No.: 8e-315 Length: 3804
 Score: 6452.00 Matches: 1135
 Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.91% Mismatches: 0
 Query Match: 32.30% Indels: 0
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 US-09-977-053-4 (1-3571) x ABA43685 (1-3804)

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 QY 2476 ThrThrThrLeuCysGlyValuAsnGlyHisTyrPLeuGlyGlyLysProThrCysValAla 2495
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 QY 2496 IleGluCysLeuLysProLysGluIleLeuAsnGlyLysPheSerTyrThrAspLeuHis 2515
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 QY 2516 TyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheAsxLeuGluGlyProSerAla 2535
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 QY 2536 LeuThrCysLeuGlyIleThrGlyAspTyrAspValAlaPheSerCysAsnAlaIleHis 2555
 DB 311 TTGACCTGTTTGAAGACAGGTATGAGATGAGATGCCCATCTTGCAATGCCATCCAC 370
 QY 2556 CysAspSerProGlnProIleGluAsnGlyPheValGluGlyValAlaAspTyrSerTyrGly 2575
 DB 371 TGTGATTCCTCCCAACCCCACTGAAATGGTTTGTGAAGAGTCAAGATTCAGCTATGGT 430
 QY 2576 AlaIleIleIleTyrSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThr 2595
 DB 431 GCCATTAATCATCTACAGATGCTCTCCCTGAGTTCAGTGGTATGCAAGCAGAC 490
 QY 2596 CysGluGluSerGlyTyrPheSerSerIleProThrCysMetProIleAspCysGlyLeu 2615
 DB 491 TGTGAAGACTCAGATGTCAGATGTCATCCCAATGATATGCAATGATGCTGCTC 550
 QY 2616 ProProHisIleAspPheGlyAspCysThrIlyLeuLysAspAspGlnGlyTyrPheGlu 2635
 DB 551 CCTCCTCATATAGATTTTGGAGACTGTACTAACTCAAGATGACCAAGGATATTTTGG 610
 QY 2636 GlnGluAspAspMetMetGluValProTyrValThrProHisProProTyrHisIleGly 2655
 DB 611 CAAGAAGACGACATGATGGAAGTTCATATGTGACTCTCACCTCTTATCAATTGGGA 670
 QY 2656 AlaValAlaIleTyrThrTyrGluAsnThrIlyGluSerProAlaThrHisSerSerAspPhe 2675
 DB 671 GCGATGGCTTAAACCTGGAAATATCAAGAGTCTCCGTACACATTCATCAAACTTT 720
 QY 2676 LeuTyrGlyThrMetValSerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnPro 2695
 DB 721 CTGTATGTAACATGATGTTTATACACTGTATCCAGATATGAACTTCTGGGGAACCT 790
 QY 2696 ValIleuIleCysGlnGluAspGlyThrTPAAsnGlySerAlaProSerCysIleSerIle 2715
 DB 791 GGTGCAATGTGCAGAGAAATGAACTTGAAATGGAGAGCACTCTGCAATTTCAATT 850
 QY 2716 GluCysAspLeuProThrAlaProGluAsnGlyPheLeuAsxPheThrGluThrSerMet 2735
 DB 851 GAATGTGACTTGTGCTTACAGTCTCTGAAATGGCTTTTTCGTTTACAGAGACTACAG 910
 QY 2736 GlySerAlaValGlnTyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuAsx 2755
 DB 911 GGAAGTGTGCTCAATATATGCTGTAACCTGACACATTTCTAGCAGGCTCTGAATTAA 970
 QY 2756 LeuCysLeuGluAsnAsxArgLysTyrSerGlyLysSerProArgCysGluAlaIleSerCys 2775
 DB 971 CTTTGTCTAGAAATGAAATGAGAGTGTGCTCTCCCACTGCAACCATTTCAATGC 1030

[illegible]

QY	3136	GIU1IAH1SPTHYTRG1USEG1UVal1LyseuamrgCyseueng1yTYTRThMeAsp	3155
Db	2111	GAGGACACACCTTAAAGAGTAAGTAAACTCAAGATCTCGAAGGTTATACATGAT	2170
QY	3156	ThAspThAspThrPheThrCyAG1uLyAspG1yATGTrPheProGluArg1LeSer	3175
Db	2171	ACAAGTACAGATACATTCACCTGTCCAGAAAGATGCTGCTGGTTCCCTGAGAGATCTCC	2230
QY	3176	CysSerProLybLybCyAPProLeuProGluAsn1LeThrs1LeLeuValHisGlyAsp	3195
Db	2231	TGCAGTCCCTAAAAATGCTCTCCCGGAAAACTPAACATATATCTGTACACAGGGAC	2290
QY	3196	AspPheSerValaAspArg1NvalSerValSerCysAlaGluGlyTYTRThPheGluGly	3215
Db	2291	GATTCAGATGAAATAGGACAGATTCGTGTCAATGTCAAGAGGATTAACCTTTGAGGCA	2350
QY	3216	ValAsn1LeSerValCyseuLeuAspG1YThrTrpLupProPheSerAspG1uSer	3235
Db	2351	GTTAAACATATCAGATATGTCACTTGATGAACTGGAGCAACATCTCCAGAAATCT	2410
QY	3236	CysSerProValSerCyseGlybLybProGluSerProGluHisGlyPheValValGlySer	3255
Db	2411	TGCATCCAGATTCCTGTGGGAAACCTGAAGTCCAAACATGGAATTTGTGTGGAGT	2470
QY	3256	LySTYTRThPheGluSerThr1Le1LeTYrGlnCyseLupProGlyTYTRGluLeuGluGly	3275
Db	2471	AAATACACCTTTGAAAGACAAATTTATATCAGTGTGAGCTGTGACTATGAACATGAGGG	2530
QY	3276	AsnATrg1uATgvalCyseGlnGluAsnArg1nTrpSerGlyValAla1LeCybLyb	3295
Db	2531	AAACAGGAACTGTCTGTGCAGAGAAACAGACAGAGTGAGGGGTGGCCAAATGTGAAA	2590
QY	3296	GluThrArgCyseGluThrProLeuGluPheLeuAsnG1yValAlaAspG1LeGluAsnArg	3315
Db	2591	GAGACAGATGTGAATCTCCACTTGAAATTTCTCATGGAAACCTGCAATTGAAAACAG	2650
QY	3316	ThrThrGlyProAsnValValTYrSerCyAsnATrg1YTYrSerLeuGluGlyProSer	3335
Db	2651	AACGATGACCCAAAGTGATATATCTCGCAACAGAGCTACAGCTTGTGAAGGGCCATCT	2710
QY	3336	Glu1IAH1SCTHrGluAsnG1YThrTrpSer1AspProValProLeuCybLybProAsn	3355
Db	2711	GAGGCACCTGCACAGAAATGAACTCGAGCCACCACTGCTCTCTGCAACCAAT	2770
QY	3356	ProCyAProValProPheVal1LeProGluAsnAlaLeuLeuSerGlyuGluPheTYr	3375
Db	2771	CCATGCCCTGTTCTTGTGTGATATCCCGAGAAATGCTCTGCTGTGAAAGAGATTTAT	2830
QY	3376	ValAspG1uAsnValSer1LeLybCyArgGluGlyPheLeuLeuGlnGlyHisGlyTLe	3395
Db	2831	GTTATGACGAATGTGCTCATCAAAATGTAGGAAAGTTTTCTGTGCAAGGGCCACGGCATC	2890
QY	3396	1LeThrCyAsnProAspGluThrTrpThrGlnThrSerAlaLybCyseGluLyb1LeSer	3415
Db	2891	ATTACCTGCACCCCGACAGAGACTGCACACAGCAAGCCCAATGTGAAAAATCTCA	2950
QY	3416	CysGlyProProAlaHisValGluAsnAla1LeAlaArgGlyValHisTYrGlnTYrGly	3435
Db	2951	TGTGTGTCCACAGCTGCACGTAGAAAATGCAATGCTCGAAGCCGTACCTTACATATAGGA	3010
QY	3436	AspMet1LeThrTYrSerCybTYrSerGlyTYrMetLeuGluGlyPheLeuAspSerVal	3455
Db	3011	GACATGATCACTTACTATGTTCAGTGAATCAATGTGAGGGTTTTCTGAGAGGTTT	3070
QY	3456	CysLeuGluAsnGlyThrTrpThrSerProPro1LeCyAsnAlaValCybArgPhePro	3475
Db	3071	TGTTTAAAGAAATGAAACATGGACATCACTCTATTTGACAGACGTGCTGTCAATTTCCA	3130
QY	3476	CysGlnAsnGlyGly1LeCyseGluArgProAsnAlaCyseSerCysProGluGlyTYrPheC	3495
Db	3131	TGTCAAGATGGGGCACTGTCCAAAGCCCAATGTCTGTCTGTGCCAGAGGGCTGGATG	3190
QY	3496	GlyArgLeuCyseGluGluPro1LeCyb1LeuProCybLeuAsnGlyArgCyVal	3515

Db 3191 GGGCCCTCTGTGAAGAACCAATCTGCAATCTTCCCTGCTACAGGAGCTGCTGTG 3250
 Oy 3516 AAlapryrYngInCyAspCyseProProglYtPThnGlySerAryCyeshIshrAlaVal 3535
 Db 3251 GCGCTTACCACTGACGTGACCCGCTGCTGACGGGCTCTGCTGATACAGCTGTT 3310
 Oy 3536 CysGInSerProCyLeuAmnGlyGlyLysCyValArgProAmnArgCysHisCyLeu 3555
 Db 3311 TGCCAGTCTCCCTGCTTAATGCTGGAATGCTGAAGCAAAACGAGTCACTGCTT 3370
 Oy 3556 SerSerTPThnGlyHisAmnCyseAryGlyArgArgTPThnGlyPhe 3571
 Db 3371 TCTTCTGACCGGACATTAATGCTTCCAGAAAGAGAGACTGGGTTT 3418
 RESULT 18
 ABO7803
 ID ABO7803 standard; DNA; 3804 BP.
 AC ABO7803;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Novel human nucleic acid SEQ ID No 43.
 XX
 KW Immunostimulant; antirheumatic; antiarthritic; neuroprotective;
 KW antiallergic; antidibetic; antiaesthetic; antiinflammatory; nootropic;
 KW immunosuppressive; anticoagulant; thrombolytic; antithrombotic;
 KW cytostatic; nephrotoxic; antiparkinsonian; gynecological; virucide;
 KW antibacterial; antihypertensive; fungicide; HCPAT05; HMAE95; HTNBM01;
 KW immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular;
 KW inflammatory condition; graft-versus-host disease; reproductive system;
 KW blood-related disorder; hyperproliferative; endocrine; neurological;
 KW respiratory; renal; infectious disease; gastrointestinal; gene therapy;
 KW neuronal growth; neuronal disorder; neuro-degenerative condition;
 KW keratinocyte growth; human; ds.
 KW
 OS Homo sapiens.
 XX
 PN US2002066330-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 17-JAN-2001; 2001US-00764893.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225268P.
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 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234397P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239335P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI, 2002-665432/71.
 XX
 XX Novel polypeptide useful for diagnosis, prognosis, prevention, and
 PT treatment of immune, hyperproliferative, renal, respiratory,
 PT cardiovascular, reproductive, endocrine, gastrointestinal and
 PT neurological disorders.
 XX
 PS Disclosure, Page 229-231, 335pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a sequence at
 CC least 90% identical to a full length protein sequence selected from 55
 CC sequences given in the specification such as a sequence of 163, 74 or 140
 CC amino acids fully defined in the specification, or the encoding sequence
 CC contained in 49 cDNA clones given in specification e.g. HCPAT05, HMAE95
 CC or HTNBM01. The protein and its encoding nucleic acid are useful for
 CC diagnosing a pathological condition or susceptibility to a pathological
 CC condition in a subject and for preventing, treating or ameliorating a
 CC medical condition. The protein, its encoding nucleic acid and an isolated
 CC antibody that can bind to the protein are useful in treating, preventing,
 CC diagnosing and/or prognosing immunodeficiencies, autoimmune disorders,
 CC allergic reactions and conditions, inflammatory conditions, graft-versus-
 CC host disease, blood-related disorders, hyperproliferative disorders,
 CC renal disorders, cardiovascular disorders, respiratory disorders,
 CC neurological disorders, endocrine disorders, reproductive system
 CC disorders, infectious diseases, and gastrointestinal disorders. The
 CC protein of the invention is useful to stimulate neuronal growth and to
 CC treat, prevent, and/or diagnose neuronal damage which occurs in certain
 CC neuronal disorders or neuro-degenerative conditions, for stimulating
 CC keratinocyte growth, to prevent hair loss, to modulate mammalian
 CC characteristic such as body height, weight, hair color, and to increase
 CC or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors or other nutritional
 CC components. The nucleic acid of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents one of the novel nucleic
 CC acids of the invention
 XX
 SQ Sequence 3804 BP; 1025 A; 859 C; 915 G; 1006 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8e-315 Length: 3804
 Score: 6452.00 Matches: 1135
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.91% Mismatches: 0
 Query Match: 32.30% Indels: 0

DB:	6	Gap:	0
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QY	2436	ValProValGluCysProGlnProGluGluIleProAsnGlyTleIleAspValGlnGly	2455
DB	11	GTTCGAGTGAATGTCCTCCCAAGCTGAGAAATCCCAATGAGATCATGATGTGCAAGGC	70
QY	2456	LeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysProGlyPheGluIleValGlyAsn	2475
DB	71	CTTGCGTAACTCAGACAGAGCTCTTAATACCTGCAAGCCAGGCTTTGAATGTGTGGAAAT	130
QY	2476	ThrThrThrLeuCysGlyGluAsnGlyYhiSTPLeuGlyGlyLysProThrCysLysAla	2495
DB	131	ACTACACACCTTTGTGTGAGAAATGGTCACTGCTGTGAGAGAAACCAACATGTATAAGCC	190
QY	2496	IleGluCysLeuLysProLysGluIleLeuAsnGlyLysPheSerTyrThrAspLeuHis	2515
DB	191	ATTGAGTGTCTTAACCCCAAGAGATTGTGAATGGCAATCTCTTACACGAGACTTACAC	250
QY	2516	TyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAla	2535
DB	251	TATGACAGACCGCTTACCTACCTCTTGCAACCGAGCTTCCGCTGGAAGTCCAGTCC	310
QY	2536	LeuThrCysLeuGluThrGlyAspTTrpAspValAspAlaProSerCysAsnAlaIleHis	2555
DB	311	TTGACCTGTTTGAACAACAGGTGATTGGAGTGAAGATGCCCATCTTGCAATCCCATCAC	370
QY	2556	CysAspSerProGluProIleGluAsnGlyPheValGluGlyValAspTyrSerTyrGly	2575
DB	371	TGTGATCTCCCAACCAACCATTAATAATGTTTTGTGAAGGTGCGAGATTAACGCTATGGT	430
QY	2576	AlaIleIleIleTyrSerCysPheProGlyPheGlnValAlaGlyYhiAlaMetGlnThr	2595
DB	431	GGCATATATCATCTACAGTTGCTTCCCTGGGTTTCAGGTGGCTGTGATGCCATGACAGC	490
QY	2596	CysGluGluSerGlyTTrpSerSerIleProThrCysMetProIleAspCysGlyLeu	2615
DB	491	TGTGAAGAGTCAGATGAGTGCAGTTTCATCCCAACATGTATGCCAATATAGACTGTGGCTTC	550
QY	2616	ProProIleAlaIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGlu	2635
DB	551	CCTCCTCATATAGATTTTGGAGACTGTACTAACTCAAGATGACCAAGGATATTTTGAAG	610
QY	2636	GlnGluAspAspMetMetGluValProTyrValThrProHisProProTyrHisLeuGly	2655
DB	611	CANAGAGACATATATGAGAGTTCCATATGTGACTCTCCACCTCTTATCATTTGGGA	670
QY	2656	AlaValAlaLysThrTyrGluAsnThrLysGluSerProAlaThrHisSerSerAsnPhe	2675
DB	671	GCAAGTGGCTAAACCTGGGAAATATCAAAAGAGTCTCCCTGCTACATCTTCAATCAAACTTT	730
QY	2676	LeuTyrTyrLysThrMetValSerTyrThrCysAsnProGlyTyrGluIleLeuGlyLysAsnPro	2695
DB	731	CTGATATGATACCATGATGTTTCAATACCTGTAAATCAGAGATTAAGAACTTCTGGGAAACCT	790
QY	2696	ValLeuIleCysGlnGluAspGlyThrTTrpAsnGlySerAlaProSerCysIleSerIle	2715
DB	791	GTCGTGATCTGCCAGAGAGATGGAACCTTGGAATGGCAGTGCACCATCTCGCATTTCAATT	850
QY	2716	GluCysAspLeuProThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMet	2735
DB	851	GAATGTGACTTGCCTACTGCTCTGAAATGGCTTTTGGCTTTTACAGAGACTGACATG	910
QY	2736	GlySerAlaValGlnTyrSerCysLysProGlyYhiSileuAlaGlySerAspLeuArg	2755
DB	911	GGAAGTGTGTGCAATATAGCTGTAAACCTGACCATTTTACAGACGCTCTGACTTAAGG	970
QY	2756	LeuCysLeuGluAsnArgLysTTrpSerGlyAlaSerProArgCysGluAlaIleSerCys	2775
DB	971	CTTTGTCTAGAGATATGAAAGTGGAGTGTGCTCTCCACGCTGTGAAAGCCATTTTCATGC	1030
QY	2776	LysLysProAsnProValMetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSer	2795
DB	1031	AAAAAGCCAAATTCAGTCAATGAAGATTCATCAAAAGCAACATCACTACCTTACG	1090
QY	2796	ThrLeuTyrTyrGluCysAspProGlyTyrValIleLeuAsnGlyThrGluArgThrCys	2815
DB	1091	ACGTTTATCTATGATGTGACCCCGGATATGTCTGTATGTGCACTGAGAGAGAAATGTC	1150
QY	2816	GlnAspAspLysAsnTTrpAspGluAspGluProIleCysIleProValAspCysSerSer	2835
DB	1151	CAGATGACAAAACTGGAGATGAGAGAGGCCCATTTGCAATCTCTGTGTGACTGCAATTCA	1210
QY	2836	ProProValSerAlaAsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIle	2855
DB	1211	CCCCAGCTCAGCAATGGCCAGAGTGAAGAGAACAGACATTCATCAAAAAGCAATT	1270
QY	2856	GluTyrThrCysAsnGluGlyPheLeuLeuGluGlyValAlaArgSerArgValCysLeuAla	2875
DB	1271	GAATACCTTGCAATGAGGGTTTCTGTGAGGAGACCGAGAGTCCGGTTTGTCTTGC	1330
QY	2876	AsnGlySerTTrpSerGlyAlaThrProAspCysValProValArgCysAlaThrProPro	2895
DB	1331	AATGGAAGTTGAGATGGAGCACTCCGACTGTGTGCTGTGCATGTGACACCCGCCA	1390
QY	2896	GlnLeuAlaAsnGlyValThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPhe	2915
DB	1391	CAACTGGCATTGGGGTGAAGAGAGGCTGCACTATGCTTCAATGAAGAAATTAACATTC	1450
QY	2916	HisCysHisGluGlyTyrIleLeuHisGlyValAspLysLeuThrCysGlnSerAspGly	2935
DB	1451	CACGTGACAGGGCTCAATCTTACACGGTGTCTCAAACTCACTGTGTGTCAGATGTC	1510
QY	2936	AsnTTrpAspAlaGluIleProLeuCysLysProValAsnGlyProProGluAspLeu	2955
DB	1511	AACGTGGATGAGAGATTTCCCTCTGTAAACAGGTCAACTGTGGACCTCTCGAAGACTT	1570
QY	2956	AlaHisGlyPheProAsnGlyPheSerPheIleHisGlyGlyYhiSileuTyrGlnCys	2975
DB	1571	GCCATGATTTCCCTAATGTGTTTCTTTATTCATGTGGGGCCATATACATGATCACTGC	1630
QY	2976	PheProGlyTyrLysLeuHisGlyLysAsnSerSerArgArgCysLeuSerAsnGlySerTrp	2995
DB	1631	TTTCTGATTTAAGCTCCAGAGAAATTCATCAAGAAAGTGCCTCTCCATAGGCTCTCG	1690
QY	2996	SerGlySerSerProSerCysLeuProCysArgCysSerThrProValIleGluTyrGly	3015
DB	1691	AGTGGAGCTACCTTCTCTGCTGCTTGCAGATGTTCCACACAGATATTAATATGGA	1750
QY	3016	ThrValAsnGlyThrAspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGly	3035
DB	1751	ACTGTCAATGGGAAAGATTTTGTGACTGTGAAAGGACCCGGATTCAGTCTTCAAAAGGC	1810
QY	3036	PheLysLeuLeuGlyLysLeuSerGluIleThrCysGlnAlaAspGlyGlnTTrpSerSerGly	3055
DB	1811	TTCAAGCTCTTGAAGCTTTCTGAATACCTGTATACCTGTATACCGATGAGCTCTGAG	1870
QY	3056	PheProHisCysGlnHisThrSerCysGlySerLeuProMetIleProAsnAlaPheIle	3075
DB	1871	TTTCCCACTGTGAACACATCTCTGTGTGTTCTCTTCCATATGATACCAATATGCTTATC	1930
QY	3076	SerGluThrSerSerTTrpLysGluAsnValIleThrTyrSerCysArgSerGlyTyrVal	3095
DB	1931	AGTAGACACAGCTCTTGAGAGAAATGTATATTAATTAACGCTGACGTCGTGATATGTC	1990
QY	3096	IleGlnGlySerSerAspLeuIleCysThrGluLysGlyValTTrpSerGlnProTyrPro	3115
DB	1991	ATACAGGCAAGTTCAAGTCTGAATTTGTACAGAAAGGGGTATGAGACCAAGCTTATCA	2050
QY	3116	ValCysGluProLeuSerCysGlySerProProSerValAlaAsnAlaValaThrGly	3135
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QY	3136	GluAlaHisThrTyrGluSerGluValLysLeuArgCysLeuGluGlyTyrThrMetAsp	3155

Db 2111 GAGGACACACCTATGAAAGTGAAGTGAAGTCTGAGAGTTATACATGAT 2170
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 Db 2411 TGCAGCTCAAGTTCTTGTGGGAAACCTGAAGTCCAGAAACATGATTTGTGGCAGT 2470
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 Db 2471 AATATCACTTTGAAAGCAAAATTTATTCAGCTGAGCTGCTATATGAATCAGAGCGG 2530
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 Qy 3296 GluTrpArgCysGluuThrProLeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArg 3315
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 Db 2831 GTTGATCAGAAATGTGTCCATCAATATAGGGAAGTTTCTGTGCAAGGCGCCACGGCATC 2890
 Qy 3396 IleThrCysAsnProAspGluThrTrpTrpGlnThrSerAlaLysCysGluLysIleSer 3415
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 AC ABV83885;
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 DT 09-DEC-2002 (first entry)
 XX
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 KW Immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antistroke; antianemic; antiarthritic; cancer;
 KW antihypertensive; hepatoprotective; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 KW antiparalytic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; neurotropic; gene therapy; vaccine;
 gene; ss.
 KW
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 PN US2002090672-A1.
 PD 11-JUL-2002.
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 XX 17-JAN-2001; 2001US-00764853.
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QY	2979	TYRILysLEuHISGLYAsnSerSerArgYpCYsLeuSerAsnGLYSerTIPSerGLYSer	2998
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QY	3039	LeuGLYLeuSerGLuILEThrCYsGLuAlaAspGLYINTIPSerSerGLYpHeProHIS	3058
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QY	3059	CysGLuHISThrSerCYsGLYSerLeuProMetILEProAsnAlaPheILESerGLYThr	3078
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QY	3079	SerSerTPLYsGLuAsnValILEThrTYrSerCYsArgSerGLYTYrValILEGLuGLY	3098
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Db	1921	AGTTCAGATCTGATATTGTACAGAGAAAGGGATATGAGACCGCTTATCCAGTCTGTGAG	1980
QY	3119	ProLeuSerCYsGLYSerProProSerValAlaAsnAlaValAlaATHGLYGLuAlaHIS	3138
Db	1961	CCCTGTCTGTGGGTCCCCACCGCTGTCTGCGCAATGCAGTGGCACTGGAGAGGCACAC	2040
QY	3139	ThTYrGLuSerGLuValLYsLeuArgCYsLeuGLuGLYTYrThrMetAspThrAspThr	3158
Db	2041	ACCTATGAAGTGAAGTGAATCACTCAGATGTCGGAAGGTATTAAGATATGATACAGATACA	2100
QY	3159	AspThrPheThrCYsGLuLYsAspGLYArgITPpHeProGLuArgILESerCYsSerPro	3178
Db	2101	GATACATTTCACTGTGCAGAAAGATGTGCGTGTCCCTGAGAGATATCTCTGCAGTCT	2160
QY	3179	LYsLYsCYsProLeuProGLuAsnILEThrHISILELeuValHISGLYAspAspPheSer	3198
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QY	3239	ValSerCYsGLYLYsProGLuSerProGLuHISGLYpHeValValGLYSerLYsTYrThr	3258
Db	2341	GTTCCTTGTGGAAATCTGAAAGTCCAAACAATGATATTGTGGTGTGGCAGTAATATACACC	2400
QY	3259	PheGLuSerThrILETYrGLuCYsGLuProGLYTYrGLuLeuGLuGLYAsnArgGLu	3278
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[illegible]

OS Homo sapiens.
 XX MO200071710-A2.
 PN
 XX 30-NOV-2000.
 PD
 XX 25-MAY-2000; 2000MO-FR001426.
 PF
 XX 25-MAY-1999; 99FR-00006587.
 PR 16-JUN-1999; 99US-0139450P.
 XX (AVERT) AVENTIS PHARMA SA.
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 XX Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C;
 PI Clepet C;
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 DR MPI; 2001-025161/03.
 DR P-PSDB; ABR37987.
 XX
 XX New nucleic acid derived from human chromosome 9, used e.g. for diagnosis
 PT and drug screening, derived from genes implicated in disorders of
 PT lipoprotein metabolism.
 XX
 XX Claim 1; Page 197-199; 269pp; French.
 XX
 XX The present sequence is the coding sequence for a human gene from
 CC chromosome 9q31-34. This sequence is likely to be involved in diseases of
 CC plasmatic lipoprotein metabolism, e.g. the reverse transport of
 CC cholesterol
 XX
 XX Sequence 3706 BP; 974 A; 837 C; 892 G; 995 T; 0 U; 8 Other;
 SQ
 Alignment Scores:
 Pred. No.: 2 47e-294 Length: 3706
 Score: 6044.00 Matches: 1063
 Percent Similarity: 99.72% Conservative: 0
 Best Local Similarity: 99.72% Mismatches: 3
 Query Match: 30.26% Indels: 0
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 DB 542 AAMCAGAGATATGAACTTCTGGGGAACCTGTGCTGATCTNCCAGAAAGATGAACTTGG 601
 QY 2706 AsnGlySerAlaProSerCysIleSerIleGluCysAspLeuProThrAlaProGluAsn 2725
 DB 602 AATGGACGTGACCAATCTGATTCATTAATGATCACTTGCTTACCTGCTCTGAAAT 661
 QY 2726 GlyPheLeuArgPheThrGlnThrSerMetCysSerAlaValGlnTyrSerCysIlePro 2745
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 DB 962 CCCATTGTCATCTCTGTGAGTGTGACATGACCCCAAGTCTACGCCAATGGCAGGTGGA 1021
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 QY 2866 GluGlyValAlaArgSerArgValCysLeuAlaAsnGlySerTrpSerGlyValAlaThrProAsp 2885
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Db	1621	TATGACTATGAAAATGGCTTGTCAATTGGACACAGGTGGCTGGGGGTGGAGCTAAATAGCTG	1680
Qy	878	AsPTyTserTYrAsPaAPPhelaeuApThVaIgingluThrAlaThrSerillegLYaAn	897
Db	1681	GATTACCTCTTAACGATGACTTCTTGACACTGTGTCAAGAAACAGCCACAGACTGTGGCAAT	1740
Qy	898	AlaLySerSerAagjileLYaArgSerAlaProLeuSerAsPTyTLYaileLYsleuile	917
Db	1741	GGCAGGTCTCAACCGATTAAAGAAAGTGGCCCATTAATCTGACTATAAATTAAGTTAATT	1800
Qy	918	PhaenilleThralaSerValProLeuProAspGluArgAsnApThrLeuGluTTPglu	937
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Qy	938	AsnGingluThraGluLeuGlnThrLeuGluThrLileThraAsnLYsleuLYsArgThrLeu	957
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Qy	958	AsnLYsAsPProMetTYrSerPheGlnLeuAlaSerGluileuLileuLilealAsPSerAsn	977
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Qy	978	SerLeuGluThrLYsLYaAlaSerProPheCysArgProGlySerValleuArgLYaArg	997
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Qy	998	MetCysValaAsnCYsProLeuGlyThrTYrTYrAsnLeuGluThrsPheThrCysGluSer	1017
Db	2041	ATGTGTGCAATYGGCTTGTGGAAACCTATTAATATCGAAGCACTTCACTGGAAGC	2100
Qy	1018	CysArgjileGlySerTYrGlnAspGluGluGlnLeuGlnCYsLYsleuCYsProSer	1037
Db	2101	TGCCGAATCGGATCTCTACAGATTAAGAAAGGCACTGAGTGTCAAGCTTGGCCCTCT	2160
Qy	1038	GlyMetTYrThngluTYrLileHiseThrAsnLileSerAsPcYsLYaAlaGlnCYsLYs	1057
Db	2161	GGGATGTACAGGAATATATCATTTCAAGAAACATCTGTGATTGTAAGCTCAGCTGTAA	2220
Qy	1058	GlnGlyThrTYrSerTYrSerGlyLeuGluThrCYsGluSerCYsProLeuGlyThrTYr	1077
Db	2221	CAAGCACTACTCTACACGTGAGCTTAAGACTGTGATGATGTGTCCACTGAGCACTTAT	2280
Qy	1078	GlnProLYsPheGlySerArgSerCysLeuSerCYsProGluAsnThrSerThrValLYs	1097
Db	2281	CAGCCAAATTTGGTTCCTGGAGCTGCTCTCGGTCTCAAGAAACACTCAACTGTAAA	2340
Qy	1098	ArgGlyAlaValaAsnLileSerAlaCYsGlyValProCYsProGluGlyLYsPheSerArg	1117
Db	2341	AGAGAGCGGTGAACATTTCTGCAATGTGGAGTCTTGTGCCAGAAAGAAATTCCTCGGT	2400
Qy	1118	SerGlyLeuMetProCYsHisProCYsProArgAsPTyTYrGlnProAsnAlaGlyLYs	1137
Db	2401	TCGGGGTTAATCCCTGTCACCAAGTCTCTGTGACTATTCACCACTTAATGCGAGGAG	2460
Qy	1138	AlaPheCYsLeuAlaCYsPhePheTYrGlyThrThrProPheAlaGlySerArgSerille	1157
Db	2461	GGCTTCTGTGAGCTGTCCCTTTATGGAACCTACCCCATGTGCTGTTCAGATTCATC	2520
Qy	1158	ThngluCYsSerSerPheSerSerThrPheSerAlaAlaGluGluSerValValProPro	1177
Db	2521	ACAGAAATTTCAAGTTTATGTTCACTTCTCAAGGCGCAAGGAAGTGTGTGCCCCCT	2580
Qy	1178	AlaSerLeuGlyHisLileLYsLYaArgHisGluLileSerSerGlnValPheHisGluCYs	1197
Db	2581	GCCTCTCTTGACATATTAATAAAGAGGCACTGAATACAGCACTCAAGTTTTCCATGAATGC	2640
Qy	1198	PhePheAsnProCYsHisAsnSerGlyThrCYsGlnGlnLeuGlyArgGlyTYrValCYs	1217
Db	2641	TTCTTTAAACCTTGGCACAAATGTGTGAACCTTCCAGCAACTTGGCGAGTGTATTTGTTGT	27000

QY	1218	LeuCSySProlenuglyYTTThnglyVleuVysCysgluThraAspIleAspGluCysSerPro	1237
Db	2701	CTGTGTCACACTGGANTATACAGGCTTAAAGTGTAACAGACATCAATGAGTGCAGCCCA	2760
QY	1238	LeuProCysLeuAenAenAnglyValCysLeysAspLeuValGlygluPheIleCysgluCys	1257
Db	2761	CTGCTCTTCCCTCAACATGAGCTTGTThPAAGACCTACTTGGGGAAATCAATTGTGAGTGC	2820
QY	1258	ProSerGlyYTTThnglygluVnaGysgluGluGluAsnIleAsnGluCysSerSerPro	1277
Db	2821	CCATCAGGCTTACACAGGCTCAGCGGTGAGAAATAATTAATGAGTGTAGCTCCAGTCT	2880
QY	1278	CysLeuAsnlyVsglyYIleCysValAspGlyValAlaGlyTYrArgCysfThCysVallys	1297
Db	2881	TGTTTAAATTAAGGAATCTGTGTGATGAGTGTGGCTGGCTTACCTTGCACATGTGTGAAA	2940
QY	1298	GlyPheValGly 1301	
Db	2941	GGATTGTAGGT 2952	
RESULT 23			
AAS03887			
ID	AAS03887	standard; cDNA; 2929 BP.	
XX	AAS03887;		
XX	29-AUG-2001 (first entry)		
XX	Human secreted protein gene #6.		
XX	Human secreted protein; autoimmune disorder; hyperproliferative disorder;		
KM	cardiovascular disorder; cerebrovascular disorder; angiogenesis; ss;		
KM	nerve system disorder; bacterial infection; viral infection; as;		
KM	fungal infection; ocular disorder; wound healing; tissue regeneration;		
KM	epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.		
XX	Homo sapiens.		
XX	WO200123598-A1.		
XX	05-APR-2001.		
XX	26-SEP-2000; 2000WO-US026324.		
XX	27-SEP-1999; 99US-0155807P.		
XX	(HDMA-) HDMA GENOMB SCT INC.		
XX	Komatsoulis G, Ruben SM, Rosen CA;		
XX	WPI: 2001-281684/29.		
XX	P-PSDB; AAU01931.		
XX	Forty nucleic acid molecules encoding human secreted proteins, useful in		
XX	the prevention, treatment and diagnosis of cancer, immune disorders,		
XX	cardiovascular disorders and neurological diseases.		
XX	Disclosure; Page 447-448; 518pp; English.		
XX	Sequences AAS03873-AAS03922 represent isolated nucleic acid molecules and		
XX	PCR primers of the invention. acid of the invention. Secreted proteins		
XX	and their related nucleic acids can be used in the diagnosis of or		
XX	susceptibility to a pathological condition by determining the presence or		
XX	absence of a mutation in a nucleic acid or by the presence or amount of		
XX	expression of a secreted protein. The sequences are used to prevent;		
XX	treat or ameliorate a medical condition in e.g. humans, mice, rabbits,		
XX	goats, horses, cats, dogs, chickens or sheep. The antibodies to the		
XX	polypeptides can also be used in alleviating symptoms associated with		
XX	disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme		
XX	linked immunosorbent assays (ELISA). The disorders include autoimmune		
XX	diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.		
XX	neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac		

CC arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis,
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.
 CC The peptides can also be used to aid wound healing and epithelial cell
 CC proliferation, to help prevent skin ageing due to sunburn, to maintain
 CC organs before transplantation, to regenerate tissues, in chemotaxis and
 CC as a food additive or preservative to alter storage capabilities

XX Sequence 2929 BP; 771 A; 662 C; 731 G; 764 T; 0 U; 1 Other;

Alignment Scores:

Prod. No.:	1.35e-242	Length:	2929
Score:	5012.00	Matches:	881
Percent Similarity:	99.89%	Conservative:	0
Best Local Similarity:	99.89%	Mismatches:	1
Query Match:	25.09%	Indels:	0
DB:	4	Gaps:	0

US-09-977-053-4 (1-3571) x AAS03807 (1-2929)

QY	2690	GlutLeuEngIYAenProValleuIleCYsgIngluaAepGIYThrTPAsnGlySerAla	2709
DB	14	GAACCTTGGGGAAACCTGTCGTATCTGCCAGAAAGATGGAATCGAATGCGAGTGC	73
QY	2710	ProSerCyAlleSerIleGIuCYaApleuProThralaProGIuaenGIYpHeuArg	2729
DB	74	CCATCTGCAATTCATTAATGATGACTGCTCTACTGCTCCGAAATGGCTTTTGGCT	133
QY	2730	PhetHrIuHrSerMetGIYSerAlaValGIuYrSerCYaIyProGIYHleIleu	2749
DB	134	TTTACAGAGATACATGAGAGAGCTGTGTGACATACCTGAACTCGAACACATTTCA	193
QY	2750	AlaGIYSerApleuAArgIeCYeIuEngIuaAenArgIYTPSerGIYAlaSerProArg	2769
DB	194	GCAGGCTCTGACTTAAGCTTTGTCTAGAGAAATGAAAGTGAAGTGGCTCCCAAGC	253
QY	2770	CysGIuAlaIleSerCYaIyApleuProAenProValMetAenGIYSerIleYsGIYSer	2789
DB	254	TGTAAACCATTTTCATGCAAAAGCAAAATCCAGTCATGAATGATCATCAAGAGAGC	313
QY	2790	AsnYrThrTYrIeAserThleuTYrTYrGIuCYaApleuProGIYTYrValIleuAenGIY	2809
DB	314	AACATCAATACCTGAGACCTGTGACTATGATGATGACCCCGATATGTCTGAATGAC	373
QY	2810	ThrGIuArgATThrCYsGIuAAspApleYAsnTPAspGIuAAspGIuProIleCYsIle	2829
DB	374	ACTAGAGAGAAACATGCCAGATGACAAAACCTGGATGAGAGATGCCCATTTGCATT	433
QY	2830	ProValAAspCYsSerSerProProValSerAlaAenGIYGIuAlaArgGIYAspGIuTYr	2849
DB	434	CCTGTGACCTGCAATTCACCCCAAGTCACCAATGCGCAGGTGAGAGAGACAGATAC	493
QY	2850	ThrPheGIuYsGIuIleGIuTYrThrCYaAenGIYpHeIleuEngIuGIYAlaArg	2869
DB	494	ACATTTCCAAAAGAGATTGAATACCTTGCAATGAAGGTTCTTCTTGAAGGACCAAG	553
QY	2870	SerATrValCYsLeuAlaAenGIYSerTPSerGIYAlaTrnProAspCYsValaProVal	2889
DB	554	AGTGGGTTTCTCTTGGCAATGGAAGTGTGAGTGAAGCACCTCCGATGTGTGCTGT	613
QY	2890	ArgCYaAlaThrProProGIuLeuAlaAenGIYAlaThrGIuGIYLeuAAspTYrIlePhe	2909
DB	614	AGATGTGCAACCCCGCAACATGCGCAATGGGTGAGCGAAGGCTTGACATATGCTTC	673
QY	2910	MetYsGIuValIleThrPheIleCYeHleGIuGIYTYrIleLeuHleGIYAlaProYsLeu	2929
DB	674	ATGAAGAGATGACATTCACATCTGATAGAGGCTTACATCTTGCAAGGCTCTCCAAATC	733
QY	2930	ThrCYsGIuAAspGIYAsnTPAspAlaGIuIleProLeuCYaIyProValAAsnCYs	2949
DB	734	ACCTGTCAGTGAGATGCGAATGCGATGACAGATTCCTCTGTAAACCAAGTCACTGT	793
QY	2950	GIYProProGIuAAspLeuAlaHleGIYpHeProAenGIYpHeSerPheIleHleGIYIle	2969

DB	794	GGACCTCTTGAAGATCTGCCAGGTTCCTTAATGATTTTCTTTATTCATGAGGAC	853
QY	2970	HleIleGIuTYrGIuCYpHeProGIYTYrIyApleuHleGIYAsnSerAArgArgCYs	2989
DB	854	CATATACATGATGATGCTTCTTCTGTATTAAGCTCCATGGAATTCATCAAGAGGTGC	913
QY	2990	LeuSerAenGIYSerTPSerGIYSerSerProSerCYsLeuProCYaArgCYsSerThr	3009
DB	914	CTTCCAAATGAGCTCTGAGAGTGCAGCTCACCTTCTCTGCTGCTTGCAGATGTTCCCA	973
QY	3010	ProValIleGIuTYrGIYThrValAAsnGIYThrAAspPheAAspCYsGIYValaAlaArg	3029
DB	974	CCAGTAATTAATTAATGAACTGTAAGGACAGATTTTGACTGTGAAAGGACACCCG	1033
QY	3030	IleGIuCYpHeIySGIYpHeIyApleuGIYLeuSerGIuIleThrCYsGIuAlaAAsp	3049
DB	1034	ATTCAATCTTCAAAGGCTTCAGCTCTTACAGATTTCTGAATACCTGTGAAGCCGAT	1093
QY	3050	GIYIleTPSerSerGIYpHeProHleCYsGIuHleIleThrSerCYsGIYSerIleuProMet	3069
DB	1094	GGCCAGTGAAGCTCTGGGTTCCCACTGTGAACACATTCGTGTGTTCTTCCAAATG	1153
QY	3070	IleProAenAlaApleIleSerGIuThrSerSerTPYsGIuAenValIleThrTYrSer	3089
DB	1154	ATACCAATGGGTCATCAGTACAGACAGCTCTTGAAAGAAATGTATTAATTTTAC	1213
QY	3090	CysAArgSerGIYTYrValIleGIuGIYSerSerApleuIleCYsThrGIuYsGIYVal	3109
DB	1214	TGCAATGTGATATGATCATACAAAGGACGTTCAATGATTTGTATACAGAAAGGGGTA	1273
QY	3110	TPSerGIuProTYrProValCYsGIuProLeuSerCYsGIYSerProProSerValAla	3129
DB	1274	TGAGAGCAGCTTATTCAGCTGTGAGCCCTTGCTGTGGGTCCCAACCGCTGTGCGC	1333
QY	3130	AenAlaValaIleThrGIuAlaHleIleThrTYrGIuSerGIuValIyLeuAArgCYsLeu	3149
DB	1334	AATGCAATGAGCACTGAGAGGACACACCTATGAAGATGAATACACAGATCTGAG	1393
QY	3150	GIuGIYTYrThrMetAAspThrAAspThrAAspThrPheThrCYsGIuYsAAspGIYArgTrp	3169
DB	1394	GAAAGTTATAGATGATGATACAGATACATCAATCACCTGTGACAAAGATGGTGGCTGG	1453
QY	3170	PheProGIuAAspIleSerCYsSerProYsIyCYsProLeuProGIuAAsnIleThrHle	3189
DB	1454	TTCCCTGAGAAATCTCTCGAGTCTTAAATAATCTCTCCCGAAACATTAACACAT	1513
QY	3190	IleLeuValHleGIYAspAAspPheSerValAAsnArgIuValSerValSerCYsAlaGIu	3209
DB	1514	ATACTTGAATGGGAGAGATTTCAAGTGAATAGGCAAGTTCTGTGTCAATGACAGAA	1573
QY	3210	GIYTYrThrPheGIuGIYValAAsnIleSerValCYsGIuAAspGIYThrTrpGIuPro	3229
DB	1574	GGGTATACCTTTAGAGGAGATTACATATCAGATATCAGCTTGAATGGAACCTGGAGCA	1633
QY	3230	ProPheSerAAspGIYSerCYsSerProValSerCYsGIYIyProGIuSerProGIuHle	3249
DB	1634	CCATTTCCGATGATCTTGAAGTCTCAGTGTCTTGTGGAAACCTGAAAGTCCAAACAT	1693
QY	3250	GIYpHeValIleGIYSerIyTYrThrPheGIuSerThrIleIleTYrGIuCYsGIuPro	3269
DB	1694	GAATTTGTGTGGAGTAATACCTTTGAAAGCAATTAATTTATTCAGTGTAGGCTT	1753
QY	3270	GIYTYrGIuEngIuGIYAsnAArgIuArgValCYsGIuIuAAsnAArgIleTPSerGIY	3289
DB	1754	GGCTATGAATAGAGAGGAGACGAGGACGTGTCTCCAGAGAAACAGACAGTGGAGTGA	1813
QY	3290	GIYValaIleIleCYsGIuGIuThrArgCYsGIuThrProLeuGIuPheIuAAsnGIYIyS	3309
DB	1814	GGGGTGGCAATATGCAAGAGACAGGTGTGAATCTCCATGAAATTTCTCAATGGAGAA	1873
QY	3310	AlaAAspIleGIuAAspArgThrThrGIYProAenValIleTYrSerCYsAAsnAArgIYTYr	3329

DB 1874 GCTGACATTGAAAACAGACAGCTGAGCCCAACGTGTATATCTCTGCAACAGAGGCTAC 1933
 QY SerLeuGluGlyProSerGluAlaHisCysThrGluAsnGlyThrTrpSerHisProVal 3349
 DB 1934 ACCTTTGAAAGGCGCATCTGAGGCACTGCAAGAAAAGAACTGGAGCCCAACGCTC 1993
 QY ProLeuGlyValProAsnProCysProValProPheValIleProGluAsnAlaLeu 3369
 DB 1994 CCTCTCTGCAACCAATTCATCCCTGCTCTTTGTATTCCTCAGATGCTCTGCTG 2053
 QY SerGluValGluPheValValAsnGluValSerIleValCysValArgGluGlyPheLeu 3389
 DB 2054 TCTGAAAAGAGCTTTATGTATGATGCAAGATGTCTCATCAAAATGAGGAGGTTTCTG 2113
 QY LeuGlnGlyHisGlyIleIleThrCysAsnProAspGluThrTrpThrGlnThrSerAla 3409
 DB 2114 CTCGAGGCGCCAGCGCTCATCTTACCTGCAACCCGACGACGCTGACACAGACAGCCGC 2173
 QY LysCysGluValIleSerCysGlyProProAlaHisValGluAsnAlaIleAlaArgGly 3429
 DB 2174 AATGTGAAAATATCATGTGTCCACAGCTCATGTAGAAAATGCATATGCTCGAGGC 2233
 QY ValHisGlyGlnThrGlyAspMetIleThrTrpSerCysGlySerGlyTrpMetLeuGlu 3449
 DB 2234 GTACATTTATCAATATGAGACATGATCACCCTACTCATGTTCAGTGATACATGTGAG 2293
 QY GlyPheLeuArgSerValCysLeuGluAsnGlyThrTrpThrSerProProIleCysArg 3469
 DB 2294 GCTTTCTGAGAGCTGTGTGTTTGAATAATGAAATGAACTGACATCCTCTTATTTGACA 2353
 QY AlaValCysArgPheProCysGluAsnGlyGlyIleCysGlnArgProAsnAlaCysSer 3489
 DB 2354 GCTGTCTGTCATTTCCATGTCAGATGAGGAGGATGCGCAACGCCCAATGCTTCTCC 2413
 QY CysProGluGlyTrpMetGlyArgLeuGluGluProIleCysAlaLeuProCysLeu 3509
 DB 2414 TGTCCAGAGGCGCTGATGAGGCGCTCTGTGAAAGCAATGTCATTTCTCTCTCTG 2473
 QY AsnGlyValArgCysValAlaProGlyGlnCysAspCysProProGlyTrpThrGlySer 3529
 DB 2474 AACGAGGTCGCTGTGTGCGCTTACAGATGATGATGCTGCGCTGAGAGGGGTCT 2533
 QY ArgCysHisThrAlaValCysGlnSerProCysLeuAsnGlyGlyIleCysValAlaPro 3549
 DB 2534 CCTGTCTATACAGCTGTGTGCGCTGCTCTCTGTTAAATGTGAGAAAATGTGTAACCA 2593
 QY AsnArgCysHisCysLeuSerSerTrpThrGlyHisAsnCysSerArgIysArgArgThr 3569
 DB 2594 AACCAATGTCACCTGTCTTCTTGTGACGAGCATTAAGTTCACAGAAAAGAGAGACT 2653
 QY GlyPhe 3571
 DB 2654 GGGTTT 2659
 RESULT 24
 ABX34482
 ID ABX34482 standard; cDNA; 2697 BP.
 AC ABX34482;
 DT 13-FEB-2003 (first entry)
 DX Human mddc cDNA seq ID 43.
 DE
 XX MDDT: human; disease detection and treatment molecule polypeptide;
 XX anti-inflammatory; immunosuppressive; osteoporotic; cytostatic; anti-HIV;
 XX haemostatic; nephrotoxic; antianemic; antiproliferative; hepatotoxic;
 XX gene therapy; protein replacement therapy; cell proliferative disorder;
 XX cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 XX anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 XX Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;
 XX psoriasis; hepatitis; gene; ss.

OS Homo sapiens.
 XX
 XX WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX
 XX 27-MAR-2002; 2002MO-US009944.
 XX
 XX 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Daffe A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GB, Hillman JL, Yu JY, Tuason O, Yap PR, Anshey SR;
 PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Rerita CH, David MR, Lewis SA, Chen AJ, Panzer SR, Harris B,
 PI Flores V, Marwaha R, Io A, Lam RY, Urashka ME;
 XX
 XX MPI; 2003-058431/05.
 DR P-PSDB; ABU11492.
 XX
 PT New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX
 PS Claim 1; SEQ ID NO 43; 339pp + Sequence Listing; English.
 XX
 XX This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteoporotic, cytostatic, anti-HIV, haemostatic, nephrotoxic,
 CC antianemic, antiproliferative and hepatotoxic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukemia, lymphoma, melanoma, myeloma or sarcoma), anemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndrome, inflammation, osteoporosis, thrombocytopenia, psoriasis or
 CC hepatitis. ABX34480-ABX34835 encode the MDDT polypeptides represented in
 CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2697 BP; 699 A; 635 C; 650 G; 713 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.41e-240 Length: 2697
 Score: 4971.00 Matches: 891
 Percent Similarity: 99.44% Conservative: 3
 Best Local Similarity: 99.11% Mismatches: 4
 Query Match: 24.89% Indels: 2
 DB: 7 Gaps: 0
 US-09-977-053-4 (1-3571) x ABX34482 (1-2697)
 QY 1671 TTTCTGLeuAsnGlnGlyGlnThrGlnProLeuProHisCysGluValIleSerCys 1690
 DB 1 TACTGTCTTACTCAACAGACAGTGACACAGCACTTCTTCACTGTAACCATTAAGCTGT 60
 QY 1691 GlyValProProLeuGluGluAsnGlyPheHisSerAlaAspAspPheArgIleGlySer 1710
 DB 61 GGGGTCCACCTCTTTGAGAAATGCGCTTCCATTCAGCGGATCATCTTATATGCGCAGC 120

QY 1711 ThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeuGlyAspSerPheGlyPheCys 1730
 DB |||||
 DB 121 ACAGTAACCTTACCAAGTGCACAAATGGCTACTATCTATGGGTGACTCAAGAGTGTCTGT 180
 QY 1731 ThrAspAsnGlySerTTPAsnGlyValSerProSerCysLeuAspValAspGluCysAla 1750
 DB |||||
 DB 181 ACAGATATATGGAGCTGGAAAGGGGTTTCAACATCTGGCTTGAATGTGATGAAGTGTGCA 240
 QY 1751 ValGlySerAspCysSerGluLysAlaSerCysLeuAsnValAspGlySerTyr1LeCys 1770
 DB 241 GTTGGATCAGATATGTATGTAGACAGTCTTCTTGGCTGAACGTAGATGATCTTACATATGT 300
 QY 1771 SerCysValProProTyrThrGlyAspGlyLysAsnGlyValGluPro1LeLysCysLys 1790
 DB 301 TCAATGTCTCCACCGTACACAGAGAGATGGGAAAACTGTGCAGAACTATTAATGTATAG 360
 QY 1791 AlaProGlyAsnProGlyLysAsnGlyHisSerSerGlyGluTyrThrValGlyAla 1810
 DB 361 GCTCCAGAAATCCGAAAAATGGCCACTCTCAGGTAGATTTATACAGTATGGTGGCAA 420
 QY 1811 ValThrPheSerCysGlnGlnGlyTyrGlnLeuMetGlyValThrLys1LeThrCysLeu 1830
 DB 421 GTCACTATTTCTGCTCAGAAAGATACCAAGTTGATGGAGATACCAAAATCAGATGTTTG 480
 QY 1831 GluSerGlyGluTTPAsnHisLeu1LeProTyrCysLysAlaValSerCysGlyLysPro 1850
 DB 481 GAGCTCGAGAAATGGAATTCATCTATATACATATGTAAAGCTGTTCATATGTGTAAACCG 540
 QY 1851 Ala1LeProGlyLysAsnGlyCys1LeGluGluLeuAlaPheThrPheGlySerLysValThr 1870
 DB 541 GCTATTCAGAAATGGTGTGATTTAGAGATTAACATTTACTTTTGGAGAAAGTGTGCA 600
 QY 1871 TyrArgCysAsnLysGlyTyrThrLeuAlaGlyAspLysGlySerSerCysLeuAlaAsn 1890
 DB 601 TATAGGTGATTAAGAAGATATACTCTGGCCGGTATTAAGAATCATCTGTCTGTGTAC 660
 QY 1891 SerSerTTPSerHisSerProProValCysGluProValLysCysSerSerProGluAsn 1910
 DB 661 AGTTCTTGAGATCATTCCTCCCTGCTGTGTGAAACAGATGAAGTGTCTAGTCCGAAAT 720
 QY 1911 LLeAsnAsnGlyLysTyr1LeLeuSerGlyLeuThrTyrLeuSerThrAlaSerTyrSer 1930
 DB 721 ATTAATATATGAATAATATATTTGAGTGGCTTACCTTCTTACTGCATCATATTTCA 780
 QY 1931 CysAspThrGlyTyrSerLeuGlnGlyProSer1Le1LeGluCysThrAlaSerGly1Le 1950
 DB 781 TCGGATACAGGATACAGCTTACAGGGCCCTTCCATATATGAATGACACGGCTTGGCATC 840
 QY 1951 TrpAspArgAlaProProAlaCysHisLeuValPheCysGlyGluProProAla1LeLys 1970
 DB 841 TGGGACAGACCGCCACCTGGCTGTCACTGTCTTGTGTGAAACCACTCGCATATAA 900
 QY 1971 AspAlaVal1LeThrGlyAsnAsnPheThrPheArgAsnThrVal1ThrTyrThrCysLys 1990
 DB 901 GATGCTCATTTTACGGGAAATTACTTCACTTTCAGAAACACCGTCACTTACACTTGCATA 960
 QY 1991 GluGlyTyrThrLeuAlaGlyLeuAspThr1LeGluCysLeuAlaAspGlyLysTTPSer 2010
 DB 961 GAAGGCTATATCTCTGTGCTTGAACACCATTAATGCTGGCCGACGGAATGTGAGT 1020
 QY 2011 ArgSerAspGlnGlnCysLeuAlaValSerCysAspGluProPro1LeValAspHisAla 2030
 DB 1021 AGAAGTGACACGACAGTCCCTGGCTGTCTCTGTATAGCAACCATTTGTGGAACCAAGCC 1080
 QY 2031 SerProGluThrAlaHisArgLeuPheGlyAsp1LeAlaPheTyrTyrCysSerAspGly 2050
 DB 1081 TCTCCAGAGCTGCTCCATGGCTTTTGGACATGTGCAATTTCTACTCTGCTTGAATGTT 1140
 QY 2051 TyrSerLeuAlaAspAsnSerGlnLeuLeuCysAsnAlaGlnGlyLysTTPValProPro 2070
 DB 1141 TACAGCTTACAGACATTTCCAGCTTCTCTGCAATGCCGACGAGAGTGTGATCCCCCA 1200

QY 2071 GluGlyGlnAspMetProArgCysAlaHisPheCysGlyLysProProSerValSer 2090
 DB |||||
 DB 1201 GAAGGTCAAGACATGCCCCGTGTATATGACTATTTGTGTAAAACTTCCATCGGATTTCC 1260
 QY 2091 TyrSer1LeLeuGlnSerValSerLysAlaLysPheAlaAlaGlySerValValSerPhe 2110
 DB 1261 TATAGCATCTTGGATCTGTGAGCAAAAGCAAAATTTGCAAGTGGCTGACTGTCGCTTT 1320
 QY 2111 LysCysMetGluGlyPheValLeuAsnThrSerAlaLys1LeGluCysMetArgGlyGly 2130
 DB 1321 AAATGCATGGAAGCTTTGTACTGACACCTCAGCAAAAGATTTGATATGATGAGTGGG 1380
 QY 2131 GluTTPAsnProSerProMetSer1LeGlnCys1LeProValArgCysGlyGluProPro 2150
 DB 1381 CAGTGAACCTTCTCCCATGTTCATCCATGTCATCTCTGTGCGGTGTGGAAGCCACCA 1440
 QY 2151 Ser1LeMetAsnGlyTyrAlaSerGlySerAsnTyrSerPheGlyAlaMetValAlaTyr 2170
 DB 1441 AGCATCATGATGGCTATGCAAGTGGATCAAACTACAGTTTGGAGCATGTGGCTTAC 1500
 QY 2171 SerCysAsnLysGlyPheTyr1LeLysGlyGluLysSerThrCysGluAlaThrGly 2190
 DB 1501 AGTGCAAACAGGGGTTCTACATCAAAAGGGAAGACACCTGGCAAGCCACAGGG 1560
 QY 2191 GluTTPSerSerPro1LeProThrCysHisProValSerCysGlyGluProProVal 2210
 DB 1561 CAGTGAAGTATCTTATACCAAGTGCACCCGGATTTGTGTGAAACCACTTAAGTT 1620
 QY 2211 GluAsnGlyPheLeuGlnHisThrThrGlyArg1LePheGluSerGluValArgTyrGln 2230
 DB 1621 GAGATGGCTTTCTGGAGCATACAACTGGCAGATCTTTGAGAGTGAAGTGAAGTATCAG 1680
 QY 2231 CysAsnProGlyTyrTyrLysSerValGlySerProValPheValCysGlnAlaAsnArgHis 2250
 DB 1681 TGTAAACCGGCTTAAATGTCAGTGGAAATCTGTATTTGTCTGTCCAGAACCAATGCGCAC 1740
 QY 2251 TrpHisSerGlySerProLeuMetCysValProLeuAspCysGlyLysProPro1Le 2270
 DB 1741 TGGCAGTGAATCCCTCTGATGTGTGTCTCTCACTGTGAAACCTCCCGCATC 1800
 QY 2271 GlnAsnGlyPheMetLysGlyGluAsnPheGluValGlySerLysValGlnPhePheCys 2290
 DB 1801 CAGATGGCTTCAAGAAAGGAAAGAACTTTGAAAGTGAAGGCTCAAGTTTCTGT 1860
 QY 2291 AsnGluGlyTyrGluLeuValGlyAspSerSerTTPThrCysGlnLysSerGlyLysTTP 2310
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 QY 2311 AsnLysLysSerAsnProLysCysMetProAlaLysCysProGluProProLeuLeuGlu 2330
 DB 1921 AATTAAGAAATCAAAATCCAAAGTGCATGCTGCAGAGGCCCAAGAGCCGCTCTGGAA 1980
 QY 2331 AsnGlnLeuValLeuLysGluLeuThrThrGluValGlyValValThrPheSerCysLys 2350
 DB 1981 AACCAAGTATGATTAAGAGATTCACACGAGGTAGAGATTTTCCGTGATAA 2040
 QY 2351 GluGlyHisValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnGlnTTPAsn 2370
 DB 2041 GAAGGGCATGTCCGCAAGGCCCTCTGTCTGTGAAATGCTTGCAATCCACACATATGAAAT 2100
 QY 2371 AsnSerPheProValCysLysAlaValLeuCysThrProProProLeu1LeSerPheGly 2390
 DB 2101 GACTCTTCCCTGTGTGTATATGTCTTTGTATCCCACTCCCTTAATTTCTTGTGT 2160
 QY 2391 ValPro1LeProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGly 2410
 DB 2161 GTCCCATTTCTTCTGTGCTCTTCAATTTGGAAGTACTGTCAAGATATCTTGTGTAGGT 2220
 QY 2411 GlyPhePheLeuAlaGlyLysAsnSerThrThrLeuCysGlnProAspGlyThrTTPSerSer 2430
 DB 2221 GGGTTTTTCCTAAGAGAAATTTTACCACTCTGCAACCTGTATGACCTGTGAGGCTCT 2280
 QY 2431 ProLeuProGluCysValProValGluCysProGlnProGluGlu1LeProAsnGly1Le 2450

DB 2281 CCACGCGAGATGTTCCATGAGATGTCCTCCCAACCTGAGGAAATCCCAATGATC 2340
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 QY 2471 GlueValG1yAsnThrThrThrleuCyG1yGluAsnG1yH1sTrpleuG1yG1yIys 2490
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 QY 2491 ProThrCyG1yAlaI1leGluCyG1yLeuIysProIysGluI1leuAsnG1yIysPheSer 2510
 DB 2461 CCACATGTAAAGCCATGAGTCCGAAACCCAGAGAAATTTGAATGCAATTCCT 2520
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 ID ABS51807 standard; cDNA; 3262 BP.
 AC ABS51807;
 XX 21-OCT-2002 (first entry)
 DT
 XX Human mdtc cDNA Incyte ID No: LI:202943.4:2001JUN12.
 DE
 XX Human; molecule for disease detection and treatment; MDT; cancer;
 KW cell proliferative disorder; arteriosclerosis; cirrhosis; asthma;
 KW autoimmune disorder; inflammatory disorder; Crohn's disease;
 KW multiple sclerosis; cytostatic; antiarteriosclerotic; antiinflammatory;
 KW hepatotropic; immunosuppressive; antistimatic; gene therapy; gene; ss.
 OS Homo sapiens.
 XX
 XX WO200255738-A2.
 XX
 XX 18-JUL-2002.
 PD
 XX
 XX 09-JAN-2002; 2002MO-US001008.
 PF
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 XX 12-JAN-2001; 2001US-0261622P.
 PR 16-JAN-2001; 2001US-0261865P.
 PR 17-JAN-2001; 2001US-0262208P.
 PR 17-JAN-2001; 2001US-0262209P.
 PR 17-JAN-2001; 2001US-0262209P.
 PR 19-JAN-2001; 2001US-0263063P.
 PR 19-JAN-2001; 2001US-0263063P.
 PR 19-JAN-2001; 2001US-0263065P.
 PR 19-JAN-2001; 2001US-0263329P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JT, Jones AL,
 PI Dam TC, Liu TF, Harris B, Flores V, Dafo A, Marwaha R, Chen AJ;
 PI Chang SC, Gerstein BH, Peralta CH, David ME, Lewis SA;
 XX WPI: 2002-590679/63.
 DR P-PSDB; ABS70334.
 XX
 XX New disease detection and treatment molecule (MDT) polynucleotides and
 PT polypeptides, useful in diagnosing, studying, preventing or treating
 PT diseases associated with MDT expression, e.g. autoimmune or inflammatory
 PT disorders.

XX
 PS Claim 1; Page 102-103; 129pp; English.
 XS
 CC The present invention relates to the isolation of novel human molecules
 CC for disease detection and treatment (MDT), and the polynucleotide
 CC sequences (mdt) encoding them. The MDT polypeptides may be used to
 CC screen for molecules that bind to, or are bound by the encoded
 CC polypeptides, and to develop a transcript image of a tissue or cell type.
 CC Probes comprising at least 20 nucleotides of the mdt polynucleotide may
 CC be used to assess the toxicity of a test compound. The MDT polypeptides
 CC and mdt polynucleotides are useful in the diagnosis, study, prevention
 CC and treatment of diseases associated with the expression of molecules for
 CC disease detection and treatment. Such disorders include cell
 CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, or cancer),
 CC and autoimmune/inflammatory disorders (e.g. asthma, Crohn's disease, or
 CC multiple sclerosis). The mdt polynucleotides may also be used as
 CC molecule markers, in microarrays, and in somatic or germline gene
 CC therapy. ABS51779-ABS51814 encode the MDT proteins of the invention
 XX
 SQ Sequence 3262 BP; 863 A; 760 C; 791 G; 848 T; 0 U; 0 Other;
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 Pred. No.: 2, 03e-238 Length: 3262
 Score: 4930.00 Matches: 947
 Percent Similarity: 95.33% Conservative: 12
 Best Local Similarity: 94.14% Mismatches: 20
 Query Match: 24,68% Indels: 28
 DB: Gaps: 4
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 DB 289 GAGTCACTGCTACCTCCTCCGACAGAGAACTCAGTAAAGAAACGTTGAGATGCTCCT 348
 QY 1610 AspPheLeuSerG1yI1leValG1yIysValI1yAsnSerIysSerI1lePheCysSer 1629
 DB 349 GATTCTTGTCAAGAAATGTGGGAAAGTGAATGATTCATTAGAGCAATTTTGTCT 408
 QY 1630 AspCyG1yProI1leG1yG1ySerValProH1sLeuAryThrI1leSerG1yAsnLeuIys 1649
 DB 409 GGTGCCCAACGCTTGAAGAGGTCAGTGCCTCATCTGAGAACTCATGTGAAGTTTAAAG 468
 QY 1650 ProG1ySerIysValAsnLeuPheCyG1yAsnProG1yPheG1nleuAlaG1yAsnProVal 1669
 DB 469 CCAAGTCCAAAGTCAATCTGTTCTGTGATCCAGGCTTCCAGCTGTGGAAACCTGTG 528
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 QY 1730 CyThrAsnAryI1Ser--TrpAsnG1yValSerProSerCyG1yAsnAryI1lePheI1y 1749
 DB 709 TGTACGATTAATGAGAGCTAGAGAACCGCTTTCACATCTCCGCGATGTGATAGTG 768
 QY 1749 salavalG1ySerAspCyG1ySerI1leI1leAsnCyG1yLeu--AsnValAryG1ySerI1y 1769
 DB 769 TGCAGTTGATCAGATTGATGATGATGATCTTCTCCCTGAAACGTAGATGATCTTACA 828
 QY 1769 IeCysSerCyG1yAlaProProI1yTrThrG1yAsnG1yIysAsnCyG1yAryI1lePheI1y 1789
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 QY 1789 Ys-IysAlaProG1y--AsnProG1yAsnG1yH1sSerSerI1yG1yI1leI1yTrThr--Va 1807

889 GCTAAGGCTCCAGGCAAGAAATCCGAAATGCGCACTCCAGGTGAGATTATACAGCT 948
1807 TGIYAla---AlaValThrPheSerCysGlnGluGlyTyr-GlnLeuMetGlyValThr 1826
949 AGGTGCCCAAGTACACATTATACAGTCTCAGAGAAAGATACCCAGTTGATGGAGATTAACA 1008
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1009 AAATTCATGTTGGTAGTACTCGGAGATGGAATCATCATTAATACCAATATGTAAGGCTGT 1068
1845 IserCysGlyIysPro-AlaIleProGluLeuSerGlyValGlu-GluLeuAla---Phe 1863
1069 TTCATGGGTAAACCGGACATATTCAGAAAATGGTGCATTGACGGAGTTAGCACTTTT 1128
1864 ThrPhe---GlySerIysValThrTyrArgCysAsnIysGlyTyrThrLeuAlaGlyAsp 1882
1129 ACCTATTGGGCGACAAAGTAGCATATAGGTATTAAGGATTAATCTCTGGCCGGTGAT 1188
1883 IysGluSerSerCysLeuAlaAsnSerSerTyrSerHisSerProValCysGluPro 1902
1189 AAAGAATCATCTGCTTGTGCTAAACAGTCTTGAGTCAATCCCTCTGTGTGAACA 1248
1903 ValIysCysSerSerProGluAsnIleAsnAsnGlyIys-TyrIleLeuSerGlyLeuTh 1922
1249 GTGAAGTCTCTAGTCCGACAAATATATCTATATGACAACTATATATAGGTGGGCTTAC 1308
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1309 CTACCTTTCTACTGSCATCATATATTCATGCGCATACAGGATTCAGGTTACAGGCCCCCTTCC 1368
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1369 ATATATGAATGCAACGGCTTCTGGCATCTGGGACAGAGCGGCACTCTGCTCTCACTCGT 1428
1961 IProCysGlyGluProProAlaIleIysAspAlaValIleThrGlyAsnAsnPheThrPh 1981
1429 CTCTGTGGAGAACACCTGTCATCAATAGATGCTGTCAITTAGGGAAATATCTTCACTTT 1488
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2001 eGluCysLeuAlaAspGlyIysTyrSerArgSerAspGlnGlyIysLeuAlaValSerCy 2021
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2029 AACTACAGTTTGGAGCCATGATGGCTTACAGCTGCAACAAAGGGTTCTACATCAAAAGCG 2088
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2201 ProValSerCysGlyIysIysProProIysValGluAsnGlyPheLeuGluHisIleThrGly 2220
2149 CCGATCTTGTGTGAAACCACTTACGTTGAGATGCTTTCTGGACATATCAATCTGGC 2208
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2209 AGAATCTTGAAGATGAAGTGAAGGTATCAAGTAAACCCGGGCTTATAGTCAGTGGAG 2268
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Db 3109 ACCGTTACTTACTTGGCAACGAGAGCTTTCGGCTCGAAGGTCCAGTGCCCTTGACTG 3168
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Search completed: May 9, 2004, 16:14:42
Job time : 3756.04 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 9, 2004, 12:50:18 ; Search time 14189.5 Seconds
(without alignments)
5626.549 Million cell updates/sec

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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
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Searched: 3470272 seqs, 2167151695 residues
Total number of hits satisfying chosen parameters: 6340544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
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41: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	10208	99.9	10878	6	AR435509 Sequence
2	10208	99.9	10878	6	AX375161 Sequence
3	9862	96.5	11152	6	AX686198 Sequence
4	9812	96.0	11158	6	AX686196 Sequence
5	8673.5	84.9	11289	10	AF206329 Sequence
6	8652.5	84.7	11230	6	AR435510 Sequence
7	8652.5	84.7	11230	6	AX375163 Sequence
8	7537	73.8	5124	6	AX880905 Sequence
9	7537	73.8	5124	6	BD158659 Sequence
10	7537	73.8	5124	9	AK027870 Sequence
11	4776	46.7	3253	9	AK122605 Sequence
12	3073	30.1	1969	6	AX880735 Sequence
13	3073	30.1	1969	6	BD158559 Sequence
14	3073	30.1	1969	6	AK023591 Sequence
15	2374	23.2	1760	6	BD229966 Sequence
16	1447	14.2	765	6	AX870332 Sequence
17	1447	14.2	765	6	BD150394 Sequence
18	1341	13.1	706	6	AX677660 Sequence
19	1328	13.0	18583	2	AC018297 Sequence
20	1328	13.0	148780	3	AC008326 Sequence
21	1328	13.0	174287	3	AC007977 Sequence
22	1328	13.0	270766	3	AE003615 Sequence
23	1304	12.8	801	6	AX869682 Sequence
24	1304	12.8	801	6	BD149744 Sequence
25	1237	12.1	3262	6	AX540417 Sequence
26	1004	9.8	167023	2	BX548016 Sequence
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38	913	8.9	96779	9	AL592463 Sequence
39	903.5	8.8	9166	5	HELKOTCH Sequence
40	901	8.8	8503	3	LCU58977 Sequence
41	893.5	8.7	7410	6	AX528263 Sequence
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50	869.5	8.5	8221	10	RROTCH Sequence
					AX57405 R.rattus mr

51	869	8.5	763	6	AX921793	AX921793 Sequence
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53	867	8.5	3362	3	SUSEPFI	L08692 Strongyloce
54	865.5	8.5	7646	3	AF000634	AF000634 Lytechinu
55	853	8.3	7332	6	AX394722	AX394722 Sequence
56	853	8.3	7332	9	HUMTMN1	M73980 Homo TAN-1
57	853	8.3	7693	9	AF308602	AF308602 Homo sapi
58	847	8.3	10452	3	DRONOTO5	M61652 Drosophila
59	847	8.3	17137	3	DRONOTO3	K03508 D.melanogas
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61	847	8.3	40933	3	DMC140611	AL003595 Drosophil
62	847	8.3	110000	3	AB003426.2	Continuatiion (3 of
63	847	8.3	179069	2	AC104144	AC104144 Drosophil
64	847	8.3	182387	3	AC116543	AC116543 Drosophil
65	845.5	8.3	7319	10	AF164486	AF164486 Rattus no
66	841.5	8.2	7943	10	MANOTC	X74760 M.musculus
67	838	8.2	763	6	AR220869	AR220869 Sequence
68	837.5	8.2	2460	6	AX531023	AX531023 Sequence
69	837.5	8.2	5516	3	AF239608	AF239608 Drosophil
70	837	8.2	8298	3	AB001327	AB001327 Halocryth
71	831.5	8.1	7615	6	AX695384	AX695384 Sequence
72	829	8.1	8091	6	A69561	A69561 Sequence 1
73	829	8.1	8091	6	AR300200	AR300200 Sequence
74	829	8.1	8091	6	BD006120	BD006120 Gene Invo
75	829	8.1	8091	9	HSU97669	U97665 Homo sapien
76	829	8.1	8257	6	AR220824	AR220824 Sequence
77	817.5	8.0	2229	3	AP397902	AP397902 Podocorym
78	816.5	8.0	3609	10	MMOTB	X68279 M.musculus
79	782	7.7	2959	5	AB027453	AB027453 Xenopus l
80	764.5	7.5	6677	6	AR199052	AR199052 Sequence
81	764.5	7.5	6677	6	AR207806	AR207806 Sequence
82	762.5	7.5	6677	10	MTU43691	U33691 Mus musculi
83	762.5	7.5	34425	3	U61946	U61946 Caenorhabdi
84	759	7.4	16122	9	HSU95299	U95299 Human Notch
85	758.5	7.4	1483	3	SUSGR	M17421 Strongyloce
86	758.5	7.4	6532	10	MUSINT33MAM	M80456 Mus musculu
87	751.5	7.4	5575	10	RATAPR	L38483 Rattus norv
88	749	7.3	4208	6	AR169937	AR169937 Sequence
89	749	7.3	4208	6	AR411902	AR411902 Sequence
90	745	7.3	3974	6	AX565642	AX565642 Sequence
91	745	7.3	3974	6	AX597042	AX597042 Sequence
92	745	7.3	3974	6	AX701333	AX701333 Sequence
93	745	7.3	3974	10	AF171092	AF171092 Mus muscu
94	745	7.3	4855	6	AX375031	AX375031 Sequence
95	745	7.3	4855	9	HSU61276	U61276 Human trans
96	745	7.3	5377	6	BC058675	BC058675 Mus muscu
97	745	7.3	6464	6	AR033974	AR033974 Sequence
98	745	7.3	6464	6	AR095920	AR095920 Sequence
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ALIGNMENTS

Alignment Scores:			
Pred. No.:	0	Length:	10878
Score:	10208.00	Matches:	1838
Percent Similarity:	99.95%	Conservative:	3
Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	99.89%	Indels:	0
DB:	6	Gaps:	0
US-09-977-053-6 (1-1842) x AR435509 (1-10878)			
QY	1	MetITPProArgLeuAlaPheCysSyrTrpGlyLeuAlaLeuValSerGlyTrpAlaThr	20
DB	11	ATNGAGCTCGCGCTGAGCCCTTTGTGTGTCTGGGGTCTGGCCCTCGTTCGGGGCTGGGAGACC	70
QY	21	PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGlnIuhAlaPro	40
DB	71	TTTCAGCAGAGTCCCGCTCGCGCAATTCACCTTCGCTCTTCCCCAGACCGGCCCC	130
QY	41	GlyAlaProGlySerLeuProAlaProProAlaProGlyAspGlyIuhAlaGlySerArg	60
DB	131	GGGGCCCCGGAGATATCCCGCGCCGCCCTCTCTGGGAGAGACCGCGGGAGACAA	190
QY	61	ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu	80
DB	191	GTGAGAGCGGCTGGGCGACGGCTTCGGGAGCGCGTGGCGCTCTGGCGGAGCTCAACGAG	250
QY	81	ArgLeuGluLeuValPheLeuValIAspAspSerSerValGlyGluValAsnPheArg	100
DB	251	CGCTCGAGAGCTGTCTTCCTCGGTGATGATTCGTCCAGCGTGGCGCAAGTCAACTTCGCG	310
QY	101	SerGluLeuMetPheValArgGlyLeuLeuSerAspPheProValValProThrAlaThr	120
DB	311	AGCGAGCTCATGTTGCTCCGACAGCTGCTGTCGACTTCCCGTGTGGCCACGGCCACG	370
QY	121	ArgValAlaIleValThrPheSerSerIysAsnIYValValProArgValAspTYrIle	140
DB	371	CGCGGGCGCATCTGACCTTCCTCGTCCAGAACCTAGTGTGCGCGCGCTGCATTCATC	430
QY	141	SerThrArgArgAlaArgGlnIleIAsyCyAlaLeuLeuGlnGluIleProAlaIle	160
DB	431	TCCACCCCGCGCGCGCGCAGACAAAGTGGCGCTCTCCCAAGAGATCCCTCGCATC	490
QY	161	SerTYrArgGlyGlyGlyThrTYrThrIysGlyAlaPheGlnGlnAlaGlnIleLeu	180
DB	491	TCCTACCGAGGTGGGGCAGCTTACCCAAAGGCGCTTCAGAGACCGCGCAAAATCTT	550
QY	181	LeuHISAlaArgGluAsnSerThrIysValValPheLeuIleThrAspGlyTYrSerAsn	200
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LOCUS	AR435509	10878 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 1 from patent US 6656707.				
ACCESSION	AR435509				
VERSION	AR435509.1	GI:40198412			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 10878)				
TITLE	Welcher,A.A. and Elliott,G.S.				
JOURNAL	Cb/cb Complement receptor-like molecules and uses thereof				
FEATURES	Patent: US 6656707-A 1 02-DEC-2003;				
SOURCE	Location/Qualifiers				
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Db	971	ACAGCTGGCCCATCGGGGACATACAAACGTAAGGCTCACACAGAGAAATCACAGATGTC	1030
Qy	341	IleProCyProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCys	360
Db	1031	ATTCCATGTCCTGATGATAAATCACACCTCTCCACTGGAAGCAATCCCTCGAAGACTGT	1090
Qy	361	ValCyAspGluGlyTyrrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla	380
Db	1091	GTCTCGAGAGAGGATACAGGGCATCTGGCCAGACCTGTGAACCTTGCCACTGCCCTGCC	1150
Qy	381	LeuLysProProGluAsnGlyTyrrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla	400
Db	1151	CTGAAACCTCCCGAAAATGGTTACTTTATCCAAAACCTTGCAACACCACTTCATGCA	1210
Qy	401	AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys	420
Db	1211	GCCTGGGGGTCCGATGTCACCTCGATTTGATCTGTGGGAAGCAGCATCATCTTATGT	1270
Qy	421	LeuProAsnGlyLeuLeuTrpSerGlySerGlySerTyrrCysArgValArgThrCysProHis	440
Db	1271	CTAACCAATGGTTTGTCGGGTCAGAGAGCTACTGCAAGATTAAGAAACATGCTCCAT	1330
Qy	441	LeuArgGlnProLysHisIleGlyHisIleSerCysSerThrArgGluMetLeuTyrrLysThr	460
Db	1331	CTCCGCGACCCGAAACATGCGCACATCAGCTGTTCTACAAAGGAAATGTTATATACACA	1390
Qy	461	ThrCysLeuValAlaCysAspGluGlyTyrrArgLeuGlyIleSerAspLysLeuThrCys	480
Db	1391	ACATGTTTGTTGCTCGTGTGATGAAGGGTACAGACTGAAGAGCAGTGAATGACTTACTGT	1450
Qy	481	GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGlnUaGlyHisCysSerThr	500
Db	1451	CAAGGAAACGCGAGTGGAGGACCAAAACCCGGGTGTGGAGCCCACTGTTCAAC	1510
Qy	501	PheGlnMetProLysAspValIleIleSerProHisAsnGlyLysGlnProAlaLys	520
Db	1511	TTTCAATGCCCAAAATATCATCATATCCCCCAACACTGTGGCAAGCCAGCCAAA	1570
Qy	521	PheGlyThrIleCysTyrrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGln	540
Db	1571	TTTGGAGCATCTGATATGTAAGTGGCCGCAAGGGTTCAATTATCTGGAAGTCAAAAGAA	1630
Qy	541	MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCysLys	560
Db	1631	ATGCTAGAGATGACCACTTCGAAAAATGAAATGTCGGAAGTTCAGGCACTGTGTAAAC	1690
Qy	561	AspValGlnAlaProGlnIleAsnGlyProLysAspIleGlnAlaLysThrLeuGlnGln	580
Db	1691	GAGGTGAAGGCTCTCAATCAACTGCTTCRAAGACATAGAGGTAAAGACTGTGAACAG	1750
Qy	581	GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyLysLys	600
Db	1751	CAAGATTCTGCGCAATGTTACTGCGAGATTCCAAAGCTAAAGCAACTCTGGTGAAGAG	1810
Qy	601	ValSerValHisValHisProAlaPheThrProProTyrrLeuPheProIleGlyAspVal	620
Db	1811	GGTCACTCCACGCTTCACGCTTTCACCCCACTTACCTTTCCAGATGGAGATGTT	1870
Qy	621	AlaIleValTyrrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle	640
Db	1871	GCATCTGATACCGGCAACTGACTATCGGCAACCAAGCCAGCTGCAATTTCCATATC	1930
Qy	641	LysValIleAspAlaGluProProValIleAspTrpCysArgSerProProProValGln	660
Db	1931	AAGGTATATGATGACAAACCACTGTATCATAGACTGGTGCAGATCTCCACTCCCGTCCAG	1990
Qy	661	ValSerGluLysValHisAlaIleSerTrpAspGluProGlnPheSerAspAsnSerGly	680
Db	1991	GTCTCGAGAAAGGTACATGCGCAAGCTGGAGTGAAGCTCATGTTCTCAAGCAACTCAGGG	2050

Qy	681	AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyLysThr	700
Db	2051	GCTGAATTGCTCATATACAGAAAGTCAATACACAAAGAGACTTTCCTCAAGGGGAGACT	2110
Qy	701	IleValGlnTyrrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle	720
Db	2111	ATAGTACAGATACAGCACTGACAGCCCTCAGGCAATACAGAGCATGTGATATCATATT	2170
Qy	721	ValIleLysGlySerProCysGlnIleProPheThrProValAsnGlyAspPheIleCys	740
Db	2171	GTCTATAAGGCTCTCCCTGTGAAATTCATTCACCTGTATATGGGATTTTATATGC	2230
Qy	741	ThrProAspAsnThrGlyValAsnGlyThrLeuThrCysLeuGlnGlyTyrrAspPheThr	760
Db	2231	ACTCCAGATATATCTGAGTCACTGATATTACTTGCTTGAGGGCTATGATTTCA	2290
Qy	761	GlnGlySerThrAspLysTyrrTyrrCysAlaTyrrGluAspGlyValITrpLysProThrTyrr	780
Db	2291	GAAGGGCTACTGACAAAGTATATTTGTATGATGAAGTGGCGTGGAAACCAACATAT	2350
Qy	781	ThrThrGlnTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe	800
Db	2351	ACCACTGAATGGCAGACCTGTGCCAAAACGTTTCTATACACAGGGTTCAAGTCTTT	2410
Qy	801	GluMetPheTyrrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGln	820
Db	2411	GAGATGTTCTACAAAGCAGCTCGTTGTATGACACAGATCGATGAAGAGATTTCGAA	2470
Qy	821	AlaPheGlnThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle	840
Db	2471	GCAATTTAAGACAGCCCTGGAAAAATGTCTCCATCATTTGTGTATGATGACAGAGACAT	2530
Qy	841	AspCysArgLeuGlnGluAsnLeuThrLysLysTyrrCysLeuGlnTyrrAsnTyrrAspTyrr	860
Db	2531	GACTGCACTGAGAGGAACTGTACCAAAAATATGGTCCAGATATATATATGACATAT	2590
Qy	861	GluAsnGlyPheAlaIleGlyProGlyGlyTyrrGlyAlaAlaAsnArgLeuAspTyrrSer	880
Db	2591	GAATAATGGCTTTCGAATTTGACCAAGTGGCTGGGGTCAAGCTATATAGGCTGATACTCT	2650
Qy	881	TyrrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAspAlaLysSer	900
Db	2651	TACATATCACTTCCGACACTGTGCAAGAAACACCAACAGCATCGGAATGCCAAGTCC	2710
Qy	901	SerArgIleLysArgSerAlaProLeuSerAspTyrrLysIleLysLeuIlePheAsnIle	920
Db	2711	TCAAGATTAAAGAGATGGCCCATTTATCTGACTATATTAATTAATTTTATACATC	2770
Qy	921	ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGlnTrpGluAsnGlnGln	940
Db	2771	ACAGCTAGTGTGCATTACCCGATGAAGAAATGATACCTTGATGAAGGAAATACAGCAA	2830
Qy	941	ArgLeuLeuGlnThrLeuGlnTrpIleThrAsnLysLeuLysArgThrLeuAsnLysAsp	960
Db	2831	CGACTCTCTCAGCAATTTGAAACATATCACAAAATTAACGTGAAMAGACTCTCAACAAGAC	2890
Qy	961	ProMetTyrrSerPheGlnLeuAlaSerGlnIleLeuIleAlaAspSerAsnSerLeuGln	980
Db	2891	CCCAATATTCCTTTCAGCTTGCATCGAATTACTTATAGCCGACAGCAATTCATTAGAA	2950
Qy	981	ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyLysMetCysVal	1000
Db	2951	ACAAAAAAGGCTTCCCTCTGCGAGACAGAGCTCATGTGAGAGAGGCGTATGTGTCTC	3010
Qy	1001	AsnCysProLeuGlyTyrrTyrrAsnLeuGlnHisPheThrCysGlyLysCysArgIle	1020
Db	3011	AATTTGCCCTTTGGAGACTTATATATCTGAAACATTTCACTGTGAAGGTGCGGATC	3070
Qy	1021	GlySerTyrrGlnAspGlnGlnGlyLysLeuGlnCysLysLeuCysProSerGlyMetTyrr	1040
Db	3071	GAATCTATCAATGAATGAAGAGGCACTTGAGTGCAGAGCTTTCCTCTCGGATGTAC	3130

1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysValAlaGlnCysIysGlnGlyThr 1060
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Db	5351	AAAAACTGTGAGAACTATTAATATGTAAGCTCCAGGAATCCGGAAATATGGCACTCC	5410
Qy	1801	SerGIuGIuIeIeYTTThVaIGIYAlaIaValThrPheSerCYGInGIuGIYTrGIIn	1820
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Db	5471	TTGATGGAGATPACCAATATCACTGTTTGAGTCTGAGATGATCATCTATATCA	5530
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DEFINITION	Sequence 1 from Patent WO0210388.		
ACCESSION	AX375161		
VERSION	AX375161.1	GI:19169916	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Welcher,A.A. and Elliot,G.S.		
TITLE	C3b/c4b complement receptor-like molecules and uses thereof		
JOURNAL	Patent: WO 0210388-A 1 07-FEB-2002;		
FEATURES			
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Alignment Scores:			
Pred. No.:	0	Length:	10878
Score:	10208.00	Matches:	1838
Percent Similarity:	99.95%	Conservative:	3
Best local Similarity:	99.78%	Mismatches:	1
Query Match:	99.89%	Indels:	0
DB:	6	Gaps:	0
US-09-977-053-6 (1-1842) x AX375161 (1-10878)			
Qy	1	MeCTTPPProArygleuAlaPheCYeCYSTrGIyleuAlaIeValSerGIYTrPAlaThr	20
Db	11	ATGAGGACCTGCGCTGGCCCTTTTGTTGCTGGGGCTCTGGCGCTGTTTCGAGCTGGGACCC	70
Qy	21	PheGIuGIuMeSerProSerAryAsnPheSerPheArygleuPheProGIuThrAlaPro	40
Db	71	TTTACGACGAGATGTCCCGCTGGCGCAATTTCAGCTTCGCGCTTCCCGGACACCGCGCC	130
Qy	41	GIYAlaPProGIYSerIleProAlaProProAlaPProGIYAspGIuAlaIAGIYSerArg	60
Db	131	GGGGCCCCCGGAGATATCCCGCGCGCGCTCTCTGCGACGAAGCGCGCGGAGCGA	190
Qy	61	ValGIuArygleuGIuAlaPheAryAryAryValArygleuAryGIuIeSerGIu	80
Db	191	GTGGAGCGGCTGGGCGACGCTTCCGCGGACGCGTGGCGCTGGCGGAGCTCAACGAG	250
Qy	81	ArygleuGIuIeValPheIeValAspAspSerSerValGIYGIuValAsnPheArg	100
Db	251	CGCGTGAAGCTTGTCTTCCTGGTGGATATTCGTCAACGATGGGAGATCACTTCGCG	310
Qy	101	SerGIuIeMeCTPheValAryIYleuIeUeSerAspPheProValProThrAlaThr	120

Db	AGGAGAGCTGANTGTTGGTCCGGAGACGTGTCGGACACTTCCCGGCGGAGCCACGAGCGACG	370
QY	ArgValAlaIleValIThrPheSerSerLysAsnTyrValValProArgValAspTyrIle	140
Db	CGCGTGGCGAATCGTAGACCTTCTCTCTCCAGAACTACAGTGGTGGCCGCGCTCGATTACATC	430
QY	SerThrArgValAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGlnIleProAlaIle	160
Db	TTCAACCCCGCCGCGCGCGCAGACACAGTGGCGCGTGGCTCTCCAGAGATCCCTGGCATC	490
QY	SerTyrArgGlyGlyGlyThrTyrThrLysGlyValAlaPheGlnGlnAlaAlaGlnIleLeu	180
Db	TTCTACCGAGAGTGGCGGACCTTACACCAAGGCGCCTTCCAGCAAGCGCGCAATTCCT	550
QY	LeuHisAlaArgGlyLeuAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn	200
Db	CTTCATGCTACAGAAACTCAACAAAGTGTATTTCTCATCACTGATGTGATATTCAAAT	610
QY	GlyGlyAspProAlaArgProIleAlaAlaIleSerLeuArgAspSerGlyValGlnIlePheThr	220
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QY	PheGlyIleTyrGlnGlyAsnIleArgGlyLeuLeuAspMetAlaSerThrProLysGln	240
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QY	GlnHisCysTyrLeuLeuHisSerPheGlnGlyLeuPheGlnAlaArgArgAlaLeu	260
Db	GAGACACTGTACCTGCTTACACAGATTGGTGAAGAAATTGAGCGCTTACGCTCGCGGGCATTG	790
QY	HisGlyLeuAspLeuProSerGlySerPheIleGlnHisAspMetValHisCysSerTyrLeu	280
Db	CATGAAAGTCTTACCTTCTGGAGATTATTAATCAATATATATGCTCACTGCTCTTAACTT	850
QY	CysAspGlnGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr	300
Db	TGTATGTAAAGGCAGACACTGCTGTACCGAATGGGAAGCTCCAAATGTGGACACACACA	910
QY	GlyHisPheGlnCysIleCysGlyLysGlyTyrTyrGlyLysGlyLeuGlnTyrGlyCys	320
Db	GGCCATATTTGAGTGCATCTGTGAAGAAAGGGGATTAACGGGAAGAGTCTGCAGTATGAAATGC	970
QY	ThrAlaCysProSerGlyThrTyrLysProGlnGlySerProGlyGlyIleSerSerCys	340
Db	ACAGCTGGCCCATGGGGACATGMAACCTGAAAGCTCACAGAGAGAAATCAGCAGATGTC	1030
QY	IleProCysProAspGlnAsnHisThrSerProProGlySerThrSerProGlnAspCys	360
Db	ATTCACATGCTCTGATGAATAATCAACCTCTCCACTGTGAAGACACATCCCTGAAGACTGT	1090
QY	ValCysArgGlnGlyTyrArgAlaSerGlyGlnThrCysGlnLeuValHisCysProAla	380
Db	GTCTGCGAAGAGGGATACAGGAGCATCTGGCGACAGCTGTGAATCTGTCCACTGCCCTGC	1150
QY	LeuLysProProGlnAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla	400
Db	CTGAAGCTCTCCGAAATATGTTACTTTATCCAAACACTTGCAACACACTTCAAGACA	1210
QY	AlaCysGlyValArgCysHisArgProGlyPheAspLeuValGlySerSerIleIleLeuCys	420
Db	GGCTGTGGGGTCCCATGTCACTCCGATTTGATCTTTGGGAGACAGACATCTTATGT	1270
QY	LeuProAsnGlyLeuTyrPserGlySerGlySerTyrCysArgValArgThrCysProHis	440
Db	CTAACCAATGTTGTGTGTGGTTCGAGAGAGCTACTGCAAGATGAACATGCTCCAT	1330
QY	LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGlnMetLeuTyrLysThr	460
Db	CTCCGCCACGCCGAACATGGCCACATCAAGCTGTCTCAAGAGGAAATGTATATTAACA	1390
QY	ThrCysLeuValAlaCysAspGlnGlyTyrArgLeuGlnGlySerAspLysLeuThrCys	480
Db	ACATGTTTGGTTCCTGTGATGAAGGGTACAGACTGAAGAGCATGTATACCTTACTTGT	1450

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 DB CAAAGAAACAGCCAGTGGATGGCCAGAACCCGGTGTGTGAGGCGCACTTCCACC 1510
 501 PheGInMetProLYaSPValIleIleSerProHisAenCySGlyLYaSPValIle 520
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 521 PheGlyThrIleCYeThrValSerCySAyGInGlyPheIleLeuSerGlyValLYaSP 540
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 541 MetLeuArgCYeThrThrSerGlyLYaSPValIleValGlnIleValIleVal 560
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 DB CAAAGATCTGCAAGATGTAACCTGACGATTCCAACAGCTTAAGCAACTGTGTAAG 1810
 601 ValSerValHisValHisProAlaPheThrProProLYeThrLeuPheProIleGly 620
 DB GTGTCAAGTCAAGCTTCACTCAAGCTTCACTTCACTTCACTTCACTTCACTTCA 1870
 621 AlaIleValIleThrAlaThrAspLeuSerGlyAenGlnIleAseCyValIlePheHis 640
 DB GTATCTGATATACAGCGCACTGACTATCCGCGCAACAGCGCCAGCTGCACTTTC 1930
 641 LysValIleLeuSPAlaGluProProValIleAspTrpCyAArgSerProProProVal 660
 DB AAGGTTATGATGACAGAACCACTGTCTATAGCTGTGGTGGAGATCTCACTCCG 1990
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 741 ThrProAspAenThrGlyValAenCySPThrLeuThrCYeLeuGlnGlyLYaSPPheThr 760
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 2231 GlnGlySerThrAspLYeThrCYeValIleGlnAspGlyValIleTrpLYeProThrTrp 780
 DB GAAAGGCTCTACAGCAAGATATATGCTATGAAAGATGAGCTGTGAAACCAACTAT 2350
 2291 GlnaSPSerThrAspLYeThrCYeValIleGlnAspGlyValIleTrpLYeProThrTrp 800
 DB ACCACTGATATGCGACCTGTGCAAAAACGTTTGTCTAACACAGGGTTCAAGTCTT 2410
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841 AspCYeArgLeuGlnGluAenLeuThrLYeLYeTrpCYeLeuGlnTrpAsnTrpAspTrp 860
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 DB TACGATGACTCTTCTGAGCACTGTGCAAGAACGCCCAACAGCATCGCAATGCCAATGCC 2710
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 DB TCAAGATTAAGAAAGTGCCTCATATATGATTAATTAATTAATTAATTAATTAATTA 2770
 2711 ThrAlaSerValIleProLeuProAspGluArgAspAspThrLeuGluTrpGluAenGln 940
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 2771 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLYeLeuLYaSPThrLeuAsnLYaSP 960
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 3191 PheGlySerArgSerCYeLeuSerCYeProGluAenThrSerThrValLYeArgGlyAla 1100
 DB TTTGTTCCCGAGGCTGCTCTGTGTCCAGAAACCACTCACTGAAAGAGAGAGGCC 3310
 3251 ValAsnIleSerAlaCYeGlyValIleProCySProGluGlyLYaSPPheSerArgSerGlyLeu 1120
 DB GTAAACATTTCTCAATGAGAGTTCCTGTGCGAAGAGAAATTTCTGCTTGGGTTA 3370
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Db	3611	CTTGCCACAAATGAGAACTGGCAGCACTTG36CGGTATGTTGTCCTGTC	3670
Oy	1221	LeuGIyYrThrGIyLeuIySeCySglunThrAspIleAspGIuCySerProLeuProCyS	1240
Db	3671	CTTGATATACAGCTTTAAGTGTGAACAAGACATCGATGATGAGGCCACTGCTTC	3730
Oy	1241	LeuAenAenGIyValCyAluYasAplLeuValGIyIuPheIleCySgluCyProSergIy	1260
Db	3731	CTCAACAATGAGATTGTGAAGACCTAGTGTGGGAATCAATTGTGATGTCCTACAGT	3790
Oy	1261	TyTrhGIyGIyAaYxCySgluGIuAasnIleAenGIuCySerSerSerProCyLeuAasn	1280
Db	3791	TACACAGGTGACGGGTGTGAAGAAAATTAATGATGATGATCTCAGTCTTGTTAAAT	3850
Oy	1281	LySglIyIleCySValAspGIyValAaGIyYrArgCySthrCySValIySglYpHeVal	1300
Db	3851	AAAGGAATCTGTGTGATGATGTGTGTGGCTGGCTATCTCTCAATGTGTGAAGATTGTA	3910
Oy	1301	GIyLeuHISCySgluThrGIuValAsnGIuCySgluSerAsnProCyLeuAasnAla	1320
Db	3911	GGCCGTGATTGTGAACAAGATCAATGAATGCCAGTCAAACCCATGCTTAATAATGCA	3970
Oy	1321	ValCySgluAspGIuValGIyGIyPheLeuCySlySProProGIyPheLeuGIyThr	1340
Db	3971	GCTGTGAAGACCAAGTGGGGGAATCTTGCAAAATCCCACTGGATTTTGGATCC	4030
Oy	1341	ArgCySglYlySAsnValAspGIuCySleuSergInProCySlySAsnGIyAlaThrCyS	1360
Db	4031	CGATGTGAAGAAAGACTGATGATGATGTCCTCAGTCAGCCATCGAATAAATGAGACTCTGT	4090
Oy	1361	LySAspGIyAlaAsnSerPheArgCySleuCyValAaGIyPheThrGIySeriICyS	1380
Db	4091	AAAGACGGTGCAAATAGCTTCAGAGCTGTGTGCACGTGGCTTCAAGATCACTGAT	4150
Oy	1381	GIuLeuAasnIleAenGIuCySgluSerAsnProCySAsnAenAlaThrCySValAsp	1400
Db	4151	GAATTGAACATCAAGAAATGATAGCTTAATCCATGATGAATAAATCAGGCCACTGTGTGAT	4210
Oy	1401	GIuLeuAasnSerYrSerCySlySCySgluInProGIyPheSergIyIaArgCySgluThr	1420
Db	4211	GAATTAAATTCAATCAGTTGTTAAATGTCAGCAGGATTTTCAGGCAAAAGTGTGAACA	4270
Oy	1421	GIuGIuSerThrGIyPheAenLeuAspPheGIuValSergIyIleYrGIyYrValMet	1440
Db	4271	GAACAGTCTACAGGCTTTAACCCTGATTTTGAAGATTCTCGCATCTAATGATATGTCATG	4330
Oy	1441	LeuAspGIyMetLeuProSerIleuHISAlaLeuThrCySthrPheThrMetIySerSer	1460
Db	4331	CTAGATGGCAATGCTCCATCTCTCATATCTCTAATCTGTACCTCTGTGATAAATCTCTCT	4390
Oy	1461	AspAspMetAsnYrGIyThrProIleSergYrAlaValAspAsnGIySerAspAsnThr	1480
Db	4391	GACGACATGAACATAGAAACACCAATCTCTCATGCAATGATGAAGCGACGACCAATACC	4450
Oy	1481	LeuLeuLeuThrAspYrAsnGIyTrpValIleuYrValAsnGIyAaGIyIuYleThr	1500
Db	4451	TTGCTCTGACGATTTATACCGCTGGGTCTTTATGTGAATGGCAGGGAAGAATTAACA	4510
Oy	1501	AsnCySProSerValAsnAspGIyAaGTTrpHISHisIleAlaIleThrTrpThrSerAla	1520
Db	4511	AACTGTCTCCGTGGTAATGATGCGAGATGCAATCATATGTGAACATCTTGAACAAGTGC	4570
Oy	1521	AsnGIyIleTrpIySValYrIleAspGIyIySleuSerAspGIyGIyAlaGIyLeuSer	1540
Db	4571	AATGGCAATCTGGAAGATCTAATACATGGGAATTTATCTGACGGTGGTCTGGCTCTCT	4630
Oy	1541	ValGIyLeuProIleProGIyGIyGIyAlaLeuValLeuGIyGIuGIuAspIySlyS	1560
Db	4631	GTTGGATTGGCCCATACCTGTGTGTGTGTCGTTAGTTCTGGGGCAAGCAAGCAAAAAA	4690
Oy	1561	GIyGIuGIyPheSerProAlaGIuSerPheValGIySeriIleSergInLeuAasnLeuTrp	1580

D8	4691	CGAAGGAGATTACAGCCAGTGAAGTCTTTTGTGTGGGCTCCATTAAAGCAGCTCAACTCTGG	4750
QY	1581	AAPYTYVALLAUSERPROGINGINVALYSESERLEUALATHISERCYSPROGIVGLULEU	1600
D8	4751	GACTATGTCCTGCTCTCCACAGAGGTGAAGTCACTGGCTCACTTCCTCCAGAGGAATC	4810
QY	1601	SERLYGELLYANVALLEUALATTPROAASPHELEUSERGIVILEVALGLYLYSVALYLS	1620
D8	4811	AGTAAAGAAAACGGTAGACATGGCCGATTTCTTGACAGAAATGTGGGAAAGTAAAG	4870
QY	1621	ILEASPSELYSSERILEPHECYSESPASPCEPFRATGLUGLYGYSERVALPROHIS	1640
D8	4871	ATGCATTTCTTAAGACATATTTTGTTCATATGGCCACGCTTAAGAGGCTCAGTCCCTCAT	4930
QY	1641	LEUALRGTHALASERGIUALSPLEULYSPROGLYSERLYSVALLENLEUPHECYEASP	1660
D8	4931	CTGAGAACCTCATCTGAAGATTATTAAGCCAGAGTTCCAAAGTCAATCTGTTCTGATCA	4990
QY	1661	GLYPHEGLILEUVALGLYANMPROVALGINTYCYSELEUANGINGLYINTPTPHGLN	1680
D8	4991	GGCTTTCACGCTGGTGGGAAACCCCTGGCAGTACCTGTGTGATCAAGACAGTGAACAA	5050
QY	1681	PROLEUPROHISCYSGIUALRGILSESCYSGIYVALPROPROPPOLEUGLIUANGLYPHE	1700
D8	5051	CCACTTCTCACTGTGAACCATTAAGCTGTGGGGTGCACCTCCTTTGAGAAATGGCTTC	5110
QY	1701	HISERLIALAPHAPHERYALAGLYSERETHIVALTHIRTYGLINCYSAENANGLYTYR	1720
D8	5111	CATTCAACCCATGACTCTTATGCTGGCAGACAGTAACTTACAGCTCAACAATGGCTTAC	5170
QY	1721	TYRILEULEUGLYASPERATRGMEPHECYETHASPAANGLYSETRPANGLYVALSER	1740
D8	5171	TATCTATTTGGGTGACTCAAGAAAGTTCTGTACAGAAATATGAGATGAGATCGAGCTTCA	5230
QY	1741	PROSERCYSELEUAPVALAEPGLUCYVALAVALGYSERASPCEYSESGIUNHIALASER	1760
D8	5231	CCATCTGCGCTTGATGTCATGAGTGTGCACTTGCGACTTGAGTCAATTTGATGAGCAGCTTCT	5290
QY	1761	CYSELEUANVALAEPGLYSERTYRILECYSESCYVALALPROBPGLYTYRTHIRGLYASPGLY	1780
D8	5291	TGCTGGAACCTAAGTGGATCTCTCAATFMTGTCATATGTTCCACCGTCAACAGAGAGATGCG	5350
QY	1781	LYASANCYVALAGLUPOLLILELYSCYVALALPROGLYANPPOGLYUANGLYHISER	1800
D8	5351	AAAAACGTGCAGAACTAATAATGTAAAGCTCCACGAAATCCGAAAAATGGCACCTCC	5410
QY	1801	SERGLYGLILETYRTHIRVALGLYVALAVALATHRPHESERCYSGINGLUGLYTYRGLN	1820
D8	5411	TCAGTATAGATTTHACATGATGATGTCGCCAAGTCACTTTTCGTCTCAGAAAGATACAG	5470
QY	1821	LEUWETGLYVALTHIRYSLIETHRCYALEUGLUSERGLYGLUTRPAANHISLEULIPE	1840
D8	5471	TTGATGGGAGATTAACAAATACATGTTTGGAGCTGTGGAATGGAATCATCTTAATACCA	5530
QY	1841	TYRQYSE 1842	
D8	5531	TATTTGT 5536	
RESULT 3			
LOCUS	AX686198		
DEFINITION	Sequence 7 from Patent WO02053915.	1152 bp	DNA
ACCESSION	AX686198		linear
VERSION	AX686198.1		
KEYWORDS	GI:29372029		
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Shinketsu, R.A., Paturajan, M., Vernet, C.A., Casman, S.J.,		
AUTHORS	Malyanekar, U., Shenoy, S., Spytek, K.A., Gangolli, B., Miller, C.,		
	Boldog, P., Li, L., Taupier, R.J., Kerkula, R., Smithson, G.,		

Zerhusen, B.D., Liu, X., Colman, S.D., Tchernev, V., Si, J., Edinger, S.,
Stone, D., Sciore, P., Miller, I. and Rothenberg, M.
Human nucleic acids and polypeptides and methods of use thereof
Patent: WO 02059315-A 7 01-AUG-2002;

FEATRES
source
Location/Qualifiers
1. 11152
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	11152
Score:	9862.00	Matches:	1781
Percent Similarity:	97.72%	Conservative:	16
Best Local Similarity:	96.85%	Mismatches:	40
Query Match:	96.51%	Indels:	2
DB:	6	Gaps:	1

US-09-977-053-6 (1-1842) x AX686198 (1-11152)

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QY      24 MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro 43
DB      143 ATGTCCCGGTGCGGAAATTCAGCTTCGCTTCCCGGACCGCGCCCGGGGCCCC 202
QY      44 GlySerIleProAlaProProAlaProGlyAspGluAlaIleGlySerArgValGluArg 63
DB      203 GGGAGTATCCCGGCGCGCGCTCTGGCGACGAAAGCGCGGGGAGAGAGTGGAGCGG 262
QY      64 LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu 83
DB      263 CTGGGCGCGCGCTC-----CGCGCGCGCTGCGCGGAGCTCAGCGAGCGCTGGAG 316
QY      84 LeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArgSerGluLeu 103
DB      317 CTGTCTTCTCTGTGGATGATTCGTCCAGCGTGGCGGAGAGTCACTTCGCGACGAGCTC 376
QY      104 MetPheValArgLeuLeuLeuSerAspPheProValProThrAlaThrArgValAla 123
DB      377 ATGTTCCGCCCAAGCTCTGTCCAGCTTCCCGGTGTCGCCACGGCGCGCGTGGCC 436
QY      124 IleValThrPheSerSerIleAsnThrValProArgValAspThrIleSerThrArg 143
DB      437 ATCGTACCTTCTGTCCAGAACTACGTGTGCGCGCGCTGATTAATCTCCACCCGC 496
QY      144 ArgAlaArgGlnIleCysAlaLeuLeuLeuGlnIleProAlaIleSerThrArg 163
DB      497 CGCGCGCGCGCGCAAGTGGCGCGCTGCTCCCAAGAGATCCCTGCCATCTCCACGA 556
QY      164 GlyIleGlyIleThrThrIleGlyAlaPheGlnGlnAlaIleGlnIleLeuLeuAla 183
DB      557 GGTGCGCGCACTTACCAAGGCGCTTCCAGCAAGCGCGCAATTTCTTCTTCAGCT 616
QY      184 ArgGluAsnSerThrIleValValPheLeuIleThrAsnGlyThrSerAsnGlyGlyAsp 203
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QY      244 TyrLeuLeuIleSerPheGluGluPheGluAlaLeuAlaArgArgAlaLeuHISGluAsp 263
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Db	2237	GGTTCCCTCGTAATTCATTTCACTCCTGTAAATGGGATTTTATATGCACTCCAGAT	2296		Qy	1104		1123
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Shimkera, R.A., Patturajan, M., Vernet, C.A., Casman, S.J.,
 Malpankar, U., Shenoy, S., Szytek, K.A., Gangoli, B., Miller, C.,
 Boldog, F., Li, L., Taupier, R.J., Kekuda, R., Smithson, G.,
 Zernusen, B.D., Liu, X., Coleman, S.D., Tchernyev, V., St. J., Edinger, S.,
 Stone, D., Sciore, P., Miller, I., and Rothenberg, M.
 Human nucleic acids and polypeptides and methods of use thereof
 Patent: WO 02059315-A 5 01-AUG-2002;
 Curesgen Corporation (US)
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"

ORIGIN

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Pred. No.:	Length:	Matches:
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US-09-977-053-6 (1-1842) x AX686196 (1-11158)

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QY AlaSerValProLeuProAspGluAlaArgAsnAspThrLeuGluThrPheLysGlnAlaArg 941
DB 2837 GCTATGTGTCATTAACCCATGAAAGAAATGATATACCTTGAAAGGAAAATACGCAACA 2896
QY LeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspPro 961
DB 2897 CTCCTTCAGACATTTGAAACTATACAAATTAATTAAGAGACTTTCACAAAGACCCC 2956
QY MetTyrSerPheGluLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThr 981
DB 2957 ATGTAATCTCTTCAGCTTCATCAAGAAATACTATATAGCGAAGCAATTCATTAAGAAACA 3016
QY LysLysAlaSerProPheCysArgProGlySerValLeuArgGluLysMetCysValAsn 1001
DB 3017 AAAAAGGCTTCCCTCTTGCAGACAGGCTCAGTCTAGAGAGGCGTATGTGTCAAT 3076
QY CysProLeuGluTyrTyrTyrAsnLeuGluLysPheThrCysGluSerCysArgIleGly 1021
DB 3077 TGCCCTTTGGGAACCTATTAATCTGAAACATTTCACTGTGAAGCTGCGGATCGGA 3136
QY SerTyrGlnAspGluGluLysGlnLeuGluCysLysLeuCysProSerGluMetTyrThr 1041
DB 3137 TCCATACAAAGTAAGAAAGGCAACTGAGTGCMACTTGGCCCTCTGGGAAATGTACACG 3196
QY GlnTyrTyrIleHisSerArgAsnIleSerAspCysValAlaGlnCysValGlnGluTyr 1061
DB 3197 GAATATATCTCATTAAGAAACATCTGTATGTAAAGCTCAGTGAACAGGCACTTAC 3256
QY SerTyrSerGlyLeuGluThrCysGluSerCysProLeuGluTyrTyrGlnProLysPhe 1081
DB 3257 TCATACAGTGAACCTTGAACCTGTGATGTGTCCACTGGGCACTTATACGCCAATAATTT 3316
QY GlysSerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaVal 1101
DB 3317 GGTGCCCCGAGCGCTCTCGTGTCCAGAAAACACTGTGAAGAGAGAGCGCGTG 3376
QY AsnIleSerAlaCysGlyValProCysProGluGluLysPheSerArgSerGlyLeuMet 1121
DB 3377 AACATTTCTGCAATGTGAAATCTCTGTGCCAAGAAAGAAATCTCGGCTCTGGGTTAAAG 3436
QY ProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysValaPheCysLeu 1141
DB 3437 CCTGTCAACCAATGTCTCTGTACTATTAACCACTTAATGCAAGGAGGAGGCTTCTGCGTG 3496
QY AlaCysProPheTyrGluThrThrProPheAlaGlySerArgSerIleThrGluCysSer 1161

DB 3497 GCCTGTCCCTTTTATGAACTACCCCATTCGCTGTTCCAGATCCATACAGAAATGTCA 3556
QY SerPheSerSerThrPheSerAlaAlaGluGluSerValValProProAlaSerLeuGly 1181
DB 3557 AGTTTATGTTCACTTCTCAGCGGAGAGAAAGTGTGTCCTGCTGCTCTTGGA 3616
QY HisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAspPro 1201
DB 3617 CATATTTAAAGAGGCATTAATCAACAGTCAAGGCAAGTCATGAATGCTCTTAAACCT 3676
QY CysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeu 1221
DB 3677 TGCACAAATAGTGAACCTGCGCAGCAACTGGGCGGTATATGTGTCTCTGTCCACTT 3736
QY GlyTyrThrGluLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeu 1241
DB 3737 GGAATATACAGGTTTAAAGTGAAGACATGAGATGAGTGCAGGCCACTGCTTGCCTC 3796
QY AsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyr 1261
DB 3797 AACATGAGGTTGTAAAGACCTAGTTGGGAAATTCATTTGTAGAGCCATCAGGTTAC 3856
QY ThrGlyGlnArgCysGluLysAsnIleAsnGluCysSerSerSerProCysLeuAsnLys 1281
DB 3857 ACAGTGAACGACTGTGAATTTGAACATCAATGATGATGATGATGATGATGATGATGAT 3916
QY GlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGly 1301
DB 3917 GCCACTGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3976
QY LeuHisCysGluThrGluValAsnGluCysGlnSerAspProCysLeuAsnAlaVal 1321
DB 3977 AAAAGGTGTGAACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4036
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DB 4037 TGTGAAGACAGGTTGGGAGATTTCTGTGCATTAATGCCACCTGGAATTTTGGTACCCGA 4096
QY CysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLys 1361
DB 4097 TGTGAAGAAACCTCAATAGATGTCTCAGTCAAGCCATGCAAAAATGAGCTACTGTAAA 4156
QY AspGlyAlaAsnSerPheArgCysLeuCysValAlaGlyPheThrGlySerHisCysGlu 1381
DB 4157 GACGGTGCCTAATAGCTTCAAGTGCCTGTGTCAGCTGCTTCAACAGATCACTGTGAA 4216
QY LeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu 1401
DB 4217 TTGAACATCAATGAATGTCAATCAATCAATGAAGAAATCAGGCTGTGTGATGAA 4276
QY LeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnAlaArgCysGluThrGlu 1421
DB 4277 TTAAATTCATACAGTTTAAATGTCAGCAGATTTTCAAGGCAAAAGGTGTGAACAGAA 4336
QY GlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeu 1441
DB 4337 CAGTTCACAGGCTTAACTGATTTTGAAGTTTCTGGCATTAATGATATGTCAAGCTA 4396
QY AspGluMetLeuProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSerAsp 1461
DB 4397 GATGGATGCTCCCATCTCCATAGCTCAATGCTGTAACCTTGAACTTCTGGAATGAATCTGTAC 4456
QY AspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThrLeu 1481
DB 4457 GACATGAACCTATGAAACCAATCTCTATGAGGATTAACAGGCAAGCAATACCTTG 4516
QY LeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyArgGlyLysIleThrAsn 1501
DB 4517 CTCCTGACGATTAATTAACGAGGTGCTTATGTGTAAGGCAAGGAGAAAGATTAACAAAC 4576
QY CysProSerValAsnAspGlyArgGlyPheHisHisIleAlaIleThrThrThrSerAlaAsn 1521
DB 4577 TGTCTCTGGTAAATGATGCAAGATGGCAATATTTGCAATCACTTGACAAATGACTGCT 4636


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QY 420 CysLeuProAsnGlyLeuTrpSerGlySerGlySerTyrcysargValaArgThrCysPro 439
DB 1481 TGTCAACCCAAATGGTTTGGTGTCTGGGAGCAAGAGCTTCTGACAGAGGAGAACGGTCCCC 1540
QY 440 HisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGlyMetLeuLeuTyrLys 459
DB 1541 CACCTCCGACAGCCCAACACGCGCACATCAGCTGCTCCACCTGGGAAAGTCTCTCAAC 1600
QY 460 ThrThrCysLeuValAlaCysAspGlnGlyTyrArgLeuGlnGlySerAspLysLeuThr 479
DB 1601 ACCCTGTGTTGGTATCTGCATGAGATGAGATTAAGAGCAGCAGCAGCTTACC 1660
QY 480 CysGlnGlyAsnSerGlnTrpAspGlyProGlnProArgCysValGlnArgHisCysSer 499
DB 1661 TGTCAAGAAATGCCCGATGGATGGCCAGAGCCCGGTGTGTAGAACCCATTTGGCC 1720
QY 500 ThrPheGlnMetProLysAspValIleIleSerProHisAsnGlyLysGlnProAla 519
DB 1721 ACCTTCAGAAAGCCCAAGGCGTCATCATTTCTCAACCCAGCTGGCGCAAGCAGCTGCC 1780
QY 520 LysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValAla 539
DB 1781 AGGCTGGAGATGACCTGTCACTAAGCTGCGCGAGGATACATTTATCCGAGGTACGA 1840
QY 540 GluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCys 559
DB 1841 GAA---GTGAGATGTCCCATCTCGGAGATGGAGTCCCAAGTTTCAGACAGCTGTGGC 1897
QY 560 LysAspValGlnAlaProGlnIleAsnGlyProLysAspIleGlnAlaLysThrLeuGln 579
DB 1898 AAGAGTGTGAGGCTCCACAAATCAGCTGTCCAAATACATTTGAGGCAAGACGTGGAG 1957
QY 580 GlnGlnAspSerLysAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGln 599
DB 1958 CAGCAGGACCTCTGTATATGTCACTGGCAGTCCCAAGCTTAAAGCAACTCTGGTGA 2017
QY 600 LysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp 619
DB 2018 AAGGTGTCACTCCACGTCCACCCAGCTTTACCCCACTTACCTTCCCAATTTGGAGAC 2077
QY 620 ValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHis 639
DB 2078 GTGGCCTACCTACACAGGCAACGCACTCATCCGGTAAACCAAGCAGCTGTGACTTAC 2137
QY 640 IleLysValIleLeuAlaGlnProProValIleAspTrpCysArgSerProProVal 659
DB 2138 ATTAAAGTCAATTGATGTGAACCGCTGTCTAGATTGGTGCATCTCCACTCCATC 2197
QY 660 GlnValSerGlnLysValHisAlaAlaSerTrpAspGlnProGlnPheSerAspAsnSer 679
DB 2198 CAGGTCTGAGAAAGAGACACCTCGCAAGCTGGAGTGAAGCTCATCTCGACACACTCC 2257
QY 680 GlyAlaGlnLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGln 699
DB 2258 GGGGCTGAATTGGTCATTACACAGCAGTCAACACAAAGCGCAATGTTTCCATGAGGAAA 2317
QY 700 ThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHis 719
DB 2318 ACGGTGTGTGTACACAGGCACTGACCCCTCAGGCAACACAGAGCCTGTGACATCCAC 2377
QY 720 IleValIleLysGlySerProCysGlnIleProPheThrProValAlaGlnLysAspPheIle 739
DB 2378 ATTGTCTAATAAGGTTCTCCCTGTGAGGTCCCTTCAACCCCTGTAAACGGGGACTTATC 2437
QY 740 CysThrProAspAsnThrGlyValAlaAsnGlyThrLeuThrCysLeuGlnGlyTyrAspPhe 759
DB 2438 TGTGCCACGATAGTGTGAGATTACGTGAGCTGCAAGGAGGAGGCTAAGATTTC 2497
QY 760 ThrGlnGlySerThrAspLysTyrTyrCysAlaTyrGlnAspGlyValIleTyrLysProThr 779
DB 2498 ACGAAGGGTCTACAGAAAGTACTACTGTGCTTTTAAGATGTATCTGAGAGACACCA 2557
QY 780 TyrThrGlnGlnTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSer 799
DB 2558 TACTTACAGAAAGGCGCAGACTGTGTATTAACGTTTGCAAAACATGGTTTCAAGTCC 2617
QY 800 PheGlnMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSer 819
DB 2618 TTTGAAATGCTATACAAACACACCTGCTGTGATGACATGATCTGTTTAAGAGTTTCT 2677
QY 820 GlnAlaPheGlnThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGlnAsp 839
DB 2678 GCAGCATTTGAGACTACCTCGGGGAAACATGATCCCGTCTTTTGAACGATGTGATAC 2737
QY 840 IleAspCysArgLeuGlnGlnAsnLeuThrLysLysTyrCysLeuGlnTyrAsnTyrAsp 859
DB 2738 ATTGACGTGACAGCTGAGGAC---CTACCAAAAATATCTCATGTAGTATATTAAC 2794
QY 860 TyrGlnAsnGlyPheAlaIleGlyProGlyValTyrGlyAlaAlaAsnArgLeuAspTyr 879
DB 2795 TATGAAATGGCTTTGCAATTGACACAGAGCTGGGGTTCAGGCGCAAGCCTGATAT 2854
QY 880 SerTyrAspAspPheLeuAspThrValGlnGlnThrAlaThrSerIleGlyAsnAlaLys 899
DB 2855 TCTTACGATCACTTCTGAGATGTGTACAGGAAACCCACCGATGTGGCGAAGCCAGA 2914
QY 900 SerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsn 919
DB 2915 TCGTCAAGGATTAAGAAAGCTGCCATGTCTACCCCAAAATTCAGCTAATTTTAA 2974
QY 920 IleThrAlaSerValProLeuProAspGlnArgAsnAspThrLeuGlnTyrGlnAsnGln 939
DB 2975 ATCAAGACTACCTGTGCACTCCACAGAGAAAGAAACATACCTTGAATGGAGATCAG 3034
QY 940 GlnArgLeuGlnGlnThrLeuGlnThrIleThrAsnLysLeuLysArgThrLeuAsnLys 959
DB 3035 CAGGACCTCATTAAGACATTGGAACATCAACCATGCGTGAAGACCTTGATATA 3094
QY 960 AspProMetTyrSerPheGlnLeuAlaSerGlnIleLeuIleAlaAspSerAsnSerLeu 979
DB 3095 GAGCCCAATGATTTTTCAGCTGCTGCGGAAACAGGTGGTGCAGACGAAATTCCTC 3154
QY 980 GlnThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCys 999
DB 3155 GAACAGAAAGGCTTTCTTCTTCTGCAAGACAGCTGTGTGAGGGGCGCATGTGT 3214
QY 1000 ValAsnGlyProLeuGlyTyrTyrAsnLeuGlnHisPheThrCysGlnSerCysArg 1019
DB 3215 GTCAAGTCCCTCGGAGACCTTACTCTGTGAGAGATCCACCTGTGAAGAGCTGCTC 3274
QY 1020 IleLysSerTyrGlnAspGlnGlnGlnLeuGlnLysLysLeuCysProSerGlyMet 1039
DB 3275 ATGGATCTTACCAAGATGAAGAGGCGAGCTGAATGCAAGCTGTGCCCAAGACT 3334
QY 1040 TyrThrGlnTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGly 1059
DB 3335 CACAGGAATACCTCCATTCAAGAAAGCTCTTAATCAACAGCTCACTGAAGCAAGC 3394
QY 1060 ThrTyrSerTyrSerGlyLeuGlnThrCysGlnSerCysProLeuGlyTyrThrGlnPro 1079
DB 3395 ACCTACTCTTCAATGGGCTGGAACCTGCGAATCGTTCGGTGGTACTTATCAACCG 3454
QY 1080 LysPheGlySerArgSerCysLeuSerCysProGlnAsnThrSerThrValLysArgGly 1099
DB 3455 GAATTGTGATCCCGAGGTGCTCTTAATCCCAAAACACACACAGCTGAAGAAAGAGA 3514
QY 1100 AlaValAsnIleSerAlaCysGlyValProCysProGlnGlyLysPheSerArgSerGly 1119
DB 3515 GCCTGTGACATCTTGTGTGTGAGATGCTGCTGCCAGTGAAGAAATTCCTCCGTTCTGG 3574
QY 1120 LeuMetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPhe 1139
DB 3575 CTAAACACCTGTCACTTGTGCTGTGAGATCATTAACCAACCAATGACGGAGAACTTCT 3634
QY 1140 CysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGln 1159
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Db	3635	TGCTCGCTGTGCTCTTTTAAAGAACTAACACATCACTGGGCGACGTCATCAACAC	1160	CysSerSerPheSerSerThrPheSerAlaIaIaGluInserValProProhIaSer	1239	ProLeuGlyIYrThrGlyIYleuIYsCysGluThrAspIleAspGluCysSerProleuPro	1240	AsnProCysHIsaenSerGlyYrThrCysGlnGluIleuGlyYrGlyYrValCysIleuYs	1255	CysIleuAsnaenGlyValCysIYsAspleuValGlyIuPheIleCysGluCysProSer	1259	GlyYrYrThrGlyIuIaYrGysGluGluIuAsnIleAsnGluIuYsSerSerProCysIleu	1279	GAGCTATTCAGGTCGAATATGTGAACAAATATTAATATGATGTATCTCAGGCTTGCTTA	1280	AsnIYsGlyIleCysValAspGlyValAlaGlyYrYrGysYrThrCysValIYsGlyIYhe	1289	AsnTAaAGAACCTGACATGACAGGCTTGCGACACTACCGCTGACCTGTGTGAAGATAC	1319	ValGlyIeuhIsCysGluIuThrGluValAlaenGluCysGlnIserAsnProCysIleuAsna	1319	ATGGGTGTGCACTGTGAAGAACAGACTCAATGAATGCCATGCAAGCCCTGCTTAAACAC	1320	AlaValCysGluAspGluValGlyIYsGlyIYheIleuCysIYsCysProProGlyIYheIleuGly	1339	GCAGTTGTGAAGAACCAAGTTGGGGGTTCTCATCAATCAATGCGCCACCGGAATTTTGGT	1339	ThrATrGysGlyIYsAsnValAspGluCysIleuSerGlnProCysIYsAsnGlyValAthr	1359	ACTCGGTGTGAAGAAATGTGATATGATATGCTCATGACCAATGCCAAATATGAGCCACT	1359	CysIYsAspGlyValAsnSerPheATrGysIleuCysAlaAlaGlyPheThrGlySerHIs	1379	TGTAAAGATGTGTGCCACAGGCTTCAAGTGTCAATGTCCAGGACGGCTTCAAGGACAC	1399	CysGluIleuAsnIleAsnGluCysGlnIserAsnProCysIYsAsnGlnAlaAthrCysVal	1399	TGTGAACATGAACATCAACAGAGTTCAGTCCAAACCATGTAGGAACAGGCAACCTGTGTG	1414	AspGluIleuAsnSerYrSerCysIYsCysGlnProGlyIYsPheSerGlyIuIaCysGluIu	1419	GATGAACATTAACCTCACTACAGTTGTAAATGTCAAGCAGAAATTTTCAAGCACAAGGTGAG	1439	ThrGluGlnIserThrGlyIYheAsnIleuAspPheGluValIserGlyIleYrGlyYrVal	1439	ACAGACAGACCTTCGGTTTAACTGTGAATTTTGAATTTTCTGCGATCTTACAGGATACCTC	1454	MetIleuAspGlyMetIleuProSerIleuHIsAlaIeuthrCysYrThrPheTrpMetIYsSer	1455	CTGCTAGATGTGAGTGTCTGCAACCTCCATATGCAATACCTGGCCTTCTGATGTAAATCC	1459	SerAspAspMetAsnYrGlyYrThrProIleSerYrAlaIaIaAspAsnGlyIserAspAsn	1479	TCCTGATGTCACTACAGGACGGCCACTCTATAGCATTAAGAAATGAACAAACACAC	1499	ThrIleuIleuThrAspYrYrAsnGlyIYrValIleuYrValAsnGlyIArgGluIuYrIle	1499	ACCTCCCTCTGACATTAACAGGCTGGGTCTTATGTGAATGGAAGAAAGAAAGATC	1519	ThraenCysProSerValAsnAspGlyIArgTrpHIsHIsAlaIleThrTrpThSer	1519		
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DB	ACCAATGCCCTCCGTAAGAAGATGGCATTTGGCATCATATATGGCAATCAATGACAAAGT	4714
Db	ACCAATGCCCTCCGTAAGAAGATGGCATTTGGCATCATATATGGCAATCAATGACAAAGT	4714
Qy	AlaangilylIeTrpIysValTyrIleapgilYlylsuSeraspGilylValagilyeu	1533
Db	ACTGGTGAAGCTGGAGGGTCTATATATAATGGGAAATTAATCTGACGGTGGTACTGGCTTC	4834
Qy	SerValGilyeuProIleProgilYglYlaleuValleuagilylGlnGlnaspIys	1555
Db	TCGATGGCAAGCCATACCTGGTGGCGCGTGCATTAGTTCTTGGGCAGAGGACAGCAAA	4899
Qy	LyseGilylGlyPheSerProalaglIserPheValGlySerIleSerGlnleuAsnleu	1579
Db	AAAGAGAGGGGTTCAACCGCGTGAAGTCTTTTGTGGCTTCATATAGCCAGTCAACTC	495
Qy	TrpAspTyrValleuSerProGlnGlnValIysSerleuValathrSerCysProGluGln	1599
Db	TGGGACTATGTCCTGTCTCCACACAGGTGAAGTGTGGCTGGCCAGCTCTGCCAGAGAA	5014
Qy	LeuSerIysGilyAsnValleuValleuTrpProaspPheIuSerGilylValGlyVal	1613
Db	CTGATCTGGGAAAGTGTATGACATGGCCGCAATTTCTGTGGGAATCAAGGGAAAGGTG	5074
Qy	LysIleAspSerIysSerIlePheCysSeraspCysProalGleuGilylYserValPro	1633
Db	AAAGTATATTCACAGAGCATTTCTGCTCTATATGTCCGCTTTAAGAAAGATCCGTGCT	5133
Qy	HisIeuatGlyThrIleSerGluAspLeuIysProGilySerIysValAsnleuPheCysasp	1655
Db	CACCTGAGACCTGCATCAGAAATTCGAAAGCCAGGCTCAAAAGTCAGCTGTCTGTGAT	5194
Qy	ProGilyPheGlnleuValGlyAsnProValGlnTyrCylleuAsnGlnGlylGlnThrPhe	1679
Db	COGGGCTTCCAGATGGTGGGAATCTGTGACGATATGTCTGAACCAAGGGCAGTGGCA	525
Qy	GlnProleuProHisCysGluAspIleSerCysGilyValProProProleuGluAsnGly	1699
Db	CACCACTCTCCCACTGAGAGCGATTCGCTGTGGGCTCTCCGCTTGGAGATATGC	5314
Qy	PheHisSerIleAspAspPheTyrIleaglYserThrValIlnTyrGlnCysAsnAsnGly	1719
Db	TTCTAATCAGCGAGAGACTTCATAGCCGGCAGCAGGTCATCATGACCAACAGTGGC	5374
Qy	TyrTyrIleuLeuGilyAspSerIarghPheCysThrAspAsnGlySerTrpAsnGlyVal	1739
Db	TACTACCTCGCTGGGTGATTCGCAATGTTCTGCACAGCAACAGGGAGCTGAGACGGCAT	5434
Qy	SerProSerCysIleuAspValAspGlyCysValIleValGlySeraspCysSerGlyHisIle	1755
Db	TCACCATCTGTCTGAGTGCAGATGAGATGTGTCACTCGGCTCGGACTGTATAGTACACGCC	5499
Qy	SerCysIleuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAsp	1779
Db	TCCTGCCCGAACAACAGATCTCGATAGTTCTCTGTAAACCAACCATACACGGAGAT	5554
Qy	GlyIysAsnCyalaGlnProIleIysCysIysValIleProGilyAsnProGluAsnGlyHis	1799
Db	GGGAAAACCTGTGACAACTGTAAATGTAGGCTCCAGAAAATCCAGAAAATGGCCAC	5614
Qy	SerSerGilylIleTyrThrValGlyAlaIleValThrPheSerCysGlnGlnGlyTyr	1819
Db	TCCTCTGTGTGATTTACACCGTGGGTACTGCAGTCAATTTCTGTGACAGAGGCAC	5674
Qy	GlnIleuIeGilyValIlnThrIleThrCysIleuGlyIuSerGilylGlnTrpAsnHisIleuIle	1839
Db	GAGCTGTGTGGAGATGAGACCACTACCGTGTGGAGACTGGCAGATGGGATCGCCTCAGG	5734
Qy	ProTyrCys 1842	
Db	CGTCTCTGT 5743	

QY 600 LysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp 619
 DB 1973 AAGGTGTCACTGCTCACTCAACCAAGCTTTTACCCCACTTACTCTTCCCAATTGGAGAC 2032
 QY 620 ValAlaIleValIleThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHis 639
 DB 2033 GTGGCCATCACTCAACGCAACCGACTCATCCGATCAACCAAGCCAGCTGCATCTTCTAC 2092
 QY 640 IleValValIleAspAlaGluProProValIleAspTyrCysArgSerProProVal 659
 DB 2093 ATTAAGTCATTGATGTGAACCGCTGTCAATGATTTGGCGATCTCCACCTCCAAATC 2152
 QY 660 GlnValSerGlyLeuValHisAlaAlaSerTyrAspGluProGlnPheSerAspAsnSer 679
 DB 2153 CAGCTGCTGAGAGAGAGACCCCTGCACTGGGAGTGAAGCTGATCTCAAGCAACTCC 2212
 QY 680 GluAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGly 699
 DB 2213 GGGGCTGAATTGGCTCAATACAGCACTCAACAAGCGACATGTTTCTCATGCGGGA 2272
 QY 700 ThrIleValGlnThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHis 719
 DB 2273 ACGGTGTGTGTACCAAGCACTGACCCCTCAAGCAACAAGACCTGTGACATCCAC 2332
 QY 720 IleValIleLeuGlySerProCysGluIleProPheThrProValAsnGlyAspPheIle 739
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 QY 740 CysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGlnGlyTyrAspPhe 759
 DB 2393 TGTGCCAGATATGCTGAGATTAACTGATGACCTGACAGGAGGCGTATGATTC 2452
 QY 760 ThrGlnGlySerThrAspIleTyrTyrCysAlaTyrGlnAspGlyValTyrIleProThr 779
 DB 2453 ACGAAGAGGTCACTGAGAACTACTGTGTTGAAGATGTATCTGAGAACCAACA 2512
 QY 780 TyrThrThrGluTyrProAspCysAlaIleValArgPheAlaAsnIleGlyPheIleSer 799
 DB 2513 TACTCTACGAATGCGCAAGCTGTGCTATAAACGTTTGCACACATGTTTCAAGTCC 2572
 QY 800 PheGluMetPheTyrIleValAlaIleArgCysAspAspThrAspLeuMetIleValPheSer 819
 DB 2573 TTTGAATGCTATACAAACCACTCGCTGTGATGACATGATCTGTTAAGAAATTTCT 2632
 QY 820 GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
 DB 2633 GCAGCATTTGAGCTACCTCGGAGAACATGCTCCCTTTGTATGATGATGCTGATGAC 2692
 QY 840 IleAspCysArgLeuGlnGluAsnLeuThrIleValTyrCysLeuGlnTyrAsnTyrAsp 859
 DB 2693 ATTGACTGCACTGAGAGAC---CTGACCAAAAATATCTGCATCGATTAATTACAC 2749
 QY 860 TyrGluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyValAlaAsnArgLeuAspTyr 879
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DEFINITION Sequence 3 from Patent WO0210388.
ACCESSION AX375163
VERSION AX375163.1 GI:19169917
KEYWORDS
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ORGANISM Mus musculus (house mouse)
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1. Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLES Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ACCESSION AX880905
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REFERENCE
  1. Ota, T., Isegai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
    Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., and Otsuki, T.
    Primers for synthesizing full-length cDNA and their use
    Patent: EP 1074617-A 15810 07-FEB-2001;
    Research Association for Biotechnology (JP)

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US-09-977-053-6 (1-1842) x AX880905 (1-5124)
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 1 (bases 1 to 5124)
 Ota,T., Iwoga,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,T.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 Primer for synthesizing full-length cDNA and use thereof
 Patent: JP 2002191363-A 13502 09-JUL-2002;
 HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 FN JP 2002191363-A/13502
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI SATO
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KENICHI NAGAI, TETSUO OTSUKI
 PC
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
 10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key

FEATURES
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FT CMS Location/Qualifiers
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ALIGNMENT SCORES:

Alignment Scores:
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Score: 7537.00 Matches: 1347
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Best Local Similarity: 99.56% Mismatches: 5
Query Match: 73.75% Indels: 0
DB: 6 Gaps: 0

US-09-977-053-6 (1-1842) x BD158659 (1-5124)

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RBSULT 10

AK027870 5124 bp mRNA linear PRI 01-AUG-2002
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DEFINITION Homo sapiens CDNA FL114964 fis, clone PLACE400581, moderately
similar to FIBROPELIN 1 PRECURSOR.
ACCESSION AK027870
VERSION AK027870.1 GI:14042858
KEYWORDS oligo capping; file (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Isogai,T., Ota,T., Hayaishi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y.,
Matsumawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuno,Y. and Sasaki,N.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 5124)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genom@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
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Best Local Similarity: 99.56% Mismatches: 5
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Pred. No.:
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QY	1315	ProCysLeuSerGlyValAlaCysGluAspGlyValGlyPheLeuGlyCysPro	1334
DB	3362	CCATGCTTAAATATGATGATCTGTGAAGACAGGTTGGGATCTCTGTGCAATGCCA	3421
QY	1335	ProGlyPheLeuGlyThrArgCysGlyValAsnValAspGlyCysLeuSerGlnProCys	1354
DB	3422	CTGTGATTTTGGGTACCCGATGTGGAAAGACGTCATGATGATCTCAGTCAGCCATGC	3481
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DB	3662	GGCAAAAGCTGTGAACAGACGTCACGCTTAACTTGAATTTGAAATTTTGGC	3721
QY	1435	LeuGlyTyrValMetLeuSerGlyMetLeuProSerLeuHisAlaLeuThrCysThr	1454
DB	3722	ATCTATGATATATCATGATGATGATGATGATGATGATGATGATGATGATGAT	3781
QY	1455	PheThrMetLeuSerSerAspAspMetAsnThrGlyThrProLeuSerTyrAlaValAsp	1474
DB	3782	TTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3841
QY	1475	AsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsn	1494
DB	3842	AACGGACGACATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3901
QY	1495	GlyArgGlyLeuValLeuThrAsnCysProSerValAsnAspGlyArgTyrHisAla	1514
DB	3902	GGCAGGGAAGAAATCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3961
QY	1515	LeuThrThrPheSerSerAsnGlyLeuTyrLeuValTyrLeuAspGlyValLeuSerAsp	1534
DB	3962	ATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4021
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DEFINITION to B-SEBECTIN PRECURSOR.			
ACCESSION AK122605			
VERSION AK122605.1 GI:34527780			
KEYWORDS oligo capping, f1s (full insert sequence).			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
1			

AUTHORS		Oshima, A., Takahashi-Puji, A., Tanase, T., Imose, N., Takeuchi, K., Ariga, M., Muraishi, K., Yuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Makamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuno, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Matsumura, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Negahori, K., Masuko, Y., Nagai, K. and Isogai, T.	
TITLE		NEDO human cDNA sequencing project	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 3253)	
AUTHORS		Isogai, T. and Yamamoto, J.	
TITLE		Direct Submission	
JOURNAL		Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kametani, Kisarazu, Chiba 292-0818, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)	
COMMENT		NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.	
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Best Local Similarity:		99.88%	
Query Match:		46.74%	
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QY	21	PheGlnGlnMetSerProSerArgAspMetPheArgLeuPheProGlnThrAlaPro	40
DB	394	TTTCAGCAGATGTCCTCCGTCGCAATTCAGCTTCCTCCCTCCGTCGCAATTCAGCT	453
QY	41	GlyValaProGlySerLeuProAlaProProAlaProGlyAspGlyAlaAlaGlySerArg	60
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DB	514	GTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	573
QY	81	ArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGlyValAlaAspPheArg	100
DB	574	CGCTGAGAGCTGCTTCTCTGATGATGATTCGTCAGACGTGGCCGAATCACTTCGCC	633
QY	101	SeGluLeuMetPheValArgGlyLeuLeuSerAspPheProValAlaProThrAlaThr	120
DB	634	AGCAGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	693
QY	121	ArgValAlaIleValThrPheSerSerArgAsnTyrValValProArgValAspTyrIle	140
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LOCUS Sequence 15640 from Patent EP1074617.

DEFINITION AX880735

ACCESSION AX880735

VERSION AX880735.1 GI:40035471

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1. 1969

AUTHORS /organism="Homo sapiens"

Isaia, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. /mol_type="unassigned DNA"

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Patent: EP 1074617-A 15640 07-FEB-2001; 415..1656

Research Association for Biotechnology (JP) /notes="unnamed protein product"

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US-09-977-053-6 (1-1842) x AX880735 (1-1969)

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Qy 718 IleHisIleValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAsp 737

Db 1201 ATCCATATGTCATAAAGGTTCTCCCTGTGAATCCCATTCACACCTGTAAATGGGAT 1260

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Db	1501	TTTTCTGAAGCATTTGGAGAGACCCCTGGGAAAAATGGTCCCATCTTTTGTAGTGATGCA	1560	Db	181	TGCCCTGCCTCGAAGCCCTCCCGAAAAATGGTTACTTTTATCCAAAACACTTTGCACACAC	240
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RESULT 13				Qy	438	CysProHisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeu	457
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SOURCE	Homo sapiens (human)			Qy	498	CysSerThrPheGlnMetProLysAspValIleIleSerProHisAsnCysGlyLysGln	517
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AUTHORS	Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.			Db	601	CCAGCCAAATTTGGGACGATCTGCTATGTAAGTTCGCCGCAAGGGTTCAATTTATCTGGA	660
TITLE	Primer for synthesizing full-length cDNA and use thereof			Qy	538	ValLysGluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAla	557
JOURNAL	Patent: JP 2002191363-A 13402 09-JUL-2002; HELIX RESEARCH INSTITUTE			Db	661	GTCAAGAAATCTCGAGATGATACCTTCTCGAAAAATGGAATGTGCGAGTTTCAAGCAGCT	720
COMMENT	OS Homo sapiens (human) PN JP 2002191363-A/13402 PD 09-JUL-2002 PP 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAOBU PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT CDS (415)..(1653).			Qy	558	ValCysLysAspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThr	577
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Percent Similarity:	99.45%	Conservative:	0	Qy	618	GlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIle	637
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ACCESSION AK023591
VERSION GI:10435568
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Ishibaishi,T., Fujimori,K.,
Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishii,S., Kawai,Y.,
Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Negahari,K.,
Masuho,Y. and Kanehori,K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1969)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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 DEFINITION Method and composition related to EGF repeat-containing polypeptide.
 ACCESSION BD229966
 VERSION BD229966.1 GI:33039736
 KEYWORDS JP 2002526077-A/6.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Ford, J.E., Mulero, J.J., Yeung, G. and Montgomery, J.
 TITLE Method and composition related to EGF repeat-containing polypeptide
 JOURNAL Patent: JP 2002526077-A 6 20-AUG-2002;
 HYSEQ INC

COMMENT
 OS Homo sapiens (human)
 PN JP 2002526077-A/6
 PD 20-AUG-2002
 PF 20-SEP-1999 JP 2000574256
 PR 18-SEP-1998 US 09/157308
 PI JOHN E FORD, JULIO J MULERO, GEORGE YEUNG, JULIE MONTGOMERY PC
 C12N15/09 A61K38/00, A61K48/00, A61P1/00, A61P1/02, A61P3/10 PC
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FEATURES
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1 (bases 1 to 1760)

Ford, J.E., Mulero, J.J., Yeung, G. and Montgomery, J.

Method and composition related to EGF repeat-containing polypeptide
 Patent: JP 2002526077-A 6 20-AUG-2002;
 HYSEQ INC

OS Homo sapiens (human)
 PN JP 2002526077-A/6
 PD 20-AUG-2002
 PF 20-SEP-1999 JP 2000574256
 PR 18-SEP-1998 US 09/157308
 PI JOHN E FORD, JULIO J MULERO, GEORGE YEUNG, JULIE MONTGOMERY PC
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1284	Qy	eValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGly	1301
1323	Db	TGTTGATGTTGTGGCTGCTATCGTTGCACATGTGTGAAGGATTTTGTAGST	1374
RESULT 16			
AX870332			
LOCUS			
Sequence 5237 from Patent EP1074617.			
AX870332			
ACCESSION			
AX870332.1			
VERSION			
KEYWORDS			
Homo sapiens (human)			
linear			
PAT 17-DEC-2003			

ORGANISM - Homo sapiens
 Rukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1
 Oka, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Makamatsu, A., Nagai, K. and Otsuki, T.
 Primers for synthesising full-length cDNA and their use
 Patent: EP 1074617-A 5237 07-FEB-2001;
 Research Association for Biotechnology (JP)

FEATURES
 Location/Qualifiers
 source 1..765
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:	5.4e-86	Length:	765
Pred. No.:	1447.00	Matches:	251
Score:	98.82%	Conservative:	0
Percent Similarity:	98.82%	Mismatches:	3
Best Local Similarity:	14.16%	Indels:	0
Query Match:	6	Gaps:	0

DB:

US-09-977-053-6 (1-1842) x AX870332 (1-765)

Qy 195 ThrAspGlyTyrSerAsnGlyGlyAspProArgProIleAlaSerLeuArgAspSer 214
 Db 2 ACTGATGGATATCCAAATGGGGAGACCTTAGACCAATTGCAGCGTCACTCGAGATTCA 61

Qy 215 GlyValGluIlePheThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMet 234
 Db 62 GGAGTGAGGATCTTCACTTTTGGGATATGGCAGGGAACTTCAGAGAGCTGAATGACATG 121

Qy 235 AlaSerThrProIysGluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAla 254
 Db 122 GCTTCCACCCCAAGGAGAGACACTGTACTCTGTACACATTTTGAGAAATTTGAGGCT 181

Qy 255 LeuAlaArgAlaLeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMet 274
 Db 182 TTAGCTCGCGGGCAATTGCATGAAGACTACTCTTCGGAGCTTTTATTCAAGATGATATG 241

Qy 275 ValHisCysSerTyrLeuCysAspGluGlyIysAspCysCysAspArgMetGlySerCys 294
 Db 242 GTCCACTGCTCATATCTTTGTGTGAAGGCAAGGACTCTGTGACCGGAATGGAGCTGC 301

Qy 295 LysCysGlyThrHisThrGlyHisPheGluCysIleCysGluIuIysGlyTyrTyrGlyLys 314
 Db 302 AAATGTGGGACACACACAGGCCATTTTGATGTGCATCTGTGAANAGGGGTATTACGGGAA 361

Qy 315 GlyLeuGlnTyrGluCysThrAlaCysProSerGlyThrTyrLysProGluGlySerPro 334
 Db 362 GGTCTGCAGTATGAATGATCACAGCTTGCCCATCGGGACATACAAACCTGAAGGCTCA 421

Qy 335 GlyGlyIleSerSerCysIleProCysProAspGluAsnHisThrSerProProGlySer 354
 Db 422 GGAGGAATTCAGACGTTGCATTTCCATGTCTCATGAAATCATCACCTCTCCACTGGAA 481

Qy 355 ThrSerProGluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGlu 374
 Db 482 ACATCCCCGTGAAGACTGTGTCTGCAGAGAGGATACAGGGCATCTGGCCAGACCTGT 541

Qy 375 LeuValHisCysProAlaLeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCys 394
 Db 542 CTTGNCCACTGCCTTGCCCTGAAGCCCTCCGAAATGTTACTTTATCCAAACACTTGC 601

Qy 395 AsnAsnHisPheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGly 414
 Db 602 AACCAACACTTCAATGCAGCCCTGTGGGTCCGATGTCAACCTCGGATTTTGATCTTGT 661

Qy 415 SerSerIleIleLeuCysLeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArg 434
 Db 662 AGCAGCATCATCTTATGTCTACCAATGGTTGTGGTCCGGNTTANAGAGACTTCGAGA 721


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QY 435 ValArgThrCysProHisLeuArgGlnProtyrHisGlyHis 448
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RESULT 17
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LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD150394
ACCESSION BD150394
VERSION BD150394.1 GI:27856152
KEYWORDS JP 2002191363-A/5237.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 5237 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN OS 2002191363-A/5237
PD 09-JUL-2002
PP 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof PH Key
Location/Qualifiers
FT source 1..765
FT /organism='Homo sapiens (human)'.
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source
Location/Qualifiers
1..765
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

ORIGIN
Alignment Scores:
Pred. No.: 5,4e-86 Length: 765
Score: 1447.00 Matches: 251
Percent Similarity: 98.82% Conservative: 0
Best Local Similarity: 98.82% Mismatches: 3
Query Match: 14.16% Indels: 0
DB: 6 Gaps: 0

US-09-977-053-6 (1-1842) x BD150394 (1-765)

QY 195 ThrAspGlyTyrSerAsnGlyGlyAspProArgProIleAlaAlaSerLeuArgAspSer 214
DB 2 ACTGATGGATATCCAAATGGGGAGACCCCTAGACCAATTCGACGCTGCAGATTCA 61

QY 215 GlyValGluIlePheThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMet 234
DB 62 GGAGTGGAGATCTTCATCTTTGGCATATGCGAAGGGAACATTCGAGAGCTGAATGACATG 121

QY 235 AlaSerThrProGlyGluHisCysTyrLeuLeuHisSerPheGluIleGluAla 254
DB 122 GCTTCACCCCAAGGAGGAGCACTGTACTCTGTACACAGTTTGAAGAAATTCAGGCT 181

QY 255 LeuAlaArgArgAlaLeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMet 274
DB 182 TTAGCTCGCCGGGCATTCGATGAGATCTACCTTCTGGGAGTTTATTTCAGATGATATG 241

QY 275 ValHisCysSerTyrLeuCysAspGluGlyLysAspCysCysAspArgMetGlySerCys 294
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242 GTCCACTGCTCATATCTTTGTGATGAAGCAAGGACTGCTGTGACCGAATGGCAAGCTGC 301
295 LysCysGlyThrHisThrGlyHisPheGluCysAlleCysGluLysGlyTyrTyrGlyLys 314
302 AAATGTGGGACACACACAGGCCATTTTGTAGTGCATCTGTGAAAAGGGGTATTACGGGAAA 361
315 GlyLeuGlnTyrGluCysThrAlaCysProSerGlyThrTyrLysProGluGlySerPro 334
362 GGTCTGCAGTATGAATGCACAGCTTGCCCATCGGGGACATACAAACCTGAAGGCTCACCA 421
335 GlyGlyIleSerSerCysIleProCysProAspGluAsnHisThrSerProProGlySer 354
422 GGAGGAATCAGCAGTTGCATTCCATTCCTGATGATGAAATCACACCTCTCCACCTGGAGC 481
355 ThrSerProGluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGlu 374
482 ACATCCCCGGAAGACTGTGTCTGCAGAGAGGAGATACAGGGCATCTGGCCAGACTGTGAA 541
375 LeuValHisCysProAlaLeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCys 394
542 CTTCGCCACTGCTGCTGCTGAGGCTCCGGAATGTTACTTTATCCAAACACTTGC 601
395 AsnAsnHisPheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGly 414
602 AACAACTTTCATATGCAGCTGTGGGTCCGATGTCCACCTCGATTTGATCTTGTGGGA 661
415 SerSerIleIleLeuCysLeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArg 434
662 AGCAGCATCATCTTATGTCTACCCCAATGTTGTGTGCTCCGNTANAGAGCTACTGCAGA 721
435 ValArgThrCysProHisLeuArgGlnProLysHisGlyHis 448
722 GTAAGAACATGCTCTATCTTTGTGAGCGACCGCAACATGNCAC 763

RESULT 18
AX677660
LOCUS Sequence 438 from Patent WO02086122.
DEFINITION AX677660
ACCESSION AX677660
VERSION AX677660.1 GI:29335065
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Legrain, P. and Daviet, L.
AUTHORS Protein-protein interactions in adipocytes
TITLE Patent: WO 02086122-A 438 31-OCT-2002;
JOURNAL Hybrigenics (FR)
FEATURES
source
Location/Qualifiers
1..706
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

ORIGIN
Alignment Scores:
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Score: 1341.00 Matches: 234
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.57% Mismatches: 0
Query Match: 13.12% Indels: 0
DB: 6 Gaps: 0

US-09-977-053-6 (1-1842) x AX677660 (1-706)

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DB 2 AACATGGAGTTGTAAAGACCTAGTTGGGAATTCATTGTGAGTGGCCATCAGGTAC 61

QY 1262 ThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLys 1281
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Db 62 ACAGGTGAGCGGTGTGAAGAAATATATAATGAGTGTAGCTCCAGTCTCTGTTAAATAAA 121
 Qy 1282 GlylleCysValAspGlyValAlaGlyTyrArgCysThrCysVallysGlyPheValGly 1301
 Db 122 GGAATCTGTGTGATGTGTGGTGTGCTATGCTGTGCACATGTGTGAAGATTTGTAGGC 181
 Qy 1302. LeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsnAlaVal 1321
 Db 182 CTGCATTGTGAAACAGAGTCAATGATGCGAGTCAACCCATGCTTAATATATGAGTC 241
 Qy 1322 CysGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArg 1341
 Db 242 TGTGAAGACAGGTTGGGGATTTCTGTGCAATGCCACCTGATTTTGGGTACCCGA 301
 Qy 1342 CysGlyValAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLys 1361
 Db 302 TGTGGAAGAACCTGCATGATGCTCTCAGTCAGTCACCCATGCAAAATGAGGACTACTGTAA 361
 Qy 1362 AspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCysGlu 1381
 Db 362 GACGGTGCCATAGCTTCAGATCCTGTGTGCGAGCTGGCTTCACAGGATCACACTGTGA 421
 Qy 1382 LeuAsnAlaAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu 1401
 Db 422 TTGAACATCAATGAATGTCAATGCTTAATCCATGTAGAAATCAGGCCACTGTGTGATGA 481
 Qy 1402 LeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlu 1421
 Db 482 TTAAATTCATACAGTTGTAAATCTCAGCCAGGAGTTTTCAGGCCAAAGAGTGTGAACAGAA 541
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 Db 542 CAGTCTACAGGCTTTAACTGGATTTTGAATTTCTGGCATCTATGATATGTCATGCTA 601
 Qy 1442 AspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSerAsp 1461
 Db 602 GATGGCATGCTCCATCTCTCCATGCTCTAACTGATCTAACTGATCTCTGATGAATCTCTGAC 661
 Qy 1462 AsnMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGly 1476
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RESULT 19

AC018297 18583 bp DNA linear HTG 09-DEC-1999
 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.

ACCESSION

AC018297.1 GI:6552894

VERSION

HTG: HTGS PHASE2.

KEYWORDS

Drosophila melanogaster (fruit fly)

SOURCE

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

ORGANISM

Adams, M. and Venter, J.C.

REFERENCE

Direct Submission

AUTHORS

Submitted (09-DEC-1999)

TITLE

Rockville, MD, USA

JOURNAL

This sequence was identified as CDM:10214228 by the submitter.

COMMENT

For more information on this record e-mail to fly@celera.com.
 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

FEATURES

Location/Qualifiers

1..18583

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

ORIGIN

Alignment Scores:

Pred. No.: 2,82e-76 Length: 18583
 Score: 1328.00 Matches: 518
 Percent Similarity: 32.44% Conservative: 256
 Best Local Similarity: 21.71% Mismatches: 718
 Query Match: 13.00% Indels: 900
 DB: 2 Gaps: 88
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 Db 8081 TCATCTTGAATCTTCTAGATGTGTGGCCACATCTCTGGCCGATGTC-CCGAGCTGCA 8139
 Qy 40 ProGlyAlaProGlySerIleProAlaProProAlaProGlyAspGluAlaAlaGlySer 59
 Db 8140 CCGGA-----ATTGGAGCTTGGCCTCCAGTCCGACACCGCTTTTCGGTAGC 8187
 Qy 60 ArgValGlu-----ArgLeuGlyGlnAlaPheArgArg-----ArgValArgLeuLeu 75
 Db 8188 CTGGTCAGCTTTACATGTCCTTCATTTGGACAGAGTTTCCACCGCCAGACCGCTGGT 8247
 Qy 76 ArgGluLeuSerGluArgLeuGluLeuValPheLeuValAspAspSerSerValGly 95
 Db 8248 ACCGATG-TCTGGCGGTGGCAACTGGAGTGTCTCTACATACCCAAAGTGTCTAG- 8304
 Qy 96 GluValAsnPhe-----GluValAsnPhe----- 99
 Db 8305 GAGTGTGCCTACCTATTTCATAATTGATATCCATAATTCATATGCAATCCCTTCCA 8364
 Qy 100 ---ArgSerGluLeuMetPheValArgLysLeuSerAspPheProValValProThr 118
 Db 8365 CAGAGGTCTACTCGGTCTGTGCCAATAATCGCAACGGTTTCTCATTTGGCTCTCGA 8424
 Qy 119 AlaThrArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAsp 138
 Db 8425 ACCTAACCTATCGGTATAGCAATGTACCACTGCTACGCGGGCTTTGCTTCGCTCGG 8484
 Qy 139 TyrIleSerThrArgArgAla-----ArgGlnHisLys 149
 Db 8485 GTGCTCGCATCGAGAGATC-TGCTGTCTCGGATGGCGCTTGGAGCGACAGCCCCAC 8543
 Qy 150 Cys---AlaLeuLeuGlnGlnIleProAlaIleSerTyr----- 162
 Db 8544 TGCATGGCTTCCCGAGTGTGCGAGCGCTGCCGGAAGTGGCACACGCCAACGTCACTCG 8603
 Qy 163 ArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHis 182
 Db 8604 AATGGAGTGGT----- 8615
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 Qy 203 AspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGly 222
 Db 8673 CATCCC-----GTGCTGACCTGTATGTCCAGCGC 8702
 Qy 223 IleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysGluGluHis 242
 Db 8703 ACCTGGAGTGTGTATGTATACCAAGTGCACG-----CGCAAGCGG 8741
 Qy 243 CysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAla----- 256
 Db 8742 TGCTTC-----GAATCCCGACCATTTGCCACGGCTTTGTGGTAGC 8783
 Qy 257 -----ArgArgAlaLeuHisGluAsp-----LeuProSerGlySer 268
 Db 8784 TCGACGCGAGCCTACCTCTTTCGGCGATGAGCGCAGGGTGCAGTGTCTCAAGGGCTACAAA 8843

Qy	269	PheIleGlnAspAspMetValHisCysSerTyr-----	-----Leu	280
Db	8844	CTGATCGGCAGCAACATCATCGCTGCAGCGCAGAGTTCGAGCAGCGCGCAG	8903	
Qy	281	CysAspGluGlyLysAspCys-----CysAspArgMetGlySerCysLysCys	296	
Db	8904	TGCAGAGACATCAACAGAGTGAGCTCTCGAGTGCAC-----CTAACCA	8960	
Qy	297	GlyThrHisThrGlyHisPheGluCysIleCysGluLysGlyTyrTyrGly---	313	
Db	8961	CAGAACACGAAAGCGCTCTTCCACTGCCAGTGCAGGACGGGATTTCAC--	9019	
Qy	313	-----	313	
Db	9020	GTGTCCGCCCGTCGGTGATTTCGGCTTGGTAATGAGGAGCATACCGGATC	9079	
Qy	314	-----LysGlyLeuGlnTyrGluCysThrAla-----	322	
Db	9080	CACCTCGGTGAGTGCAGCGGCTACACGAAGGAGCAGCTCGCTTGAAAC	9139	
Qy	323	-----CysProSerGlyThrTyrLysProGluGlySer-----	333	
Db	9140	GTGGGTGGCTCTTCGAGAGCTGTGTGCCAACTGGATACTCATCGACTG	9199	
Qy	333	-----	333	
Db	9200	CATTCTGCTGGCTTCGCGACCATGTCCGTGAGCGTCCCGATGGCAAATG	9259	
Qy	333	-----	333	
Db	9260	CTCGCGGTGGTCTGCAGTACACCAAGANTGACGGATGTGTCAAGGATTAT	9319	
Qy	333	-----	333	
Db	9320	TCCCGACGGCACTCGCTCGAATTCGCGATCTTGGAGCCCCAGCTCTCCAT	9379	
Qy	334	-----ProGly-----	335	
Db	9380	GCCCTGCCATCGAAGCTCGCTATATTGCTTCGCGATCCAGSACTACGTA	9439	
Qy	336	-----Gly-IleSerSerCys-----IleProCysProAspGluAenHis	349	
Db	9440	CTGTCTCGCATGAGCTGATGGGCTGCACGCGCTTGATGTGTGACATCA	9499	
Qy	349	rSerProGlySerThrSerProGluAspCysVal-----	361	
Db	9500	CAGCAAGAACATGGCGCTGTGACAGAGTGCATCACTCACCGGCGGATTTG	9559	
Qy	362	-----CysArgGluGlyTyrArg-----	367	
Db	9560	TGGCTGCAACACTGGCTTACCAGCTGTATACCTCCACAGCGACGGCTAT	9619	
Qy	368	-----AlaSerGlyGln-----ThrCysGluLeu	375	
Db	9620	ACGCTCCGAATCCGCGCAACGTGATGGTGACACCTATCAGCGCAACAG	9679	
Qy	375	uValHisCysProAlaLeuLysProProGluAenGlyTyrPheIleGlnAen	395	
Db	9680	TCTCATGTGTCCCGAAGCTGGGGCCCGAGATGGTCACTCTGAGCGACGA	9739	
Qy	395	nAsnHisPheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeu	415	
Db	9740	CTATCACTTTGGCGATGTGGTGGCTTCCAGTGCACCTTTGGCTACATCA	9799	
Qy	415	rSerIleIleLeuCysLeuProAenGlyLeuTyrSerGlySer-----Glu	433	
Db	9800	CTGGCGGCGCTGTGGCTCTCCAGCGGTGAGTGAACGCCAGCGGTACCG	9859	
Qy	433	sArgValArgThr-----	437	
Db	9860	TAAGTTTATACATTTCAGATTCTCAATGAATTCCTTACTTAACAACGA	9919	
Qy	437	-----	437	

9920	TTTTCAGATGCAAAATGGCTTTCCCTGCGCCGATGACAGTTTGAGGGTCTGACTGTGGCC	9979
438	-----CysProHisLeuArgIn-----	443
9980	CGCCCGATCCCGAATCGTTCTAGTGGCCCTTCCGGTGACAAATGTGACCAATTACGTGCGGA	10039
443	-----	443
10040	TCGCGGACGCCAACTGAGAGCCACCGCTTCTCTGGTTTCGGGAGTGGGTGTACGAT	10099
444	-----ProLysHisGlyHisIleSerCys-----	451
10100	CCCAAGCCCGGTCTCCCGAATTACTGCTATCCGGAATGAGCCCTCTTGTCCCGAGTG	10159
452	-----SerThrArgGluMetLe-----	457
10160	GATTGCTACTCACCCATGCCAAGCCCGCGGCGAGATACGACAGTATTGTG-GACACTCG	10218
457	uTyrlsThrThrCysLeuValalaCysAspGluGlyTyArgLeuGluGly	474
10219	CTATCAGAGACGCTCTCTTTGGTGCAGAACACCTTTTAAGTTGGCTGGACAGACGG	10278
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10279	TCGTCACACAAATGGTTCTGTTTGGAGCCGATGTATCTGGACTTTGGAGATCTTG	10338
492	9CysValGluArgHisCysSerThrPheGlnMetProLysAsp-----	506
10339	CTGTGAGGACCTGTGTGCGAGGATCCGGGAAGACCGCGAGATGGTCCGCCAGATTGCACG	10398
507	-----ValIleIle-----	509
10399	CAGCTATGAGCAGACTCGAGGTGTATCTCGGCTGCAATGCTCGGCTACATCTCTGAT	10458
509	eSerProHisAen-----	513
10459	CAATCCGCGACCAATTCATGTCATACGCGAGCCAGAGTCAAGGTGATCAAGCCTTTGGG	10518
513	-----	513
10519	ATTAAATTCCGGCAGGATTCGGGATTCGGCTGCAATGCTCGAGCGACCCAAATTA	10578
514	-----CysGlyLysGln-----	517
10579	CGAGCCCAAGAACATCCGTCTCAACTCGGCCACTGCTGGTGGGACGAGGAGGCGCTT	10638
517	-----	517
10639	CACCTATGTGAGCGTGGATCTGGTCAGATCTATCGAGTCAAGGCGATTCGTGGAAGGG	10698
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10699	TGTGTTTACCAACGACATTTGGGAGGCCCAAGGAGATTCGGTCTTCTTCAACAACAGC	10758
518	-----ProAl-----	519
10759	TGAGAGCGAGAACTAGTGGTGTACTTCCCAATTTCAATCTGACCATCGAGATCCAGG	10818
519	alysPheGlyThrIleCysTyrValSer-----CysArgGlnGlyPheIleLe	535
10819	CAACTACGGCGAGCTGGCCATGATCACGCTGCCCAAGTTCGTGAGGAGCGCTGTTGAT	10878
535	uSerGlyValLys-----GluMetLeuArgCysThr	545
10879	CTTGGAAATAGTGAAGTACATAGCAACACCGCTGTCTGAAGTTGAGTTGATGGCTGCGA	10938
545	rThrSerGlyLys-----TirAenValGlyValIleAlaIalValCysLy	560
10939	GGAGCGGAACAGGAACCACTCTCGCTACGACTACGGCTAC-----TCCCGGTGGT	10992
560	aspValGluAlaProGlnIle-----AsnCysProLysAsp-----IleGluAlaLysThrLe	578

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Db 11053 TGAGAAATGGAGGAGTACTACCGGTAACTTCCAGCAACCCAGCGGGTGACCACTCCGG 11112
Qy 598 yGluLysValSerValHisValHisProAla-----PheThrProProTyrLeuPhePr 616
Db 11113 ATCGATTGCCCGCTGGAGATCAAGCCACACAGAACTCCGACACACCCAGCTACATTTTCAA 11172
Qy 616 olleGlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCy 636
Db 11173 G-----GATACGGTGTAAAGTACGGGCTTTGACTACGATGGCAATGTGGCCATCTG 11226
Qy 636 sIlePheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArgSerPr 656
Db 11227 CGAGATCAACATCAGCGTGCCGATGTAACACACCACTGCTGCAG---TGC----- 11275
Qy 656 oProProValGlnValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSe 676
Db 11276 -CCCGAGAGCTATGTGATTGAGCTAGTGATGCGCAGGACAGCTACACTGTGAACITCAA 11334
Qy 676 rAspAsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeu----- 694
Db 11335 CGATACCCGGAAGG-----ATCAAGACCTCCGACGACACAGGAGATGTGAGTT 11385
Qy 695 -----PheProGlnGlyGluThrIle-----ValGlnTyrTh 705
Db 11386 GCAGTTTCAGCCCGAGAGTGCACATCAAGATCGGAACTTCGAGAACGTGACCGTCAC 11445
Qy 705 rAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleLysGlySe 725
Db 11446 GGCAACGGATAAGTACACACACCGCGCGCTGCCACTTCAGGTCTCTGTGAAGGCTTC 11505
Qy 725 rProCys-----GluIleProPheThrProValAsnGlyAspPheIleCysThrPr 742
Db 11506 ACCCTGGTGGAGCTGGGAGCTCCAG---CCGCGCGGAAATGGTGCCATCAATGCTGCC 11562
Qy 742 oAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluG1 762
Db 11563 TGGTGATCGTGGTATCGAATGCAATGTCACGTGCAAGCCAGGATTCGGTTTCCCGACGG 11622
Qy 762 ySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysAspProThrTyrThrTh 782
Db 11623 CGAAACCACTGAAGACCTTCTCTCGGAGACATCATCGTCTGTGGGCTCCACGTCCTGGGT 11682
Qy 782 rGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLys---SerPheG1 801
Db 11683 G-----CCGAGCTGGTGTGGAGACACGAGACGCGCGCTTACCACGTGACCGCTC 11736
Qy 801 uMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAl 821
Db 11737 CATTACTACCGCGCAATGAGCAGTGGGCCAATCTCTGTGGTGTGATGAGGAGATGGGT 11796
Qy 821 aPheGluThrThrLeuGly-----LysMetValProSerPheCysSerAsp----- 836
Db 11797 GCTGGCACACCACTATGGCGAGCTCAACACGATGCTCTCGAGCGCTGCTCCGCGGTGAA 11856
Qy 837 -----AlaGluAspIleAspCysArgLeuGluGluAsnLeuTh 849
Db 11857 TGTCAACATGAATGTGACCTTTGTGAAGTCTGTGCCCATCTGCTGGAGGAGATGGGT 11916
Qy 849 rLysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPheAlaIleGlyProG1 869
Db 11917 CAAGATG----- 11923
Qy 869 yGlyTyrGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrValG1 889
Db 11924 -----GACTTCATCTCTCCAT-- 11941
Qy 889 nGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaProLe 909
Db 11942 -----CTGCCGCTGTGGTGCAGCGCGAGCTGTACGACCT 11976

Qy 909 uSerAspTyrLysIleLysLeuIlePheAsnIleThrAlaSerValProLeuProAspG1 929
Db 11977 GTGGCGCTCCACGCTGAACCTGATCTTTGATCTG-----AGTGTACCTATGCGAGTGC 12030
Qy 929 u---ArgAsnAspThrLeuGluTyrGluAsnGlnArgLeuLeuGlnThrLeuGluTh 948
Db 12031 CGTGATCGATGACCTTTTGAACATTCGCAACATCGTAACAGTGTCTCCGCTACGCGC 12090
Qy 948 rIleThrAsnLysLysArgThrLeuAsnLysAspProMetTyrSerPheGlnLeuAl 968
Db 12091 CCTCAAGTCGCAATCTCGGAGGATTTAACTGCAAT-----GT 12129
Qy 968 aSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysAlaSerProPheCy 988
Db 12130 GGGCGAGTACTCAACATGACACCGCATGTCCG----- 12166
Qy 988 sArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThrTyrTy 1008
Db 12167 -----CGTTGCTGCACCTGTCCCGCGCAACGTATGT 12198
Qy 1008 rAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAspGluGluG1 1028
Db 12199 GTCAGAGGGTTCAGAACAGCTGCACTACTGCCCGAGGGGCTTACTACCAAGAACCGTGACCG 12258
Qy 1028 yGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAs 1048
Db 12259 CAGGGAACTTCTGCTGCGTCCCGCGCGGAACTTACACAGAGGAGGCGCCACAGTC 12318
Qy 1048 nIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyrSerGlyLeuGluTh 1068
Db 12319 GCAGCGGACTGCATTCCTCCGCTCTGGGTATGCGACCTACTCACCCACCGGACTGTGCC 12378
Qy 1068 rCysGluSerCysProLeuGlyThrTyr-----GlnProLysPheGlySerArgSe 1085
Db 12379 GTGCTCGAGTGTCCGGTAACTCATTCCTGCGGAACCAACACCGGTGATTCAGGA 12438
Qy 1085 rCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValAsnIleSerAl 1105
Db 12439 TTGCAGCGCTGTCCGCGACAGACTTCCTACACCGCGCTGCTCGAACAGGATCT 12498
Qy 1105 aCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCysHisPr 1125
Db 12499 GTGTGGCGCCAGTGTGGCGCGGAGCTACTCCGCCACCGGACTGGCACCTGTCTGCC 12558
Qy 1125 oCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysProPh 1145
Db 12559 CTGCCCACTGCATCATTCACAGGAGCGCGGGTGGCGAGAGCTGCACACGAGTGTCCGAG 12618
Qy 1145 eTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSerSerPheSerSe 1165
Db 12619 TAACATGAGAACCCGNTTACCCGCTCCAGGGAGCGGACAGTGC----- 12664
Qy 1165 rThrPheSerAlaAlaGluGluSerValProProAlaSerLeuGlyHisIleLysLy 1185
Db 12665 -----AAGCGGTGGTA----- 12676
Qy 1185 sArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsnProCysHisAsnSe 1205
Db 12677 -----TGTGGTGAAGGTGCTTCCACGACGCG 12702
Qy 1205 rGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrThrG1 1225
Db 12703 CGAGCTGTGTGTCCTCCATGGCCATGATCCAGTGTCTTCTGTCCGCGCGGATCTCTGG 12762
Qy 1225 yLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsnGlyVa 1245
Db 12763 ACCTGCTGGGAAACAGGACATTCGACGAGTGGCGCTCCAGCGCTGTCTCAATATGGTGTCA 12822
Qy 1245 lCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGlyGlnAr 1265
Db 12823 GTGCAGAGTATTCGCGCAGGGCTATCGCTGTGAGTGGCGGCTGTGATCTCGGCGATCA 12882

[illegible]

QY 333 ----- 333
DB 32518 CTGGGGGTGGTCTGCGATGACCAACGATCTGACGGATGTGTCAAGGATTAAGCCAA 32459
QY 333 ----- 333
DB 32458 TCCGAGGGCACTGCGTGAATTCCGCATCTCGGAGCCACGCTCTCCATCTTAACCT 32399
QY 334 -----ProGly----- 335
DB 32398 GCCCTGCCATCGAAGCTCGCTATATTCGTTCCGCATCCAGGACTACGTGGGTGGCC 32339
QY 336 -----Gly-IleSerSerCys-----IleProCysProAspGluAsnHisTh 349
DB 32338 CTGCTCGCATGAGCTGATGGCTGACAGCGCTTGGATTGGTGACATCAACGAGTG 32279
QY 349 rSerProGlySerThrSerProGluAspCysVal----- 361
DB 32278 CAGCAAGAACATGGCGGTGTGACCAAGATGATCACTACCGGGCGGATTTGGCTG 32219
QY 362 ----CysArgGluGlyTyrArg----- 367
DB 32218 TGGCTGCAACACTGGCTACCGATGTACACTCCAAAGCGCAAGCTGGCTATCACATCGA 32159
QY 368 -----AlaSerGlyGln-----ThrCysGluLe 375
DB 32158 AGCTCCGAATCCGGCAAGCTGATGGTGACACTATACGCGCAACAAGACCTGTGTTC 32099
QY 375 uValHisCysProAlaLeuLysProProGluAsnGlyTyrPheIleGluAsnThrCysAs 395
DB 32098 TCTGTGTGTCGCGAATCGGAGCGCGCGGAGATGGTCAACTCTCGAGCGCAAGAAGCA 32039
QY 395 nAsnHisPheAsnAlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlyse 415
DB 32038 CTATCACTTTGGGATGTGGTGGCTTCCAGTGGCCACTTTTGGCTATCATCATGAGCGCAG 31979
QY 415 rSerIleIleLeuCysLeuProAsnGlyLeuTrpSerGlySer-----GluSerTyrC 433
DB 31978 CTGGGGCGCCCTGTGCTCTCCAGCGCTCAGTGGAGAGCGCCAGCTACCGGAGTGCATTTG 31919
QY 433 sArgValArgThr----- 437
DB 31918 TAGGTGTATACATTGAGATTCTCAATGAATTCCTCATTTTACTAACACGAATGTGCAC 31859
QY 437 ----- 437
DB 31858 TTTTCAGATGCCAAATGGCTTCCCTCGCCCGATGACAAAGTTGGAGGCTCTGACTGTGGCC 31799
QY 438 -----CysProHisLeuArgGln----- 443
DB 31798 CGCCCGATCCCGAATCCGTTCTAGTGGCCCTTCGGTGACAAATGACCAATTACGTGCGGA 31739
QY 443 ----- 443
DB 31738 TCCCCGGAGCGCACTGAGAGCCACGCTTCCTCTGGTTTCGGCGAGTCGGTGTAGGAT 31679
QY 444 -----ProlyHisGlyHisIleSerCys----- 451
DB 31678 CCAAGCCCGGTCTGCGCGATTAAGTCTACCGAATGCGAGCCCTCTTGTCCCGCGAGTG 31619
QY 452 -----SerThrArgGluMetLe 457
DB 31618 GATTGTCTACTACCCATGCCAAGCGCGCGCAGAAATACGGACAGTTTGTG-GACACTCG 31560
QY 457 uTyrLysThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGly----- 474
DB 31559 CTATCAGAGCGCTTCTCTTGGCTGCGCAAGACACTTAAAGTTGGCTGGACAGAGCGG 31500
QY 475 -----SerAspLysLeuThrCysGlnGlyAsnSerGlnTrpAspGlyProGluProAr 492
DB 31499 TCGTCACGACAATGTGTTGTGGAGCGGATGTATCTGGGACTTTGGAGATCTTCTG 31440

QY 492 gCysValGluArgHisCysSerThrPheGlnMetProLysAsp----- 506
DB 31439 CTGTGAGGAGACCTGTGTGCGAGGATCCGGGAAGACCCGGAGATGGTCCAGATTGCACG 31380
QY 507 -----ValIleI 509
DB 31379 CAGCTATGAGCAGAGCTCGGAGGTGTACTTTCGGCTGCAATCGTCTGGCTACATCTGAT 31320
QY 509 eSerProHisAsn----- 513
DB 31319 CAATCCGCGACCCATTACATGATACGCGAGCCAGAGTCAAGGTATCAAGCCTTTGGG 31260
QY 513 ----- 513
DB 31259 ATTAAGTTCCGGCAGGATTCGGATTCGGCCATCAATGCCACCTCGGAGCGACCAATTA 31200
QY 514 -----CysGlyLysGln----- 517
DB 31199 CGAGGCCAAGAACATCCGTCTCAACTCGGCCACTGGCTGTGGTGGCAAGCAGAGGCGCTT 31140
QY 517 ----- 517
DB 31139 CACTATGTGAGCGTGTATCTGGGTGATCTATGAGTCAAGCGGATTCGTGTGAAGGG 31080
QY 517 ----- 517
DB 31079 TGTGGTTACCAAGACATTTGTGGGCGGCCCAAGGATTCGGTTCTTCTACAACAAGC 31020
QY 518 -----ProAl 519
DB 31019 TGAGAGCGAGAACTACGTGTGTACTTCCCAATTTCAATCTGACCATCGAGATCCAGG 30960
QY 519 aLysPheGlyThrIleCysTyrValSer-----CysArgGlnGlyPheIleLe 535
DB 30959 CAACTAGCGGAGCTGGCCATGATCAGCTGCCCAAGTTGCGAGGCTCCCTTTGTGAT 30900
QY 535 uSerGlyValLys-----GluMetLeuArgCysTh 545
DB 30899 CCTTGAATAGTAGCTACATGACCAAGCGCTGTCTGAAGTTCGAGTTGATGGCTGCGA 30840
QY 545 rThrSerGlyLys-----TrpAsnValGlyValGlnAlaValCysLy 560
DB 30839 GGAGCGCAAGCAAGCAACCACTCTCGGTACGACTACGGCTAC-----TCCCGGTGGT 30786
QY 560 sAspValGluAlaProGlnIle-----AsnCysProLysAsp-----IleGluAlaLysThrLe 578
DB 30785 GGAACAAGCAACCACTCTCCAAATCTCCCGCAGCAACCAATTTGGTGGCGACGCGA 30726
QY 578 uGluGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGl 598
DB 30725 TGAGATGGAGGAGTACTACCGGTAACTTTCACGGAACCCACGCGGTGGACAACTCCGG 30666
QY 598 yGluLysValSerValHisValHisProAla-----PheThrProTyrLeuPhePr 616
DB 30665 ATCGATTCCCGCTCGAGATCAAGCCACAGAACTTCCGCACACCCAGCTACATTTCAA 30606
QY 616 oIleGlyAspValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCy 636
DB 30605 G-----GATACCGTTGTAAAGTACGTGGCTTTGACTACGATGGCAATGGCCATCTG 30552
QY 636 sIlePheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArgSerPr 656
DB 30551 CGAGATCAATCCGTCGCGCGATGTAAACACCACTCTCTGCG-----TGC----- 30503
QY 656 oProProValGlnValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSe 676
DB 30502 -CCCCAGAGCTATGTATTGAGCTAGTGGATCGCCAGGACAGCTACACTGTGAACACTTCAA 30444
QY 676 rAspAsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeu----- 694
DB 30443 CGATACCCGGAAGAG-----ATCAAGACCTCCGACGACACAGAGATGTAGGTT 30393
QY 695 -----PheProGlnGlyGluThrIle-----ValGlnTyrTh 705


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Db 30392 GCAGTTACGCCCGAGAGTCCCAACATCAAGATCGGAACCTTGGAGAACGTGACCTCCAC 30333
Qy 705 rAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIleValIleValGlySe 725
Db 30332 GCGAACGGATAAGATCAACAACCGCCGCTCCACATCTCCAGGTCTCTGTGAAGCTTC 30273
Qy 725 rProCys-----GluIleProPheThrProValAsnGlyAspPheIleCysThrPr 742
Db 30272 ACCCTGCGTGGAGTGGAGCTCAG---CCGCCGGGGAATGGTCCCATCAATTGCTCTGCC 30216
Qy 742 oAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGluGl 762
Db 30215 TGGTGATCGTGTATCGAATGATTCGCCAGCTGCAAGCCAGGATTCGGTTTACCAGCG 30156
Qy 762 ySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThrTyrThrTh 782
Db 30155 CGAACCACTGAAGACCTTCTCTCGGAGACATACAGTCTCTGTGGCGTCCACGCTCGTGT 30096
Qy 782 rGluTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLys---SerPheGl 801
Db 30095 G-----CCCGACTGCTGTGCGAGAACACGGAGCAGCGCGCTACCAGTGACCGCCTC 30042
Qy 801 uMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAl 821
Db 30041 CATTACCTACCGCGCAATGGAGCAGTGGCCCAATCTCTCTGGGTCACTACAGGAGT 29982
Qy 821 aPheGluThrThrLeuGly-----LysMetValProSerPheCysSerAsp----- 836
Db 29981 GCTGGCAGACCATATGGCGGACTCAACCGATGTCTTCGCAGCGTCTCGCCCGTGAA 29922
Qy 837 -----AlaGluAspIleAspCysArgLeuGluGluAsnLeuTh 849
Db 29921 TGTCAACATGAATGACCTTGTGAAGTCTGTGCCCATGCTGCTCGAGAGATGTGT 29862
Qy 849 rLysLysTyrCysLeuGluTyrAsnTyrAspTyrGluAsnGlyPheAlaIleGlyProGl 869
Db 29861 CAAGATG----- 29855
Qy 869 yGlyTrpGlyAlaAlaAsnArgLeuAspTyrSerTyrAspAspPheLeuAspThrValGl 889
Db 29854 -----GACTTCATCTCTCCATT-- 29837
Qy 889 nGluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaProLe 909
Db 29836 -----CTGCCCGCTGTGCGTACGCCAGCTGTACAGACT 29802
Qy 909 uSerAspTyrLysIleLysLeuIlePheAsnIleThrAlaSerValProLeuProAspGl 929
Db 29801 GTGCGGCTCCACGCTGAACCTGTATCTTGTATCTG-----AGTGATACCTATGCCAGTGC 29748
Qy 929 u---ArgAsnAspThrLeuGluTrpGluAsnGlnGlnArgLeuLeuGlnThrLeuGluTh 948
Db 29747 CGTGATCGATGATGACCTTTTGAACATTTGCCAACATCGGTAAACAGTGTCTCCGCTACGCG 29688
Qy 948 rIleThrAsnLysLeuLysArgThrLeuAsnLysAspProMetTyrSerPheGlnLeuAl 968
Db 29687 CTTCAAGTCGGAATCTCCGAGGATTTAATCTGCAAT-----GT 29649
Qy 968 aSerGluIleLeuIleAlaAspSerAsnSerLeuGluThrLysLysLysAlaSerProPheCy 988
Db 29648 GGGCGAGGTACTGAACTGACACACACCGAGCATGTGCGC----- 29612
Qy 988 sArgProGlySerValLeuArgGlyArgMetCysValAsnCysProLeuGlyThrTyrTy 1008
Db 29611 -----CGTTGCTGTGCACTGTCCCGCGCGGACGTATGT 29580
Qy 1008 rAsnLeuGluHisPheThrCysGluSerCysArgIleGlySerTyrGlnAspGluGluGl 1028
Db 29579 GTACAGGGTCAAGACAGCTGACCTACTGCGGAGGGGCTACTACAGAACCGTGACCG 29520
Qy 1028 yGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAs 1048
Db 1028 yGlnLeuGluCysLysLeuCysProSerGlyMetTyrThrGluTyrIleHisSerArgAs 1048
Db 29535 CGAGCAAAAGATCGATCTCTGCTATCGGAACCATGCAAGCATGGC---ACCTGCGTGA 28479
Qy 1048 nIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyrSerTyrSerGlyLeuGluTh 1068
Db 29459 GCAAGCGGACTGCATTTCCGCTGTGCGGTTATGCACTACTACCCACCGGACTGTGTC 29400
Qy 1068 rCysGluSerCysProLeuGlyThrTyr-----GlnProLysPheGlySerArgSe 1085
Db 29399 GTGCTTGGAGTGTCCGTAATCTATCTACTCGGAACCAACCAACCGTGGATTCAGGA 29340
Qy 1085 rCysLeuSerCysProGluAsnThrSerThrValLysArgGlyAlaValaAsnIleSerAl 1105
Db 29339 TTGCCAGCTGTGCGGCACAGAGCTTCACTACCAAGCCGCTGCTCGAACAGGATCT 29280
Qy 1105 aCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMetProCysHisPr 1125
Db 29279 GTGTGCGCCNAAGTGTGCGCCGGAACGTACTCCGCCACCGAGACTGGCACCTCTCGCC 29220
Qy 1125 oCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeuAlaCysProPh 1145
Db 29219 CTGCCCATCTGCATCATATCCAGGAGCCGCGGTGCGCAGAGCTGCAACGAGTGTCCGAG 29160
Qy 1145 eTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSerSerPheSerSe 1165
Db 29159 TAACATGAGAACCGATTACCCGCTTCAAGGAGCGCAACAGTGC----- 29114
Qy 1165 rThrPheSerAlaAlaGluGluSerValValProProAlaSerLeuGlyHisIleLysLy 1185
Db 29113 -----AAGCCGTGTGTA----- 29102
Qy 1185 sArgHisGluIleSerSerGlnValPheHisGluCysPheAsnProCysHisAsnSe 1205
Db 29101 -----TGTGTGAAGCTCTTCCACGACCG 29076
Qy 1205 rGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysProLeuGlyTyrThrGl 1225
Db 29075 CGGACTGTGTGTCGCCCATGAGCCATCATCATCCAGTGTCTTGTCTCGGCCGATCTCTCTGG 29016
Qy 1225 yLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeuAsnAsnGlyVa 1245
Db 29015 AGTCTGCTCGAACACAGACATCGACAGTGCCTTCCAGCCCTGTCTACATGTGTGTCA 28956
Qy 1245 lCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyrThrGlyGlnAr 1265
Db 28955 GTGCAAGATCTGCCCGCAGGGCTATCGTGTAGTGTCCCGCTGGTACTTCCGGGCATCAA 28896
Qy 1265 gCysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLysGlyIleCysVa 1285
Db 28895 TTGCCAGGAGGAGGCGCAGTGTGTGCAACGACACCTGTCTCGGCCAGGCCATGTGCAA 28836
Qy 1285 lAsp-----GlyValAlaGly----- 1290
Db 28835 GAACGAGCCGGGCTACAGAACGTGACCTGTCTGTGCGCGAGTGTGTACACCGCGCATCA 28776
Qy 1290 ----- 1290
Db 28775 GTGCGAGTGCACCATCGATCCGTGACGGCGAATGCAATCCGTGCGGAACCGAGCCAG 28716
Qy 1291 -----TyrArgCysThrCysValLysGlyPheValGlyLe 1302
Db 28715 CTGCCAGGCTTTGGAGCAGGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 28656
Qy 1302 uHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaValCy 1322
Db 28655 CCACTGTGAGCAGAAATATCAATGATCTTTCGGAAGAATCCCTGCTGTGTGTGTGTGTGTGT 28596
Qy 1322 sGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThrArgCy 1342
Db 28595 CACAGATCTGGTCAATGACTTCCAGTGGCGCTGTCCGCCAGGATTTACGGCGCAGCGATG 28536
Qy 1342 sGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLysAs 1362
Db 28535 CGAGCAAAAGATCGATCTCTGCTATCGGAACCATGCAAGCATGGC---ACCTGCGTGA 28479
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QY	1362	polyalaahenserpheargCysLeuCyalaalaglyPheThrThrGlySerHisCysGluLeu	1382	QY	1703	aaaspPheThrAlaGlySerThrValThrTyrGln	1715
DB	28478	TCGTCGTTCGATCAGGAGTGTGTTGGCCATCCGGCTGGACGGATCCGCTGGACAT	28419	DB	27752	GGAT-----TACTCGGGCATTTGGGTGTCAGTACGATACGCGATGCGAGGAGCATGT	27699
QY	1382	uasnlleangluCysGlnSerAsnProCysArganglnAlaThrCysValaspGluLeu	1402	QY	1716	-CysAasnanglyTyrTyrLeuLeuGlyAspSerArgMetPheCysThrAspAasnGlySe	1735
DB	28418	CAACATCAGCAGCTCGGAGAACCGACCCCTGCCCAATGAGGAACTCGCTGCATCGT	28359	DB	27698	CTGTCAAGATGGC-----GCCACTTGTGTGGACATGGTGC	27663
QY	1402	uasnseryrserCysLysCysGlnProGlyPheSerGlyGlnArgCysGlu-ThrGluG	1422	QY	1735	rTrpAanglyValserProserCys-----LeuAs	1745
DB	28358	CGACGGCTATAGTCAACTGTGAACCCCGCTACACGGCGCAAGATTGCCACACCAT	28299	DB	27662	T-----GGCTACAGCTGCCAGTCCACCTGGCTTTCACCGGTGGCAATTGGCAACAGGA	27609
QY	1422	InSerThrGlyPheAasnLeuaspPheGluValserGlyIleTyrGlyTyrValMetLeuA	1442	QY	1745	pValaspGluCysAlaValGlySerAspCysSerGluHisAlaserCysLeuAasnValas	1765
DB	28298	CGACGACTCGC-----	28288	DB	27608	CATCTGTCGATCAAGGACAACTCT---TGCCACCGGGCGCCACCTGGTGTGATCTAC	27552
QY	1442	spGlyMetLeuProSerLeuHisAlaLeuThrCys-----ThrPheTrpMetL	1458	QY	1765	polySeryrileCysSerCysValProProTyrThrGlyAspGlyLysAasnCysAlaG	1785
DB	28287	-----CCTCGAATCCCTGCCAGCAGCCGCGCCACTGTGTGGACCACTGGATGG	28239	DB	27551	CAACGGCTTCTACTGTGCTGTC-----CCCTTCAATATGACCGGAGACGATTGCCGCA	27498
QY	1458	ysSerSerAspAspMetAsnTyrGlyThrProIleSerTyrAlaValaspAasnGlySerA	1478	QY	1785	uProIleLys	1788
DB	28238	CTTTCAGTCGAATGCCCGCTGGTACTGTGGTCTCTCTCTCGC-----	28195	DB	27497	GGCCATCCAA	27488
QY	1478	spAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValaspGlyArgGluL	1498	RESULT 21			
DB	28194	-----AGGCCGA	28188	AC007977/c			
QY	1498	ysIleThrAsnCysProSerValaspGlyArgTyrPheHisIleAlaIleThrTrpT	1518	LOCUS			
DB	28187	GATCGACGAGTCTCGAGCGACCCCTGCATCCGGTGGCGCAGG-----	28144	DEFINITION			
QY	1518	hrSerAlaasnGlyIleTyrLysValTyrIleaspGlyLysLeuSeraspGlyGlyValag	1538	AC007977			
DB	28143	--AGCGCTCGCTCGATCTGGACAAAT-----TCGAGTGGTGTGGCG	28101	174287 bp			
QY	1538	lyLeuSer-ValGlyLeuProIleProGlyGly-----GlyAlaLeuVal	1552	Drosophila melanogaster			
DB	28100	GGACGATTCAAGGACCCCTGTGGCGCCAGCAGCATCGATGACTCGAGGGCGCGACCGCTG	28041	linear			
QY	1553	-Leu-----GlyGlnGluGlnAspLysGlyGlu-----GlyPheSerProal	1567	INV 05-APR-2001			
DB	28040	TCTGAACAACGCGATCTGTGGGATCGCTCGGTGGCTTTGAGTGGCTGGACCCAGG	27981	Drosophila melanogaster (fruit fly)			
QY	1567	aGluSerPheValGlySerIleSerGlnLeuAasnLeuTyrAspTyrValLeuSerProgl	1587	Eukaryota; Insecta; Pterygota;			
DB	27980	A-----TGAGTGGCATCGCTGGCGAGCA	27957	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
QY	1587	nGlnVallysserLeuAlaThrSerCysProGluGluLeuSerLysGlyAasnValLeuAl	1607	Ephydroidea; Drosophilidae; Drosophila.			
DB	27956	GCAGGTGACCACTGGCGAGCTCAGCGCGCTGCCAGAACGATGCCAGCTGCATCGACCT	27897	1 (bases 1 to 174287)			
QY	1607	atrPrpAappheLeuSerGlyIleValGlyLysVallySileAaspSerLysSerIleph	1627	2 (bases 1 to 174287)			
DB	27896	GTTCAGGACTAC-----TT	27882	Celniker, S.E., Aqbavani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,			
QY	1627	eCysSeraspCysProArgLeuGlyGlySerValProHisLeuArgThrAlaserGluAs	1647	Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,			
DB	27881	CTGCGTG---TGTCCAGC---GGACCATGGCAAGAACTCGAGACCGCTCCCGAA--	27830	Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,			
QY	1647	pleuLysProGlySerLysValaspLeuPheCysaspProGlyPheGlnLeuValGlyAs	1667	Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,			
DB	27829	-----CGCTGCATCGGTGA	27816	Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,			
QY	1667	nProValGlnTyrCysLeuasnGlnGlyClnTrpThrGlnProLeuProHisCysGluL	1686	Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,			
DB	27815	TCCT-----TGATGCAGCGGTGGCAAG-----TGCCAGGA	27796	Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,			
QY	1687	-----ArgIleSerCysGlyValProProLeuGluAasnGlyPheHisSerAl	1703	Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and			
DB	27785	CTTTCGCTCTGCTTAACTGCACTGTCCT-----GC	27753	Rubin, G.M.			
				Direct Submission			
				Submitted (06-JUL-1999)			
				Laboratory, MS 64-121, Berkeley, CA 94720, USA			
				On Apr 5, 2001 this sequence version replaced gi:6015173.			
				Sequence submitted by:			
				Berkeley Drosophila Genome Project			
				Lawrence Berkeley National Laboratory, MS 64-121			
				Berkeley, CA 94720			
				This sequence was assembled using end sequences from a whole genome			
				shotgun and from subclones of this BAC and its neighboring clones.			

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to bdg@fruitfly.berkeley.edu.

FEATURES

source
Location/Qualifiers
1. 174287
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/chromosome="2L"
/map="27C-27C"
/clone="BACR13J07 (D857)"
/clone_lib="pEC1-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in pBACE3.6)"
/notes="BACR13J07 (D857) was sequenced as a bridge. BACR13J07 extends from a minimal overlap with its distal neighbor DS01321 (D143) at bp 1 to BAC end at bp. 142,141."

ORIGIN

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Score: 1328.00 Matches: 518
Percent Similarity: 32.44% Conservative: 256
Best Local Similarity: 21.71% Mismatches: 718
Query Match: 13.00% Indels: 900
DB: 3 Gaps: 88

US-09-977-053-6 (1-1842) x AC007977 (1-174287)

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QY 20 ThrPheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAla 39
DB 90399 TCAATCTTGATCTTCTAGATGTTGGCCACATCTCGGCCGATGTC-CGGAGCTCCAA 90341
QY 40 ProGlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySer 59
DB 90340 CCGCGA-----ATTGAGCCTTGGCTCCAGTCGACACCGCTTGGGTACG 90293
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DB 90292 CTGGTCAGCTTTACATGTCCCATTTGGACGAGGTTTGCCACCGCGCAAGCGCACTGGTT 90233
QY 76 ArgGluLeuSerGluArgLeuGluLeuValPheLeuValAspSerSerValGly 95
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QY 362 ---CysArgGluGlyTyrArg----- 367

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Qy 437 ----- 437
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Drosophila melanogaster chromosome 2L section 24 of 83 of the
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AE003615.2 GI:22945803

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 270766)

Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galie,R.F.,
George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D.,
Wan,K.H., Doyle,C., Baxter,B.G., Helt,G., Nelson,C.R., Gabor,G.L.,
Abrill,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D.,
Ballwe,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,G.M.,
Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S.,
Borkova,D., Botchan,M.R., Bouck,J., Brokstein,P., Brotter,P.,
Burtis,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A.,
Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B.,
Davies,P.A., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I.,
Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S.,
Dunkov,B.C., Dunn,P., Durbin,K.J., Evganellista,C.C., Ferraz,C.,
Ferrier,S., Fleischmann,W., Fosler,C., Gabriellian,A.E., Garg,N.S.,
Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z.,
Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J.,
Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J.,
Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z.,
Kennisson,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Nushekern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Skupski,M.P., Smith,T., Spicer,B., Spradling,A.C., Turner,R.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinstock,G.M., Weissbach,J., Williams,S.M., Woodage,T.,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
Zhong,J.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,B.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)

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2 (bases 1 to 270766)

Celniker,S.E., Adams,M.D., Krommiller,B., Wan,K.H., Holt,R.A.,
Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y.,
Banzon,J., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Ferrier,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzales,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phonaneavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Tyler,D.,
Williams,S.M., Zaveri,J.S., Smith,H.O., Venter,J.C. and Rubin,G.M.
Sequencing of Drosophila melanogaster genome
Unpublished

3 (bases 1 to 270766)

AUTHORS

Misra, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L., Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochownik, S.E., Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W., de Celinkner, S., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de Grey, A.D.N.J., Harris, N.B., Kronmiller, B., Marshall, B., Millburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E., Shu, S., Smutnak, F., Whitfield, E.J., Ashburner, M., Gelbart, W.M., Rubin, G.M., Mungall, C.J., and Lewis, S.E.

Annotation of Drosophila melanogaster genome

JOURNAL

Unpublished

REFERENCE

4 (bases 1 to 270766)

AUTHORS

Adams, M.D., Celinkner, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.

TITLE

Direct Submission

JOURNAL

Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

REFERENCE

5 (bases 1 to 270766)

AUTHORS

PlayBase

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Direct Submission

JOURNAL

Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA

REFERENCE

6 (bases 1 to 270766)

AUTHORS

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CONSTRM

Direct Submission

JOURNAL

Submitted (23-JAN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA

COMMENT

On Sep 16, 2002 this sequence version replaced gi:2797167.

FEATURES

Location/Qualifiers

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/locus_tag="CG11321-RA"

/notes="CG11321 gene product from transcript CG11321-RA"

/codon_start=1
/product="CG11321-PA"

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Percent Similarity:	32.44%	Conservative:	256
Best Local Similarity:	21.71%	Mismatches:	718
Query Match:	13.00%	Indels:	900
DB:	3	Gaps:	88

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Qy	1265	sCysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLysGlyIleCysVa	1285	Qy	1567	aGluSerPheValGlySerIleSerGlnLeuAsnLeuTyrAspTyrValLeuSerProGl	1587
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Qy	1291	-----TyrArgCysThrCysValLysGlyPheValGlyLe	1302	Qy	1627	eCysSerAspCysProArgLeuGlyGlySerValProHisLeuArgThrAlaSerGluAs	1647
				Db	221092	CTGGGTG---TGTCACG---GGCACCGATGGCAAGAACTGCGAGACCGCTCGGAA--	221041

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 QY 1667 nProValGlnTyrCysLeuAsnGlnGlyGlnTrpThrGlnProLeuProHisCysGlu-- 1686
 Db 221026 TCCT-----TGCAATGACGGTGGCAAG-----TGCCAGGA 220997
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 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Ota, T., Sugiyama, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
 Primers for synthesizing full-length cDNA and their use
 Patent: EP 1074617-A 4587 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES
 Location/Qualifiers
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 Pred. No.: 1,41e-76 Length: 801
 Score: 1304.00 Matches: 247
 Percent Similarity: 91.18% Conservative: 1
 Best Local Similarity: 90.81% Mismatches: 16
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 QY 358 GluAspCysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHis 377
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 ACCESSION BD149744
 VERSION BD149744.1 GI:27855502
 KEYWORDS JP 2002191363-A/4587.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 801)
 Ota, T., Sugiyama, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
 Primers for synthesizing full-length cDNA and use thereof
 Patent: JP 2002191363-A 4587 09-JUL-2002;
 HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002191363-A/4587

PD 09-JUL-2002
PP 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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PT Location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.41e-76 Length: 801
Score: 1304.00 Matches: 247
Percent Similarity: 91.18% Conservative: 1
Best Local Similarity: 90.81% Mismatches: 16
Query Match: 12.76% Indels: 8
DB: Gaps: 0

US-09-977-053-6 (1-1842) x BD149744 (1-801)

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DB 61 AGCAGTTGATTCATGTCCTCCGATGAATACACCTCTCCACCTGGAAGCACATCCCT 120

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QY 478 LeuThrCysGlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGluArgHis 497
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QY 498 CysSerThrPheGlnMet-ProLysAspValIleIleSerProHisAsnCys-GlyLysG 517
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DEFINITION
Sequence 29 from Patent WO02055738.
AX540417
VERSION
AX540417.1 GI:25273450
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Panzer, S.R., Lincoln, S.E., Altus, C.M., Dufour, G.E., Hillman, J.L.,
Jones, A.L., Dam, T.C., Liu, T.F., Harris, B., Flores, V., Daffo, A.,
Marwaha, R., Chen, A.J., Chang, S.C., Gerstin, B.H., Peralta, C.H.,
David, M.H. and Lewis, S.A.
Molecules for disease detection and treatment
Patent: WO 02055738-A 29 18-JUL-2002;
Incyte Genomics, Inc. (US)
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US-09-977-053-6 (1-1842) x AX540417 (1-3262)

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QY 1650 ProGlySerLysValAsnLeuPheCysAspProGlyPheGlnLeuValGlyAsnProVal 1669
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QY 1670 GlnTyrCysLeuAsnGlnGlyGlnTrrThrGlnProLeuProHisCysGluArgIleSer 1689
DB 529 CAGTACTGTCTGAATCAGGACAGTGGACACCACTTCTCTCACTGTGAACGATTAGC 588

QY 1690 CysGlyValProProLeuGluAsnGlyPheHisSerAlaAspPheTyrAlaGly 1709


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Db 829 TATGTTTCATGTGTCCTCCACCGTACACAGAGATGGGAAAACTGTGCAGAACCTATAAAT 888
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Job time : 15424 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: May 9, 2004, 12:50:18 ; Search time 27508.5 Seconds
(without alignments)
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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Total number of hits satisfying chosen parameters: 6940544

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Listing first 100 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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3	19616	98.2	11152	6	AX686198 Sequence
4	19586	98.0	11158	6	AX686196 Sequence
5	16736	83.8	11289	10	AF206329 Mus muscu
6	16707	83.6	11230	6	AR435510 Sequence
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8	9400	47.1	5421	6	BD127949 Primer fo
9	9400	47.1	5421	6	AK075235 Homo sapi
10	8427	42.2	6153	6	AX350821 Sequence
11	8157	40.8	4701	9	BSX37918 Homo sapi
12	7537	37.7	5124	6	AX880905 Sequence
13	7537	37.7	5124	6	BD158659 Primer fo
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15	7486	37.5	4385	9	BSX38049 Homo sapi
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18	6950	34.8	4088	9	AK075234 Homo sapi
19	6693	33.5	3914	9	AL832416 Homo sapi
20	6218	31.1	194835	9	AL158158 Human DNA
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23	5086.5	25.5	152909	10	AL929406 Mouse DNA
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25	4776	23.9	3253	9	AK122605 Homo sapi
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67	1606.5	8.0	5420	9	HSCR1R	X05309 Human mRNA
68	1604.5	8.0	5420	6	AR364182	AR364182 Sequence
69	1465.5	7.3	109766	2	AC117712	AC117712 Mus muscu
70	1447	7.2	765	6	AX870332	AX870332 Sequence
71	1447	7.2	765	6	BD150394	BD150394 Primer fo
72	1443.5	7.2	18583	2	AC018297	AC018297 Drosophil
73	1443.5	7.2	148780	3	AC008326	AC008326 Drosophil
74	1443.5	7.2	174287	3	AC007977	AC007977 Drosophil
75	1443.5	7.2	270766	3	AE003615	AE003615 Drosophil
76	1379	6.9	3896	6	AX149475	AX149475 Sequence
77	1349	6.8	3905	6	AX149473	AX149473 Sequence
78	1341	6.7	706	6	AX677660	AX677660 Sequence
79	1304	6.5	801	6	AX869682	AX869682 Sequence
80	1304	6.5	801	6	BD149744	BD149744 Primer fo
81	1225.5	6.1	771	6	BD126501	BD126501 Primer fo
82	1217	6.1	4094	9	HUMEB2CR2	J03565 Human Epste
83	1209.5	6.1	3518	9	AK127129	AK127129 Homo sapi
84	1184	5.9	3934	6	AR380521	AR380521 Sequence
85	1184	5.9	3934	9	HUMEBVR	M26004 Human CR2/C
86	1182	5.9	8010	6	AX685959	AX685959 Sequence
87	1173.5	5.9	728	6	BD125275	BD125275 Primer fo
88	1173.5	5.9	728	6	BD126535	BD126535 Primer fo
89	1170.5	5.9	3923	6	AX774975	AX774975 Sequence
90	1170.5	5.9	3923	9	HSBLCR2	Y00649 Human mRNA
91	1126.5	5.6	3187	10	MUSCR2B	M61132 Mouse compl
92	1124.5	5.6	3220	10	MUSCR2AA	M35684 Murine comp
93	1124.5	5.6	5463	9	AB067471	AB067471 Homo sapi
94	1117.5	5.6	251269	2	AC145193	AC145193 Gallus ga
95	1114.5	5.6	4020	4	AF038131	AF038131 Ovis arie
96	1086.5	5.4	761	6	BD125309	BD125309 Primer fo
97	1060	5.3	594	6	BD125308	BD125308 Primer fo
98	1059	5.3	4849	3	AK113070	AK113070 Ciona int
99	1058.5	5.3	6004	6	AX537467	AX537467 Sequence
100	1045.5	5.2	4003	4	SSC278470	AJ278470 Sus scrof

ALIGNMENTS

RESULT 1

AR435509

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1 (bases 1 to 10878)
Welcher,A.A. and Elliott,G.S.
C3b/c4b complement receptor-like molecules and uses thereof
Patent: US 6656707-A 1 02-DEC-2003;
Location/Qualifiers
1..10878
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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Alignment Scores:

Pred. No.: 0 Length: 10878
Score: 19958.00 Matches: 3566
Percent Similarity: 99.94% Conservative: 3
Best Local Similarity: 99.88% Mismatches: 2
Query Match: 99.92% Indels: 0
DB: 6 Gaps: 0

US-09-977-053-4 (1-3571) x AR435509 (1-10878)

Qy	1	MetTTPProAqLeuAlaPheCysCysTTPGlyLeuAlaLeuValSerGlyTTPAlaThr	20
Db	11	AVGTGGCCCTGGCTGGCCCTTTTGTGCTGGGCTGGCGCTGGTTCGGGCTGGGGAGC	70
Qy	21	PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro	40
Db	71	TTTCAGCAGATGTCCTCCGTGGCGCAATTTACGCTTCGGCTCTTCCCGAGACGGGCC	130
Qy	41	GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg	60
Db	131	GGGGCCCCGGGAGTATCCCCGGCGCCGCTCTTGGCGAGCAGAGCGCGGGAGCAGA	190
Qy	61	ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu	80
Db	191	GTGGAGCGGCTGGGCGCGCGGTTCCGGCGACCGCTGCTGGGAGCTCAGCGAG	250
Qy	81	ArgLeuGluLeuValPheLeuValAspSerSerSerValGlyGluValAsnPheArg	100
Db	251	CGCTGGAGCTGTGCTTCTGTGTGATGNTTGTCCAGGTGGCGGAGTCACTTCGCG	310
Qy	101	SerGluLeuMetPheValArgLysLeuSerAspPheProValValProThrAlaThr	120
Db	311	AGCGAGCTCATGTTGTCGTCGCAAGCTGCTGTCGAGCTTCCCGTGGTGGCCAGCG	370
Qy	121	ArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIle	140
Db	371	CGCTGGCGCATCGTGACCTTCTGTCGAAGAATAGTGTGGCGCGCTCGATTACATC	430
Qy	141	SerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnIleProAlaIle	160
Db	431	TCCACCGCGCGCGCGCGCAGCACAAGTGGCGCTCTCTCCAGAGATCCCTGCGCATC	490
Qy	161	SerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaGlnIleLeu	180
Db	491	TCCTACCGAGGTGGCGGCACCTACACCAAGGCGCTTCCAGCAAGCGCGCAATTCYT	550
Qy	181	LeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn	200
Db	551	CTTCATGCTAGAGAAAACCTCAACAAAAGTTGTATTTCATCACTGATGATATTCAT	610
Qy	201	GlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThr	220
Db	611	GGGGGAGACCCCTAGACCAATTCAGCGTCACTGCGAGATTTCAGGAGTGAGATCTTCACT	670
Qy	221	PheGlyIleTTPGlnGlnIleArgGluLeuAsnAspMetAlaSerThrProLysGlu	240
Db	671	TTTGGCAATGCGAAGGGAACATTCAGAGCTGAATGACATGGCTTCCACCCCAAGGAG	730
Qy	241	GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeu	260
Db	731	GAGCATGTGTACCTGCTACACAGTTTTCAGAAATTTGAGGCTTTAGCTCGCGGGCATG	790
Qy	261	HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu	280
Db	791	CATGAAGATCTACCTCTGGGAGTTTATTCAAGATGATATGTCCTCACTCTTATCTT	850
Qy	281	CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr	300
Db	851	TGTGATGAAGGCAAGGACTGCTGTGACCGAATGGGAAGCTGCAATGTGGGACACACA	910
Qy	301	GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys	320

Db 911 GGCCATTTTTCAGTGCATCTCTGAAAGGGGTATTACGGGAAAGGTCTTCAGTATGAATGC 970
Qy 321 ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlySerSerCys 340
Db 971 ACAGCTTGGCCATCGGGGACATACAAACCTGAAAGGCTCACAGGAGGAATCAGCAGTGC 1030
Qy 341 IleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAspCys 360
Db 1031 ATTCCATGCTCTGATGAAATATCACTCTCCACCTGGAAAGCAATCCCTCGAAGACTGT 1090
Qy 361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
Db 1091 GTCTGCAGAGAGGATACAGGGCATCTGGCCAGACCTGTGAACTTGTCCACTGCCCTGCC 1150
Qy 381 LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla 400
Db 1151 CTGAAGCCTCCCGAAATGTTACTTTATCCAAACACATTCGAACCAACCACTTCAATGCA 1210
Qy 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCys 420
Db 1211 GCCTGTGGGGTCCGATGTACCCCTGGATTTGATCTTGTGGGAAGCAGCATCATCTTATGT 1270
Qy 421 LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
Db 1271 CTACCCCAATGGTTTGTGTCGGTTCCAGAGACTACTGCAGAGTAAGAACATCTCTCAT 1330
Qy 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
Db 1331 CTCCCGCAGCCGAAACATGSCCACCATCAGCTGTTCTACAGGGGAAATGTTATATAAGACA 1390
Qy 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
Db 1391 ACATGTTTGGTTCCTCTGTGATGAAGGTACAGACTAGAGGCGAGTGAAGCTTACTTGT 1450
Qy 481 GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr 500
Db 1451 CAAGGAAACAGCCAGTGGGATGGCCAGAACCCCGGTGTGTGGAGCGCACTGTTCACC 1510
Qy 501 PheGlnMetProLysAspValIleSerProHisAsnCysGlyLysGlnProAlaLys 520
Db 1511 TTTTCAGATGCCAAAGATATCATCATATCCCCCACAACTGTGGCAGCAGCCAGCCNAA 1570
Qy 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
Db 1571 TTTGGAGCATCTGCTATGTAAGTTCGCCCAAGGGTTCATTTTATCTGGAGTCAAGAA 1630
Qy 541 MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaValCysLys 560
Db 1631 ATGCTGAGATGTACCACTCTCGAAATGGAATGTCCGAGTTCAGGCAGCTGTGTGTAAA 1690
Qy 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln 580
Db 1691 GAGCTGGAGGCTCTCCAAATCACTGTCTCTAAGGACATAGAGGCTAAGACTCTGTGAACAG 1750
Qy 581 GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys 600
Db 1751 CAAGATCTCGCCAAATGTATCTGGGAGATTCACAGCTAAAGACAACTCTGTGTGAAAG 1810
Qy 601 ValSerValHisValHisProAlaPheThrProTyrLeuPheProIleGlyAspVal 620
Db 1811 GTGTCACTCCAGCTTCATCCAGCTTTCACCCCACTTACCTTTTCCAGTTGGAGATGT 1870
Qy 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
Db 1871 GCTATCGTATACAGGCAACTGACCTATCCGGCAACAGCCAGCCAGCTGCAATTTTCCATATC 1930
Qy 641 LysValIleAspAlaGluProProValIleAspTrpCysArgSerProProValGln 660
Db 1931 AAGGTTATTGATGCAGAACCACTGTCTATAGACTGTGTGAGATCTCCACTCCCTCCAG 1990
Qy 661 ValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGly 680
Db 1991 GTCTCGAGAGGTATACGCGCAAGCTGGATGAGCCTCAGTTCTCAGACAACTCAGGG 2050

Qy 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyLysThr 700
Db 2051 GCTGAATTTGTCTCATACCAGAGTATACACAAAGGAGACCTTTTCCCTCAAGGGAGACT 2110
Qy 701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
Db 2111 ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATAACAGGACATGTGATATCCATAT 2170
Qy 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
Db 2171 GTCATAAAGGTTCTCCCTGTGAAATTCATTCACCTGTAAATGGGATTTTATATGC 2230
Qy 741 ThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
Db 2231 ACTCCAGATTAATACTGGAGTCAACTGTACATTAACCTTGTGGAGGGCTATGATTTTACA 2290
Qy 761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTrpLysProThrTyr 780
Db 2291 GAAGGCTTACTGACAAAGTATTAATGTGCTTATGAGATGGCGTCTGGAAACCAACATAT 2350
Qy 781 ThrThrGluTrpProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPhe 800
Db 2351 ACCACTGAATGGCCAGACTGTGCCAAAAACGTTTGTCTAAACCAACGGGTTCAAGTCTCTT 2410
Qy 801 GluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGlu 820
Db 2411 GAGATGTTCTACAAAGCAGCTCGTTGTGATGACACAGATCTGTATGAAGAGTTCGTGAA 2470
Qy 821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
Db 2471 GCATTTGAGAGCACCCTGGGAAATGTTGCCATCATTTTGTAGTGATGACAGAGACATT 2530
Qy 841 AspCysArgLeuGluGluAsnLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyr 860
Db 2531 GACTGCAGACTGGGAGGAGAACTGACCAAAAAATATTTCCTAGAAATAATAATTATGACTAT 2590
Qy 861 GluAsnGlyPheAlaIleGlyProGlyTyrGlyValAlaAlaAsnArgLeuAspTyrSer 880
Db 2591 GAAAAAGCTTTGCAATTTGACCAAGTGGCTGGGTGCGTACGTAATAGCTGGATACTCT 2650
Qy 881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSer 900
Db 2651 TAGCATGACTTCTCTGCACACTGTGCAAGAAACAGCCACAGCATCGGCAATGCCAAGTCC 2710
Qy 901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsnIle 920
Db 2711 TCACGGATTAAGAAAGTGCCTCATTTATCTGACTATATAAATAAAGTTTAAATTTTAAACATC 2770
Qy 921 ThrAlaSerValProLeuProAspGluArgAsnAspThrLeuGluTrpGluAsnGlnGln 940
Db 2771 ACAGCTAGTGTGCTATACCCGATGAAGAAATGATACCTTTGAAATGGGAAATCAGCNA 2830
Qy 941 ArgLeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAsp 960
Db 2831 CGACTCTTCAGACATTTGAAACTATCACAAATAAATGAAAGAGGACTCTCAACAAAGAC 2890
Qy 961 ProMetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGlu 980
Db 2891 CCCATGTATTCTCTTCAGCTTGCATCAGAAATAATCTATAGCCGACAGCAATTTCAATTAGA 2950
Qy 981 ThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysVal 1000
Db 2951 ACAAAAGAGCTTTCCCTCTTCGACACAGGCTCAGTGTGAGAGGGCGCTATGTGTGTC 3010
Qy 1001 AsnCysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIle 1020
Db 3011 AATTGCCCTTTGGAACTTATTAATCTCGAACATTTTACCTGTGAAAGCTGCGGATC 3070
Qy 1021 GlySerTyrGlnAspGluGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyr 1040
Db 3071 GGATCTCTATCAAGTGAAGAGGCAACTTGGAGTGCAGCTTTTGCCTCTCTGGATGTAC 3130

Qy 1041 ThrGluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThr 1060
Db 3131 ACGGAATATATCCATTCAGAAACATCTCTGATTGTAAGCTCAGTGTAACAGGCACC 3190
Qy 1061 TyrSerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLys 1080
Db 3191 TACTCATACATGAGCTTGAAGCTTGTGAATCGTGTCACCTGGGCACTTATCAGCCAAA 3250
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Db 3311 GTGAACATTTCTGCATGTGAGTTCCTGTGTGTCAGAAAGGAAATTCCTGCGTTCTGGTTA 3370
Qy 1121 MetProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCys 1140
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Db 3431 CTGGCTCTCTCTTTATGGAATACCCCATTCGCTGTTCCAGATCCATCACGAATGT 3490
Qy 1161 SerSerPheSerThrPheSerAlaAlaGluGluSerValValProProAlaSerLeu 1180
Db 3491 TCAAGTTTTAGTTCAACTTTCTCAGCGGCAGAGGAAAGTGTGTGCTCCCTCTCTT 3550
Qy 1181 GlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePheAsn 1200
Db 3551 GGAATATATAAAGAGGACATGAATACAGCATGAGTTCAGTTTTCATGAATGCTTCTTTAAC 3610
Qy 1201 ProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCysPro 1220
Db 3611 CCTTCCACATAGTGGAACTGCCAGCACTTGGCGTGTATGTTGTCTCTGTCCA 3670
Qy 1221 LeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCys 1240
Db 3671 CTTGGATATACAGGCTTAAAGTGTGAACACAGACATCGATGATGTCAGCCACCTGCTTGC 3730
Qy 1241 LeuAsnAsnGlyValCysLysAspLeuValGlyLupheIleCysGluCysProSerGly 1260
Db 3731 CTCACATAGTGGATTTGTAAAGACTAGTGTGGGAATTCATTTGTGAGTGCCCATCAGGT 3790
Qy 1261 TyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeuAsn 1280
Db 3791 TACACAGTTCAGCGGTGTGAAGAAAAATATAAATCAGTGTAGCTCCAGTCTCTGTTAAAT 3850
Qy 1281 LysGlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheVal 1300
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Qy 1321 ValCysGluAspGlnValGlyGlyPheLeuCysLysCysProProGlyPheLeuGlyThr 1340
Db 3971 GTCTGTGAAGACCAAGTTGGGGATTCCTGTGCAAAATGCCACCTGGATTTTGGGTACC 4030
Qy 1341 ArgCysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCys 1360
Db 4031 CGATGTGAAGAGACGTCATGAGTGTCTCAGTCAGCCATGCAAAAATGGAGCTACCTGT 4090
Qy 1361 LysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHisCys 1380
Db 4091 AAAGCGGTGCATAGCTTTCAGTTCCTGTGTGAGCTGCTGAGCTGCTCACAGGATCACACTGT 4150
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Db 4151 GAATTGAACATCAATGAATGTCACTTAATCCATGTAGAAATCAGGCCACCTGTGTGGAT 4210
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Db 4211 GAATTAAATTCATACAGTTGTAAATGTCCAGCAGGATTTTCAGGCAAAAGGTGTGAACA 4270
Qy 1421 GluGlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMet 1440
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Qy 1441 LeuAspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheTrpMetLysSerSer 1460
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Qy 1461 AspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsnThr 1480
Db 4391 GACGACATGAATATGGAACACCAATCTCTATGCAAGTTGATAACGGCAGCAGCAATACC 4450
Qy 1481 LeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAsnGlyValArgGluLysIleThr 1500
Db 4451 TTGCTCTCAGCTGATTAACGGCTGGGTCTTTATGTGAATGGCAGGGAAGAATATACA 4510
Qy 1501 AsnCysProSerValAsnAspGlyValArgTrpHisIleAlaIleThrTrpThrSerAla 1520
Db 4511 AACTGTCTCCGTGGAATGATGGCAGATGGCATCATATTGCAATCACTTGGACAAGTGCC 4570
Qy 1521 AsnGlyIleTyrLysValTyrIleAspGlyLysLeuSerAspGlyGlyAlaGlyLeuSer 1540
Db 4571 AATGGCATCTGGAAAGTCTATATCGATGGGAAATTTATCTGACGGTGGTCTGCTCTCT 4630
Qy 1541 ValGlyLeuProIleProGlyGlyAlaLeuValLeuGlyGlnGluAspLysLys 1560
Db 4631 GTTGGTTGGCCCATCTCTGTTGGTGGTGGTGTCTTCTGGGGCAGAGCAGCAAAAAA 4690
Qy 1561 GlyGluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrp 1580
Db 4691 GGAGAGGGAATTCAGCCACAGCTGAGTCTTTTGTGGGCTCCATAAGCCAGCTCAACTCTGG 4750
Qy 1581 AspTyrValLeuSerProGlnGlnValLysSerLeuAlaThrSerCysProGluLeu 1600
Db 4751 GACTATGTCTCTTCCACAGCAGGTGAAGTCACTGGCTACTCTCTGCCAGAGAACTC 4810
Qy 1601 SerLysGlyAsnValLeuAlaTrpProAspPheLeuSerGlyIleValGlyLysValLys 1620
Db 4811 AGTAAGGAACAGTGTAGCATGGCTGATTTCTTGTTCAGGAATTTGTGGGAAGTGAAG 4870
Qy 1621 IleAspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHis 1640
Db 4871 ATCGATTTAAGACATATTTTGTCTGATTTGCCACGCTTAGGAGGCTCAGTGGCTCAT 4930
Qy 1641 LeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspPro 1660
Db 4931 CTGAGAACTGCATCTGAAGATTTAAAGCCAGGTTCCAAAGTCAATCTGTTCTGTATCCA 4990
Qy 1661 GlyPheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTrpThrGln 1680
Db 4991 GECTTCAGCTGGTGGGAACCCCTGTGTCAGTACTGTCTGTAATCAAGGACAGTGGACAAA 5050
Qy 1681 ProLeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPhe 1700
Db 5051 CCATCTCTCATCTGGAACGCAATTAGCTGTGGGGTGGCCACCTCTCTTGGAGAAATGGCTTC 5110
Qy 1701 HisSerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyr 1720
Db 5111 CATTCAGCCGATGATCTTATGCTGGCAGCAAGTACCTACCACTGACGACACATGGCTAC 5170
Qy 1721 TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSer 1740
Db 5171 TATCTATTGGGTGACTCAAGGATGTTCTGTACAGATAATGGAGCTGGAAACGGCGTTTCA 5230
Qy 1741 ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer 1760
Db 5231 CCATCTCTCTGATGTGATGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGAT 5290
Qy 1761 CysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGly 1780

Db 5291 TGCTGAACGTAGATGATCTACATATGTTTCATGTGTCCACCGTACACAGGATGGG 5350
Qy 1781 LysAsnCyAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer 1800
Db 5351 AAAAACTGTGCAGAACCTATAAAATGTAAGGCTCCAGGAAATCCGAAAAATGCCACTCC 5410
Qy 1801 SerGlyGluIleThrValGlyAlaAlaValThrPheSerCysGlnGluGlyThrGln 1820
Db 5411 TCAGGTGAGATTTATACAGTAGTAGTGCGAAGTCACATTTTCGTGTGAGGAGGATACACAG 5470
Qy 1821 LeuMetGlyValThrLysIleThrCysLeuGluSerGlyLysTrpAsnHisLeuIlePro 1840
Db 5471 TTGATGGAGTACCAAAATACATGTTTGGAGTCTGGAGATGGAATCATCTAATACCA 5530
Qy 1841 TyrCysLysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGlu 1860
Db 5531 TATTTGTAAGAGCTGTTTCATGTGTTAAACCGGCTATTTCGAAAAATGGTTGCAATTGAGGAG 5590
Qy 1861 LeuAlaPheThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAla 1880
Db 5591 TTAGCATTTTACTTTTGGCAGCAAGTGACATATAGGTGTATTAAGGATATATCTTGACC 5650
Qy 1881 GlyAspLysGluSerCysLeuAlaAsnSerSerTrpSerHisSerProProValCys 1900
Db 5651 GGTGATAAAGATCATCTCTGTGTCTGTAAACAGTTCTTGAGTCAATCCCTCCCTGTGTGT 5710
Qy 1901 GluProValLysCysSerSerProGluAsnIleAsnAsnGlyLysTyrIleLeuSerGly 1920
Db 5711 GAACCAAGTGAAGTGTCTAGTCCGAAAAATATAAATAATCGAAAAATATATTTTGAGTGGG 5770
Qy 1921 LeuThrTyrLeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuGlnGlyPro 1940
Db 5771 CTTACCTACTTCTTACTGATCATATATTCATGCGATACAGATACAGCTTACAGGCGCCCT 5830
Qy 1941 SerIleIleGluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeu 1960
Db 5831 TCCATTATTGAATGATCAAGGCTCTGCGCATCTGGCAGACAGCGCCACCTGCTGTCTACCTC 5890
Qy 1961 ValPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThr 1980
Db 5891 GTCTCTGTGGAGAACCCCTGCGCATCAAGATGCTGTCAATACGGGGAATACTTCAC 5950
Qy 1981 PheArgAsnThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThr 2000
Db 5951 TTCAGGACACCTGCTACTTACACTTGCATAAGAGGCTATACTCTTCTGCTGTGACACC 6010
Qy 2001 IleGluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnGlnCysLeuAlaValSer 2020
Db 6011 ATTGAATGCTGGCCGACGCAAGTGGAGTAGAAGTAGACCAAGTGCCTGGCTGTCTCC 6070
Qy 2021 CysAspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGly 2040
Db 6071 TGTGATGAGCCACCAATTTGGACCAACGCTCTCCAGAGACTGCCCATCGGCTCTTTTGA 6130
Qy 2041 AspiLeaAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAsnAsnSerGlnLeuLeu 2060
Db 6131 GACATTTGCAATTTCTACTTACTTCTGTGTTACGCTTACGCTACGACAAATTTCCAGCTTCTC 6190
Qy 2061 CysAsnAlaGlnGlyLysTrpValProProGluGlyGlnAspMetProArgCysIleAla 2080
Db 6191 TGCATGTCCCGCCAGGAGTGGGTACCCCGACAGAGGTCAAGACATGCCCTGGTGTATAGCT 6250
Qy 2081 HisPheCysGluLysProProSerValSerTyrSerIleLeuGluSerValSerLysAla 2100
Db 6251 CATTTCTGTGAAAAACCTCCATCGGTTTCTATAGCATCTTGGAAATCTGTGAGCAAGCA 6310
Qy 2101 LysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThr 2120
Db 6311 AAATTTGCAAGCTGGCTCAGTTGTGAGCTTTAATGATGATGAGGCTTTGTACTGACACC 6370
Qy 2121 SerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGln 2140
Db 6371 TCAGCAAGATTTGAATGTATGAGAGGTGGGAGTGGAAACCTTTCCCCCATGTCTCATCCAG 6430

Qy 2141 CysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySer 2160
Db 6431 TGCATCCCTGTGCGGTGTGGAGAGCCACCAAGCATCATGAATGGCTATGCAAGTGGATCA 6490
Qy 2161 AsnTyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGly 2180
Db 6491 AACTACAGTTTTTGGAGCCATGGTGGCTTACAGCTGCAACCAAGGGTCTTACATCAAGGG 6550
Qy 2181 GluLysLysSerThrCysGluAlaIleThrGlyGlnTrpSerSerProIleProThrCysHis 2200
Db 6551 GAAAGAGAGACGACCTGCGAAGCCACAGGCGAGTGGAGTAGTCTCTATACCGACGTGCCAC 6610
Qy 2201 ProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrThrGly 2220
Db 6611 CCGTATCTTTGTGGTGAACCACTTAAGGTTGAGATGGCTTTCTGAGAGCATACAACTGGC 6670
Qy 2221 ArgIlePheGluSerGluValArgTyrGlnCysAsnProGlyTyrLysSerValGlySer 2240
Db 6671 AGCATCTTTGAGAGTGAAGTGAGGTATCACTGTAAACCGGGCTATAAGTCAGTCGGAAGT 6730
Qy 2241 ProValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysVal 2260
Db 6731 CCTGTATTTGTGTGCCAAGCAATCGCCACTGGCACAGTGAATCCCTCTGTATGTGTGT 6790
Qy 2261 ProLeuAspCysGlyLysProProIleGluAsnGlyPheMetLysGlyGluAsnPhe 2280
Db 6791 CCTCTGACGTGTGGAACCTCCCGCATCGAGATGGCTTCATGAAGGAGAAACTTT 6850
Qy 2281 GluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSer 2300
Db 6851 GAAGTAGGTTCCAAAGGTTCAAGTTTTCTGTAAAGAGGTTATGAGCTGTGGTGACAGT 6910
Qy 2301 SerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetPro 2320
Db 6911 TCTTGGACATGTGCAGAAATCTGGCAAATGGAATAAGAAAGTCAATCCAAAGTGCATGCT 6970
Qy 2321 AlaLysCysProGluProProLeuLeuGluAsnGlnLeuValLeuLysGluLeuThrThr 2340
Db 6971 GCCAGTGGCCAGAGCGCCCTCTTGGAAAAACAGCTAGTATTAAGGAGTTGACCAACC 7030
Qy 2341 GluValGlyValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerVal 2360
Db 7031 GAGGTAGGAGTTGTGACATTTCTCTGTAAAGAGGCGATGCTCTGCAAGGCCCTCTGTCT 7090
Qy 2361 LeuLysCysLeuProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeu 2380
Db 7091 CTGAAATGCTGTGCCATCCAGCAATGGAATGACTCTTTCTCTGTTGTGAAGATTGTCTT 7150
Qy 2381 CysThrProProProLeuIleSerPheGlyValProIleProSerSerAlaLeuHisPhe 2400
Db 7151 TGTACCCCACTCCCTAATTTCTTTGGTGTCCCATCTCTCTCTCTCTCTCTCTCTCT 7210
Qy 2401 GlySerThrValLysTyrSerCysValGlyPhePheLeuArgGlyAsnSerThrThr 2420
Db 7211 GGAAGTACTGTCAAGTATCTCTGTGTAGTGGGTTTTTCTTAAGAGAAATTTTACCACC 7270
Qy 2421 LeuCysGlnProAspGlyThrTrpSerSerProLeuProGluCysValProValGluCys 2440
Db 7271 CTCTGCCAACCTCTGATGGCACCCTGCCAGCTGCCAGATGTGTTCAGTAGAATGT 7330
Qy 2441 ProGlnProGluGluIleProAsnGlyIleIleAspValGlnGlyLeuAlaTyrLeuSer 2460
Db 7331 CCCCACTGTAGGAATCCCAATGGAATCTTGTGTGAGGCTTGTGCTATCTCAGC 7390
Qy 2461 ThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCys 2480
Db 7391 ACAGCTCTCTATACCTGCAAGCCAGGCTTTGAATTTGTGGGAAATCTACCCACCCTTGT 7450
Qy 2481 GlyLysGlnGlyHisTrpLeuGlyLysProThrCysLysAlaIleGluCysLeuLys 2500
Db 7451 GGAGAAAAATGTCATGCTGTGGAGGAAAAACCAACATGTAAGGCCATTGATGCTGCTGAAA 7510

QY	2501	ProLysGluIleLeuAsnGlyLysPheSerThrAspLeuHisThrGlyGlnThrVal	2520	DB	8591	GAAGGGTCTTCTGCTTGGAGGAGCCAGGAGTGGGGTCTTGTCTTCCCAATGGAAGTTGGAGT	8650
DB	7511	CCCAAGGAGATTTTGAATGGCAAAATCTCTTACACGGACCTACACTATGGACAGACCGTT	7570	QY	2881	GlyAlaThrProAspCysValProValArgCysAlaThrProGlnLeuAlaAsnGly	2900
QY	2521	ThrTyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGlu	2540	DB	8651	GGAGCCACTCCCGACTGTGTGCTGTGCAGATGTGCCACCCGCCCACTGGCCATGGG	8710
DB	7571	ACCTACTCTTGCAACCGAGGCTTTGGCTCGAAGGTCCAGTGCCTTGACCTTGTTAGAG	7630	QY	2901	ValThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGluGly	2920
QY	2541	ThrGlyAspTyrAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGln	2560	DB	8711	GTGACGGAAGGCTGGACTATGGCTTCATGAAGGAAGTAACATTCCTCATGTCTATGAGGC	8770
DB	7631	ACAGGTGATGGATGTAGATGCCCATCTTGCAATGCCATCCACTGTGTATCCCCACAA	7690	QY	2921	TyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGlyAsnTyrAspAlaGlu	2940
QY	2561	ProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIleIleTyr	2580	DB	8771	TACATCTTGGACGGTGTCCAAACTCACTGTCACTGAGTCAGATGGCAACTGGGATGCAGAG	8830
DB	7691	CCCATTTGAAAATGGTTTGTAGAGGTGCAGATTACAGCTATGGTGCCATATCATCTAC	7750	QY	2941	IleProLeuCysLysProValAsnCysGlyProProGluAspLeuAlaHisGlyPhePro	2960
QY	2581	SerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGly	2600	DB	8831	ATTCTCTCTGTAAACCACTCAACTGTGGACCTCTCTGAAGATCTTGCCCATGGTTCCCT	8890
DB	7751	AGTTGCTTCCCTGGGTTCAGGTGGCTGTGTATGCCATGCAACCTGTGGAAGTCAAGA	7810	QY	2961	AsnGlyPheSerPheIleHisGlyHisIleGlnTyrGlnCysPheProGlyTyrLys	2980
QY	2601	TyrSerSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAsp	2620	DB	8891	AAATGGTTTTTCTTTATTCATGGGGGCCATATACAGTATACAGTGTCTTCTGGTTATAAG	8950
DB	7811	TGGTCAAGTTCCATCCCAACATGATATGCAATAGACTGTGGCTCTCCCTCATATAGAT	7870	QY	2981	LeuHisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTyrSerGlySerSerPro	3000
QY	2621	PheGlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAspAspMet	2640	DB	8951	CTCCATGGAAATTCATCAGAAGGTGCCTCTCCAATGGCTCTCTGGAGTGGCAGCTCACCT	9010
DB	7871	TTTGGAGACTGTACTAAACTCAAGATGACCAAGGATATTTTTGAGCAAGAACACACATG	7930	QY	3001	SerCysLeuProCysArgCysSerThrProValIleGluTyrGlyThrValAsnGlyThr	3020
QY	2641	MetGluValProTyrValThrProHisProTyrHisLeuGluValAlaIleLysThr	2660	DB	9011	TCCTGCTGCTTGCAGATGTTCCACCCAGTAATTAATATGAATGTAATGTCATGGGACA	9070
DB	7931	ATGGAAATTCATATGTGACTCTCTACCTCTCTTATTCATTTGGAGCAGTGGCTTAACCC	7990	QY	3021	AspPheAspCysGlyLysAlaIleGlnCysPheLysGlyPheLysLeuLeuGly	3040
QY	2661	TyrGluAsnThrLysGluSerProLathrHisSerSerAsnPheLeuTyrGlyThrMet	2680	DB	9071	GATTTTGACTGTGGAAGGCAGCCGGATTCAGTGTCTTCAAGGCTTCAAGCTCCTAGGA	9130
DB	7991	TGGGAAAATACAAAGGAGTCTCTGCTACACATTCATCAAACTTCTGTATGGTACCATG	8050	QY	3041	LeuSerGluIleThrCysGluAlaAspGlyGlnTyrSerSerGlyPheProHisCysGlu	3060
QY	2681	ValSerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCysGln	2700	DB	9131	CTTCTGAAATCCTCTGAGACCCGATGACCAGTGGAGCTCTGGGTCCCCCACTGTGAA	9190
DB	8051	GTTCATACACCTGTAATCCAGATATGAACCTCTGGGGAACCCCTGTGCTGATCTGCCAG	8110	QY	3061	HisThrSerCysGlySerLeuProMetIleProAsnAlaPheIleSerGluThrSerSer	3080
QY	2701	GluAspGlyThrTyrAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuPro	2720	DB	9191	CACACTTCTGTGGTCTCTCTCCAAATGATACCAATCGCTTCATCAGTGGACAGCTCT	9250
DB	8111	GAAGATGGAACCTTGGATGCGAGTGCACCATCTGCAATTCATTAATGAATGTGACTTGCCT	8170	QY	3081	TyrLysGluAsnValIleThrTyrSerCysArgSerGlyTyrValIleGlnGlySerSer	3100
QY	2721	ThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGln	2740	DB	9251	TGGAAGGAAAATGTGATAACTTACAGCTGCAGGTCTGGGATATGTCTATACAGGCGATTCA	9310
DB	8171	ACTGCTCTGAAAATGGCTTTTGGCTTTCACAGAGACTAGCATGGGAAGTGTGTGCAG	8230	QY	3101	AspLeuIleCysThrGluLysGlyValTyrSerGlnProTyrProValCysGluProLeu	3120
QY	2741	TyrSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsn	2760	DB	9311	GATCTGATTTGTACAGAAAGGGGTATGGAGCCAGCTTATCCAGCTCTGTGAGCCCTTG	9370
DB	8231	TATAGCTGTAAACCTGGACACATTCCTTGTGGGTCTGACTTAAGGCTTTGTCTAGAGAAAT	8290	QY	3121	SerCysGlySerProProSerValAlaAsnAlaValAlaThrGlyGluAlaHisThrTyr	3140
QY	2761	ArgLysTyrSerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProAsnPro	2780	DB	9371	TCCTGTGGGTCCCAACCGTCTGTGCCAATGCAGTGGGCAACTGGAGAGGCACACCTAT	9430
DB	8291	AGAAAGTGGAGTGGTCCCTCCCAAGCTGTGAAGCCATTTTCATGCAAAAAGCCAAATCCA	8350	QY	3141	GluSerGluValLysLeuArgCysLeuGluGlyTyrThrMetAspThrAspThrAspThr	3160
QY	2781	ValMetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGlu	2800	DB	9431	GAAGTGAAGTGAACCTCAGATGTCTGGAAGGTATACCATGTGATACAGATACATACA	9490
DB	8351	GTCCATGAATGGATCCATCAAGGAAGCACTACATACCTCAGCAGCTGTGTACTATGAG	8410	QY	3161	PheThrCysGlnLysAspGlyArgTyrPheProGluArgIleSerCysSerProLysLys	3180
QY	2801	CysAspProGlyTyrValLeuAsnGlyThrGluArgArgThrCysGlnAspAspLysAsn	2820	DB	9491	TTTCACTGTACAGAAAGTGTGCTGTCTCCCTGAGAGAAATCTCTTCAGTCTCTAAAAA	9550
DB	8411	TGTGACCCCGGATATGTCTGATGCTGATGCTGAGAGGAAACATGCCAGGATGACAAAC	8470	QY	3181	CysProLeuProGluAsnIleThrHisIleLeuValHisGlyAspAspPheSerValAsn	3200
QY	2821	TyrAspGluAspGluProIleCysIleProValAspCysSerSerProProValSerAla	2840	DB	9551	TGTCCTCTCCCGAAAAACATAACACATATCTTGTTCATGGGAGCAAGTTTCAGTGTGAAT	9610
DB	8471	TGGGATGAGGATGAGCCCAATTTGCATCTCTGTGAGCTGCAGTTTCACTCCAGTCTCAGCT	8530	QY	3201	ArgGlnValSerValSerCysAlaGluGlyTyrThrPheGluGlyValAsnIleSerVal	3220
QY	2841	AsnGlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIleGluTyrThrCysAsn	2860	DB	9611	AGGCAAGTTTCTGTGTCTATGTGCAAGGTTATACCTTTTGGAGGAGTTAACATATCAGTA	9670
DB	8531	AAATGGCCAGGTGAGAGGAGCAGTACATTTCCAAAAAGAGATTGAATACACTTGCAT	8590	QY	3221	CysGlnLeuAspGlyThrTyrGluProProPheSerAspGluSerCysSerProValSer	3240
QY	2861	GluGlyPheLeuLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTyrSer	2880				

QY 221 pheGlyileTrpGlnGlyAenlleArgGluLeuAenAspMetAlaSerThrProLysGlu 240
DB 671 TTTGGCATATGCAAGGGAACATTCGAGAGCTCAATGACATGGCTTCCACCCCAAGGAG 730
QY 241 GluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLeu 260
DB 731 GAGCACTGTTCCTGCTACACAGTTTTGAAGAAATTTGAGGCTTTAGCTCGCGGGCATTG 790
QY 261 HisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeu 280
DB 791 CATGAGATCTACCTTCTGGAGTTTATTCAGATGATATGTTCCACTGCTTATCTT 850
QY 281 CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr 300
DB 851 TGTGATGAAGGAAGGACTGCTGTGACCAATGGGAAGCTGCAAAATGTGGGACACACACA 910
QY 301 GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyValGlyLeuGlnTyrGluCys 320
DB 911 GGCCATTTTGGTGCATCTGTGAAGGGGTATTTACGGGAAGGNTTGCAGATATGAATGC 970
QY 321 ThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSerCys 340
DB 971 ACAGCTTGGCCATCGGGACATACAAACCTGAAGGCTCACAGGAGGATCAGAGTTGC 1030
QY 341 IleProCysProAspGluAenHisThrSerProProGlySerThrSerProGluAspCys 360
DB 1031 ATTCCATGTCTGATGAAATCACACCTCTCCACCTGGGAAGCACATCCCTGAAGACTGT 1090
QY 361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
DB 1091 GTCTGAGAGAGGGATACAGGGGATCTGGCCAGACCTGTGAACCTTGTCCACTGCCCTGCC 1150
QY 381 LeuLysProProGluAenGlyTyrPheIleGlnAenThrCysAenAenHisPheAenAla 400
DB 1151 CTGAAGCTTCCGAAAATGTTACTTATTCAAAACACTTGCACACCACTTCAATGCA 1210
QY 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuCys 420
DB 1211 GCCTGTGGGGTCCGATGTCCCTGGAATTTGATCTTGTGGGAAGCAGCATCATCTTATGT 1270
QY 421 LeuProAenGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
DB 1271 CTACCAATGGTTTGTGGTCCGGTTCAGAGAGCTACTGCAGAGTAAGAACAATGCTCTCAT 1330
QY 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
DB 1331 CTCCGCCAGCCGAACATGCGCCACATCAGCTGTCTTACAAAGGMAATGTTATATAAGACA 1390
QY 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
DB 1391 ACATGTTTGGTTCCTGTGATGAAGGGTACAGACTAGAAAGGCGATGAATGAAGCTTACTGT 1450
QY 481 GlnGlyAenSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr 500
DB 1451 CAAGGAACAGCCAGTGGATGGCCGAACCCCGGTGTGTGAGGCGCCACTGTTCAC 1510
QY 501 PheGlnMetProLysAspValIleLeuSerProHisAenCysGlyLysGlnProLys 520
DB 1511 TTTTCAGATGCCCAAGATATCATATATATATATATATATATATATATATATATATATAT 1570
QY 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
DB 1571 TTTGGGACGATCTGCTATGATTTAGTTTGGCCCAAGGGTTTATTTATCTGGGATCAAGAA 1630
QY 541 MetLeuArgCysThrThrSerGlyLysTrpAenValGlyValGlnAlaAlaValCysLys 560
DB 1631 ATGCTGAGATGTACCACTTCTCGAANAATGGAATGCGAGTTTCAGGAGCTGTGTGTA 1690
QY 561 AspValGluAlaProGlnIleAenCysProLysAspIleGluAlaLysThrLeuGluGln 580
DB 1691 GACGTGGAGGCTTCTCAATCAACTGCTCTAAGGACATAGAGGCTTAAGACTCTGGAACAG 1750

QY 581 GlnAspSerAlaAenValThrTrpGlnIleProThrAlaLysAspAenSerGlyGluLys 600
DB 1751 CAAGATTTCTGCCAATGTTTACCTGGCAGATTCCAACAGCTAAAGACAACCTCTGTGTGA 1810
QY 601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620
DB 1811 GTGTGATTCAGTTCATTCAGCTTTCACCCACCTTACCTTTCCAGTTGGAGATGTT 1870
QY 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAenGlnAlaSerCysIlePheHisIle 640
DB 1871 GCTATCGTATACACGGCAACTGACCTATCCGGCAACAGCGCCAGCTGCAATTTTCCATATC 1930
QY 641 LysValIleAspAlaGluProProValIleAspTyrCysArgSerProProProValGln 660
DB 1931 AAGGTTATTGATGTCAGAACCACTGTCTAGACTGGTGCAGATCTCCACCTCCGTCAG 1990
QY 661 ValSerGluLysValHisAlaIleSerTrpAspGluProGlnPheSerAspAenSerGly 680
DB 1991 GTCTGGAGAGGTACATGCGCAGCTGGATGAGCTTCAGTTCTCAGACACACTCAGGG 2050
QY 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
DB 2051 GCTGAATTTGTTTCAATACCAAGAGTTCATACCAAGGAGACCTTTTCCCTCAAGGGAGACT 2110
QY 701 IleValGlnTyrThrAlaThrAspProSerGlyAenAenArgThrCysAspIleHisIle 720
DB 2111 ATAGTACAGTATACAGCCACTGACCCCTCAGGCAATTAACAGGACATGTGTATATCCATAT 2170
QY 721 ValIleLysGlySerProCysGluIleProPheThrProValAenGlyAspPheIleCys 740
DB 2171 GTCATAAAGGTTCTCCCTGTGNAATTCATTCACACCTGTAAATGGGGATTTTATATGC 2230
QY 741 ThrProAspAenThrGlyValAenCysThrLeuThrCysLeuGluGlyTyrAspPheThr 760
DB 2231 ACTCCAGATAATACCTGGAGTCAACTGTACATAAATTCCTTGTGGAGGCTATGATTTTCA 2290
QY 761 GluGlySerThrAspLysTyrTyrCysAlaTyrGluAspGlyValTyrLysProThrTyr 780
DB 2291 GAAGGTCCTACTGACAGAGTATTTTGTCTTATGAAGTGGCGCTGTGGAACCAACACATAT 2350
QY 781 ThrThrGluTrpProAspCysAlaLysLysArgPheAlaAenHisGlyPheLysSerPhe 800
DB 2351 ACCACTGAATGGCCAGACTGTGCCAAAACCGTTTGTCTTAACCAACCGGTTCAAGTCTTT 2410
QY 801 GluMetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGlu 820
DB 2411 GAGATGTTCTACAAAGCAGCTGCTGTGTGATGACACAGATCTGATGAAGAAGTTTCTGAA 2470
QY 821 AlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIle 840
DB 2471 GCATTTGAGACGACCTCGGNAANAATGTTCCCATCATTTTGTAGTATGCAAGAGACNTT 2530
QY 841 AspCysArgLeuGluAenLeuThrLysLysTyrCysLeuGluTyrAenTyrAspTyr 860
DB 2531 GACTGCAGACTGGAGGAGAACCTGCACAAAATAATATGCTAGATAATAATATATGACTAT 2590
QY 861 GluAenGlyPheAlaIleGlyProGlyTyrGlyValaAlaAenArgLeuAspTyrSer 880
DB 2591 GAAATGGCTTTGCAATTTGGACAGGTGCTGGGTGGAGTCAATTAAGGTGGAATACTCT 2650
QY 881 TyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAenAlaLysSer 900
DB 2651 TACGATGACTTCTGACACTGTGCAAGAAACAGCCACAGCATCCGCAATGCCAAGTCC 2710
QY 901 SerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAenIle 920
DB 2711 TCACGGATTAAGAAGTGGCCCATTTATCTGACTATAAATAAATTAAGTTAATTTTAAATC 2770
QY 921 ThrAlaSerValProLeuProAspGluArgAenAspThrLeuGluTrpGluAenGlnGln 940
DB 2771 ACAGCTAGTGTGCCATATACCGATGAAGAAATGATACCTTGAATGGGAAATTCAGCAA 2830
QY 941 ArgLeuLeuGlnThrLeuGluThrIleThrAenLysLeuLysArgThrLeuAenLysAsp 960

1681 ProLeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPhe 1700
1701 HisSerAlaAspPhePheThrAlaGlySerThrValThrThrGlnCysAsnAsnGlyThr 1720
5111 CATTCAGCCGATGACTTCTATGCTGGCAGCACAGTAACCTACCAAGTGCACCAATGGCTAC 5170
1721 TyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSer 1740
5171 TATCTATGGTGACTCAGAGATGTTCTGTACAGATAATGGAGCTGGACGGCTTTCA 5230
1741 ProSerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSer 1760
5231 CCATCTGCCTGATGTCGATGAGTGTGCGAGTGGATCAGATTGTAGTACGATGCTTCT 5290
1761 CysLeuAsnValAspGlySerThrIleCysSerCysValProProThrThrGlyAspGly 1780
5291 TGCCTGAACGTAGATGGATCTCATATGTTCTATGTGTCTCCACCGTACACAGAGATGGG 5350
1781 LysAsnCysAlaGluProIleLysCysLysAlaProGlyAsnProGluAsnGlyHisSer 1800
5351 AAAAAGTGTGCAGAACCTATAAATGTAGGCTCCAGGAAATCCGGAATATGGCCACTCC 5410
1801 SerGlyGluIleThrValGlyAlaAlaValThrPheSerCysGlnGluGlyThrGln 1820
5411 TCAGGTGAGATTTATACAGTAGGTGTCGGAAGTCAATTTCTGTCAGGAAGGATACCA 5470
1821 LeuMetGlyValThrLysIleThrCysLeuGluSerGlyGluTrpAsnHisLeuIlePro 1840
5471 TTGATGGAGTAAACCAAAATCACATGTTTGGAGTCTGGAGATGGAATCATCTAATACCA 5530
1841 TyrCysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGlu 1860
5531 TATTGTAAAGCTGTTCTGTTGCTAAACCGGTATTTCCAGAAATGTTGCAATTGAGGAG 5590
1861 LeuAlaPheThrPheGlySerLysValThrTyrArgCysAsnLysGlyThrThrLeuAla 1880
5591 TTAGCATTTACTTTTGGCAGCAAGTGACATATAGGTGTATAAATGGAATATATTTGAGTGG 5650
1881 GlyAspLysGluSerSerCysLeuAsnSerSerTrpSerHisSerProProValCys 1900
5651 GGTGATAAAGATCATCTGCTGTCTGCTAAACAGTTCCTGGAGTCAATCCCTCTCTGTGT 5710
1901 GluProValLysCysSerProGluAsnIleAsnAsnGlyLysThrIleLeuSerGly 1920
5711 GAACCAAGTGAAGTGTCTAGTCCGGAAATATAAATATGGAATATATTTTGAAGTGG 5770
1921 LeuThrThrLeuSerThrAlaSerTyrSerCysAspThrGlyThrSerLeuGlnGlyPro 1940
5771 CTTACCTTACCTTTCTACTGCATCATATTTCTATGCGATACAGGATACAGCTTACAGGGCCT 5830
1941 SerIleIleGluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeu 1960
5831 TCCATTTATGAATGACCGGCTTCTGGCATCTGGGACAGAGCGCCACTGCTGTACCTC 5890
1961 ValPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThr 1980
5891 GTCTTCTGTGGAGNACCACCTGCCATCAAGATCTGTCTATTACGGGAATAAATTCACT 5950
1981 PheArgAsnThrValThrThrCysLysGluGlyThrLeuAlaGlyLeuAspThr 2000
5951 TTCAGGAACACCGTCACTTACATTCGAAAGAAGGCTATATCTTGTCTGTCTTGCACACC 6010
2001 IleGluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnGlnCysLeuAlaValSer 2020
6011 ATTGAATGCTGCGCGCAGCGCAAGTGGAGTAGAAGTGCACAGAGTGCCTGCTGTCTCC 6070
2021 CysAspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGly 2040
6071 TGTGATGAGCCACCATTTGTGGACCAACGCTCTCCAGAGAGCTGCCCATCGCTCTTTTGA 6130

2041 AspIleAlaPheThrTyrCysSerAspGlyThrSerLeuAlaAspAsnSerGlnLeuLeu 2060
6131 GACATTTGCTTACTACTCTCTGATGGTTACAGCCTAGCAGACAATTTCCAGCTTCTC 6190
2061 CysAsnAlaGlnGlyLysTrpValProProGluGlyGlnAspMetProArgCysIleAla 2080
6191 TGCATGCCCHAGGCAAGTGGGTACCCCAAGAGTCAAGACATGCCCGTTGTATAGCT 6250
2081 HisPheCysGluLysProProSerValSerTyrSerIleLeuGluSerValSerLysAla 2100
6251 CATTTCTGTGAAAAAOCCTCCATCGGTTTCTATAGCATCTTGGAAATCTGTGAGCAAGCA 6310
2101 LysPheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThr 2120
6311 AAAATTTGACGTGGCTCAGTTGTGAGCTTTAAATGCATGGAAGGCTTTGTACTGAACACC 6370
2121 SerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGln 2140
6371 TCAGCAAAAGATTGAATGTATGAGAGGTGGCGCATGTGGAACCTTCCCCCATGTCCATCCAG 6430
2141 CysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySer 2160
6431 TGCATCCTGTGCGGTGTGAGAGCCACCAAGCATCATGAATGGCTATGCAAGTGGATCA 6490
2161 AsnTyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGly 2180
6491 AACTACAGTTTTGGAGCCATGTGGCTTTACAGCTGCAACAGGGGTTCTACATCAAGGG 6550
2181 GluLysLysSerThrCysGluAlaThrGlyGlnTrpSerSerProIleProThrCysHis 2200
6551 GAAAGAGAGAGCACCTGCGAAGCCACAGGCGAGTGGAGTAGTCTCTATACCGAGGTGCCAC 6610
2201 ProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHisThrThrGly 2220
6611 CCGGTATCTTGTGTTGAAACCACTTAAGTTGAGAATGGCTTTCTGGAGCATACACTGGC 6670
2221 ArgIlePheGluSerGluValAlaGlyThrCysAsnProGlyTyrLysSerValGlySer 2240
6671 AGGATCTTTGAGAGTGAAGTGAAGTATCAGTGTAAACCGGCTATTAAGTCAAGTGGAGT 6730
2241 ProValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysVal 2260
6731 CCTGTATTTGTCTGCCAAGCCATGCGCACCTGGCACAGTGAATCCCTCTCATGTGTGT 6790
2261 ProLeuAspCysGlyLysProProProIleGlnAsnGlyPheMetLysGlyGluAsnPhe 2280
6791 CCTCTCGACTGTGAAAAACCTCCCGCATCCAGATGGCTTTTCATGAAGAGGAGAAACTTT 6850
2281 GluValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSer 2300
6851 GAAGTAGGGTCCAGGGTTCAGTTTTTCTGTAAATGAGGTTATGAGCTTGTGTGACAGT 6910
2301 SerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetPro 2320
6911 TCTTGGACATGTGAGAAATCTGGCAATGGAATGAAGTCAAATCCAAAGTGCATGCT 6970
2321 AlaLysCysProGluProProLeuLeuGlnAsnGlnLeuValLeuLysGluLeuThrThr 2340
6971 GCCAAGTGGCCAGAGCGCCCTCTTGGAAAAACCAAGCTAGTAGTATTAAAGAGTGGACACC 7030
2341 GluValGlyValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerVal 2360
7031 GAGTAGAGATTGTGACATTTCTGTAAAGAGGGCATGTCTCTGCAAGGCCCCCTCTCTC 7090
2361 LeuLysCysLeuProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeu 2380
7091 CTGAATGCTTGCATCCAGCAATGGAATGACTTTTCTCCCTGTGTGTGTGAAGATTGTCTT 7150
2381 CysThrProProProLeuIleSerPheGlyValProIleProSerSerAlaLeuHisPhe 2400
7151 TGTACCCCACTCCCTCAATTTCTTGGTGTGCCCATTCCTTCTTCTGCTCTTCTTCTT 7210
2401 GlySerThrValLysTyrSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrThr 2420

Db	7211	GGAGTACTGTCAAGTATCTCTGTAGTGGGTTTTCTTAAGGAAATTTCTACCA	8291	AGAAAGTGGAGTGGCTCTCCACGCTGTGAAGCCATTTTCATGCAAAAAGCCAAATCCA
Qy	2421	LeuCysGlnProAspGlyThrTrpSerSerProLeuProGluCysValProValGluCys	2781	ValMetAsnGlySerIleLysGlySerAsnTrpThrTrpLeuSerThrLeuTrpGlu
Db	7271	CTCTGCCAACCTGATGGCACCTGGAGCTCTCCACATGCCAGAAATGTGTTCAGATGAATGT	8351	GTCAATGAATGGATCCATCAAGGAAGCAACTACACATACCTTGAGCAGCTGTGTACTATGAG
Qy	2441	ProGlnProGluGluIleProAsnGlyIleAspValGlnGlyLeuAlaTrpLeuSer	2801	CysAspProGlyTrpValLeuAsnGlyThrGluArgArgThrCysGlnAspAspLysAsn
Db	7331	CCCCAACCTGAGGAAATCCCAATGGAAATCAATGATGGCAGGCCCTTGCCATCTCAGC	8411	TGTGACCCCGGATATGTGTGAATGGCACTGAGAGGAGAACATGCGCAGGATGCAAAAC
Qy	2461	ThrAlaLeuTrpThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCys	2821	TrpAspGluAspGluProIleCysIleProValAspCysSerSerProProValSerAla
Db	7391	ACAGCTCTCTATACCTGCAAGCCAGGCTTGAATTTGGTGGGAATACTACCAACCTTTGT	8471	TGGATGAGGATGAGCCCAATTTGCATCTCTGGACTGCAGTTTCAACCCCACTCTCAGCC
Qy	2481	GlyGluAsnGlyHisTrpLeuGlyGlyIleAspProThrCysLysAlaIleGluCysLeuLys	2841	AsnGlyGlnValArgGlyAspGluTrpThrPheGlnLysGluIleGluTrpThrCysAsn
Db	7451	GGAGAAATGGTCACTGGCTTGGAGGAAACCAACATGTAAGCCATTGAGTGCCTGAAA	8531	AATGCCAGGTGAGAGGAGAGAGTACATTTCCAAAAGAGATTTGAATACACTTGGCAAT
Qy	2501	ProLysGluIleLeuAsnGlyIlePheSerTrpThrAspLeuHisTrpGlyGlnThrVal	2861	GluGlyPheLeuLeuGluGlyValArgSerArgValCysLeuAlaAsnGlySerTrpSer
Db	7511	CCCAAGAGATTTTGAATGGCAAAATTTCTTACACGGACCTTACACTATGGACAGACCGTT	8591	GAAGGGTTCTTGCTTGAGGGAGCCAGAGTCCGGTTTGTCTTGCCAATGGAAATGGAGT
Qy	2521	ThrTrpSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGlu	2881	GlyAlaThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGly
Db	7571	ACCTACTCTTGCACCGAGGCTTTCGCTCGAAGTCCAGTCCCTTGACCTGTTAGAG	8651	GGAGCCACTCCCGACTGTGTGCTGTGATGTGCACACCCCGCCACAACTGGCCAAATGGG
Qy	2541	ThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGln	2901	ValThrGluGlyLeuAspTrpGlyPheMetLysGluValThrPheHisCysHisGluGly
Db	7631	ACAGGTGATTTGGGATGTAGATGCCCATCTTGCATATGCCATCCACTGTGATTTCCCAAA	8711	GTGACGGAAGGCCCTGGACTATGGCTTTCATGAAGGAAGTAAATTCCTCTCATGAGGGC
Qy	2561	ProIleGluAsnGlyPheValGluGlyValAspTrpSerTrpGlyAlaIleIleTrp	2921	TyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAlaGlu
Db	7691	CCCATTTGAAATGGTTTTGTAGAGGGTGCAGATTACAGCTATGGTGCATATCATCTAC	8771	TACATCTTGACGGTGTCTCCAAACTCACCTGTGATGAGTGGCACTGGGATGCAGAG
Qy	2581	SerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGly	2941	IleProLysCysLysProValAsnCysGlyProProGluAspLeuAlaHisGlyPhePro
Db	7751	AGTTGCTCTCCCTGGGTTTCAGGTGGCTGCTCATGCCATGCAGACCTGTGAAGAGTCAGGA	8831	ATTCCTCTCTGTAACCACTCACTGGACCTCTCTGAAGATCTTGGCCATGGTTTCCCT
Qy	2601	TrpSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAsp	2961	AsnGlyPheSerPheIleHisGlyGlyHisIleGlnTrpGlnCysPheProGlyTrpLys
Db	7811	TGGTCAAGTTCCATCCCAACATGATGCCAATAGACTGTGGCTCTCCCTCATATAGAT	8891	AATGGTTTTCTTTATTCATGGGGCCATATACAGTATCAGTGTCTTCTGGTTATAG
Qy	2621	PheGlyAspCysThrLysLeuLysAspAspGlnGlyTrpPheGluGlnGluAspMet	2981	LeuHisGlyAsnSerSerArgCysLeuSerAsnGlySerTrpSerGlySerSerPro
Db	7871	TTTGGAGACTGTACTAACTCAAAGATGACACAGGATATTTTGACGAAGAGACGACATG	8951	CTCCATGGAATTCATCAAGAGGTGCTCTCTCCAATGGCTCTCTGGAGTGGCAGCTCACCT
Qy	2641	MetGluValProTrpValThrProHisProProTrpHisLeuGlyAlaValAlaLysThr	3001	SerCysLeuProCysArgCysSerThrProValIleGluTrpGlyThrValAsnGlyThr
Db	7931	ATGGAGTTCCATATGATGACTCTCCCTCCTCATCTTATGGGAGCAGTGGCTTAAACCC	9011	TCCTGCTGCTTGCAGATGTTCCACACCACTGAATTTGAATATGGAACCTGTCAATGGGACA
Qy	2661	TrpGluAsnThrLysGluSerProAlaThrHisSerSerAsnPheLeuTrpGlyThrMet	3021	AspPheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGlyPheLysLeuLeuGly
Db	7991	TGGGAAATACAAAGGAGTCTCTGCTACACATTCATCAAACTTTCTGTATGGTACCATG	9131	GATTTTGACTGTGGAAGGCGCCGGATTCAGTGCTTCAAGGGCTTCAGCTCTCAGGA
Qy	2681	ValSerTrpThrCysAsnProGlyTrpGluLeuLeuGlyAsnProValLeuIleCysGln	3041	LeuSerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGlyPheProHisCysGlu
Db	8051	GTITTCATACACCTGTAAATCCAGGATATGAATCTCTGGGGAAACCTCTGCTGATCTGCAG	9191	CTTTCTGAATCACTCTGTGAAGCCGATGGCCAGTGGAGCTCTGGGTTCCTCCCACTGTGAA
Qy	2701	GluAspGlyThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuPro	3061	HisThrSerCysGlySerLeuProMetIleProAsnAlaPheIleSerGluThrSerSer
Db	8111	GAAGATGGAACTTGAATGGCAGTGCACCATCTCTGCATTTCAATTTGAATGTGACTTGCT	9251	CACACTTTCTGTGTCTCTTCCAAATGATACCAATTCGTTTCATCAGTGAGACCACTCT
Qy	2721	ThrAlaProGluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGln	3101	TrpLysGluAsnValIleThrTrpSerCysArgSerGlyTrpValIleGlnGlySerSer
Db	8171	ACTGCTCTGAAAATGGCTTTTTCGTTTTTACAGAGACTAGCATGGGAAGTGTGTGCAG	9311	TGGAGGAAATGTGATAACTTACAGCTGCAAGTCTGGATATGTCTATCAAGGCACTTCA
Qy	2741	TrpSerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsn	3121	AspLeuIleCysThrGluLysGlyValTrpSerGlnProTrpValCysGluProLeu
Db	8231	TATAGCTGTAAACCTGGACACATTTCTAGTGGGCTCTGACTTAAGGCTTTGTCTAGAGAT	9371	GATCTGATTTGTACAGAGAAAGGGGTATGGAGCCAGCTTATCCAGTCTGTGAGGCCCTTG
Qy	2761	ArgLysTrpSerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProAsnPro	9431	TCCTGTGGGTCCCCACCGTCTGTTCGCAATGTCAGTGGCACTGGAGAGGCAACACCTAT

1564 PheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTrpAspTyrVal 1583
4757 TTCAACCCGGCTAGTCTTTTGTGGGCTCATTAAGCCAGCTCAACCTCTGGGACTAAGTC 4816
1584 LeuSerProGlnGlnValIlyssSerLeuAlaThrSerCysProGluGluLeuSerIlyysGly 1603
4817 CTGTCTCCACAGCAGGTGAAGTCACTGGCTACCTCTGCGCCAGAGGAACTCAGTAAGAAG 4876
1604 AsnValLeuAlaTrpAspPheLeuSerGlyIleValGlyIlyssValIlyssIleAspSer 1623
4877 AACGTGTTAGCATGGCTCTGATTTCTTGTGAGGAATTTGTGGGAAGTGAAGATCGATTTCT 4936
1624 LysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHisLeuArgThr 1643
4937 AAGAGCATATTTTGTCTGATTCGCCACGCTTGGAGGGTCAGTGCCTCATCTGAGAACT 4996
1644 AlaSerGluAspLeuIlyssProGlySerLysValAsnLeuPheCysAspProGlyPheGln 1663
4997 GCATCTGAAGATTTAAACCCAGGTTCCAAAGTCAATCTGTTCTGTGAACCCAGGCTTCCAG 5056
1664 LeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTrpThrGlnProLeuPro 1683
5057 CTGTGCGGAAACCTCTGTGAGTACTGTCTGTAATCAAGGACAGTGGACACAACTCCCTCC 5116
1684 HisCysGluArgIleSerCysGlyValProProLeuGluAsnGlyPheHisSerAla 1703
5117 CACTGTGAACGCAATTCGCTGTGGGGTGGCCACCTCTCTTTGGAGAAATGGCTTCCATTCAGCC 5176
1704 AspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyrLeuLeu 1723
5177 GATGACTCTATGCTGCGAGCACAGTAACCTACAGTGCACAACTGGCTACTATCTATTG 5236
1724 GlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSerProSerCys 1743
5237 GGTGACTCAAGGATGTTCTGTACAGATAATGGGAGCTGGAACGGCTTTCACCATCTCTC 5296
1744 LeuAspValAspGluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAsn 1763
5297 TTAGATGTCGATGAGTGTGAGTGTGATCAGATTGATGAGGATGCTTCTTCTGCTGAAC 5356
1764 ValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyIlyssAsnCys 1783
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1804 IleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeuMetGly 1823
5477 ATTTATACAGTAGTCCGAGTACATTTTCTGTCAGGAGGATACCAATGTTGATGGGA 5536
1824 ValThrLysIleThrCysLeuGluSerGlyGluTrpAsnHisLeuIleProTyrCysLys 1843
5537 GTAACCAAAATCACATGTTTGGAGTCTGGAGATGGAATCATCTAATACCATATTGTAAA 5596
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5597 GCTGTTTCAATGTGTAACCCGGCTATTCAGAAAAATGGTTGCAATGAGGAGTGTAGCATTT 5656
1864 ThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAlaGlyAspLys 1883
5657 ACTTTTGGCAGCAGGAGTACATATAGTGTATTAAGGATATACTCTGCGCGGTGATAAA 5716
1884 GluSerSerCysLeuAlaAsnSerSerTrpSerHisSerProProValCysGluProVal 1903
5717 GAATCATCTCTGCTTCAACAGTCTCTGGAGTCAATTCCTCTCTGTGTGTGAACCAAGT 5776
1904 LysCysSerSerProGluAsnIleAsnAsnGlyIlyssTyrIleLeuSerGlyLeuThrTyr 1923
5777 AAGTGTCTTAGTCCGGAATAATAATAATGGAATAATATTTTGTGAGGCTTACCTAC 5836
1924 LeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuGlnGlyProSerIleIle 1943

5837 CTTTCTACTGCATCATATTTCATGCGATACAGGATACAGCTTACAGGGCCCTTCCATTATT 5896
1944 GluCysThrAlaSerGlyIleTrpAspArgAlaProProAlaCysHisLeuValPheCys 1963
5897 GAATGCACGGCTTCTGGCATCTGGGACAGAGCCACCTGCTGTCACCTCGTCTTCTGT 5956
1964 GlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThrPheArgAsn 1983
5957 GGAGAACCACTCCCATCAAGATGCTGTCATTACGGGGAATAACTTCACTTTCCAGAAC 6016
1984 ThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThrIleGluCys 2003
6017 ACCGTCACTTACACTTGCAGGAAGGCTATCTTGTCTGTCTGTGACACCATTTGAATGC 6076
2004 LeuAlaAspGlyIlyssTrpSerArgSerAspGlnGlnCysLeuAlaValSerCysAspGlu 2023
6077 CTGGCCGAGCGCAAGTGGAGTAGAAGTGACAGCAGTCCCTGGCTGTCTCTGTGATGAG 6136
2024 ProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGlyAspIleAla 2043
6137 CCACCATTTGGGACCACGCTCTCCAGAGACTGCCCATCGGCTCTTTGGAGACATTTGCA 6196
2044 PheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeuCysAsnAla 2063
6197 TTCTACTACTGCTCTGATGTTACAGCTAGCAGACAAATTTCCAGCTTCTCTGCAATGCC 6256
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6317 GAAAACTTCCATCGGTTTCTATAGCATCTTGGAACTCTGTGAGCAAGCAAAATTTGCA 6376
2104 AlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThrSerAlaLys 2123
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2124 IleGluCysMetArgGlyGlyGlnTrpAsnProSerProMetSerIleGlnCysIlePro 2143
6437 ATTGAATGTATGAGAGGTGGCAGTGGAAACCTTCCCGCATGTCCATCCAGTGCATCCCT 6496
2144 ValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySerAsnTyrSer 2163
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6617 AGCACCTGGCAAGCCACAGCGCAGTGGAGTAGTCTTATACCGAGCTGCCACCCGCTATCT 6676
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6677 TGTGGTAACCCACTAAGGTTGAGAAATGGCTTCTGGAGCATACACTGCGAGATCTTT 6736
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6737 GAGAGTGAAGTAGGTATCAGTGTAAACCCCGGCTATAAGTCAGTCGGAAGTCTCTGTATT 6796
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6797 GTCTGCCAAGCCCAATCGCCACTGGCAGTGAATCCCTCTGATGTGTGTCTCTCTCGAC 6856
2264 CysGlyLysProProIleGlnAsnGlyPheMetLysGlyGluAsnPheGluValGly 2283
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2284 SerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSerSerTrpThr 2303

Db 6917 TCCAAAGGTTTCAGTTTCTGTAATCAGGGTTATGAGCTTGTGGTGCAGAGTTCTTGGACA 6976
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Db TGTCCAGAAATCTGGCAATGGAATGAAGTCAATCCAAAGTGCATGCTGCCAAGTGC 7036
Qy ProGluProProLeuLeuGluGlnLeuValLeuLysGluLeuThrThrGluValGly 2343
Db CCAGAGCCGCCCTCTTGTGAAAACCAAGCTAGTATTAAGAGGAGTTGACCAACAGAGTAGGA 7096
Qy ValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerValLeuLysCys 2363
Db GTTGTGACATTTCTGTAAAGAGGCGATGCTTCGAAAGCCCTCTGTCTGAAATGC 7156
Qy LeuProSerGlnGlnTrpAsnAspSerPheProValCysLysLeuValLeuCysThrPro 2383
Db TTGCCATCCAGCAATGAAATGACTCTTTCCTGTTTGTAAAGATTTGTTCTTGTATCCCA 7216
Qy ProProLeuLysPheGlyValProLysProSerSerAlaLeuHisPheGlySerThr 2403
Db CCTCCCTTAAATTTCTTGTGGTGTCCCATTCCTTCTTCTGCTCTTCATTTTGGAAAGTACT 7276
Qy ValLysTrpSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrThrLeuCysGln 2423
Db GTCAAGTATTTCTGTGTAGTGGTGGTTCCTTAAGAGGAATCTACCACTCTTGCCTC 7336
Qy ProAspGlyThrTrpSerProLeuProGluCysValProValGluCysProGlnPro 2443
Db CTGATGCGACCTGGAGCTCTCCATGCGCAGAAATGTTTCCAGTAGAATGTCCCAACT 7396
Qy GluGluLeuProAsnGlyLeuLeuValGlnGlyLeuValLeuValLeuSerThrAlaLeu 2463
Db GAGGAATATCCCAATGGAATCAATGATGCAAGGCTTGGCTATCTCAGCACACTCTC 7456
Qy TyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsn 2483
Db TATACCTGCAAGCCAGGCTTGAATGGTGGGAATACTACCACTTGTGGAGAAAT 7516
Qy GlyHisTrpLeuGlyGlyLysProThrCysLysAlaLeuGluCysLeuLysProLysGlu 2503
Db GGTCACTGGCTGGAGGAAACCAACATGTAAGCCATTTGAGTGCCTGAAACCCCAAGGAG 7576
Qy IleLeuAsnGlyLysPheSerTrpThrAspLeuHisTyrGlyGlnThrValThrTrpSer 2523
Db ATTTTGAATGGCAATTTCTTTACAGGACCTTACACTATGGACAGACCGTTACCTACTCT 7636
Qy CysAsnArgGlyPheArgLeuGlyProSerAlaLeuThrCysLeuGluThrGlyAsp 2543
Db TGCAACCGAGGCTTTGGCTCGAAGTCCAGTGCCTTGAACCTGTTTAGAGACAGTGTGT 7696
Qy TrpAspValAspAlaProSerCysAsnAlaLeuHisCysAspSerProGlnProLysGlu 2563
Db TGGATGTAGATGCCCCATCTTGCATGCCATCCACTGTGATTTCCCAACCCCACTTGA 7756
Qy AsnGlyPheValGluGlyValAspTrpSerTrpGlyAlaLeuIleLeuThrSerCysPhe 2583
Db AATGTTTTTGTAGAGGTGCAGATTACAGCTATGGTGCCATTAATCTCTACAGTTGCTTC 7816
Qy ProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrpSerSer 2603
Db CCTGGTTTTCAAGTGGCTTGTGTCATGCCATGCAGACCTGTGGAAGAGTCAAGTGTCAAGT 7876
Qy SerIleProThrCysMetProLysPheGlyLeuProProHisIleAspPheGlyAsp 2623
Db TCCATCCCAACATGTATGCCAATAGACTGTGGCTCTCCCTCTCATATAGATTTTGGAGAC 7936
Qy CysThrLysLeuLeuAspAsnGlnGlyTrpPheGluGlnGluAspAspMetMetGluVal 2643
Db TGTACTAACTCAAGATGACAGGATATTTTGGCAAGAGAGACATGATGGAAGTT 7996
Qy ProTrpValThrProHisProTrpHisLeuGlyAlaValAlaLysThrTrpGluAsn 2663
Db CCATATGTGACTCTCCACCTCTTATCATTTGGGAGGCTGAGTAAACCTGGGAAAT 8056

Qy ThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTrp 2664
Db ACAAGAGAGTCTCTGCTACACATTCATCAAACTTCTCTATGGTACCATGGTTTCATAC 8116
Qy ThrCysAsnProGlyTrpGluLeuGlyAsnProValLeuIleCysGlnGluAspGly 2703
Db ACCTGTAATCCAGGATATGAATCTCTGGGGAAACCTCTGTCTGTATCTGCCAGGAAGTGA 8176
Qy ThrTrpAsnGlySerAlaProSerCysIleSerIleGluCysAspLeuProThrAlaPro 2723
Db ACTTGAATGGCAGTGCACCATCTTGCAATTCATTTGAATGTGACTTGTCTACTGCTCCT 8236
Qy GluAsnGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGlnTrpSerCys 2743
Db GAAAAATGGCTTTTTCGCTTTTACAGAGACTAGCATGGGAAGTGTCTGTGAGTATAGATCTGT 8296
Qy LysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArgLysTrp 2763
Db AAACCTGGACACATTTCTAGCAGGCTCTGACTTAAGCTTTTGTCTAGGAATAGAAAGTGG 8356
Qy SerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProAsnProValMetAsn 2783
Db AGTGTGCTCTCCCAAGCTGTGAAGSCATTTTCATGCAAAAGCCAAATCCAGTCATGAAT 8416
Qy GlySerIleLysGlySerAsnTrpThrTrpLeuSerThrLeuTrpTrpGluCysAspPro 2803
Db GATCCATCAAAGGAAGCAACTACACATACCTTGAGCAGCACTGTCTATGAGTGTGACCC 8476
Qy GlyTrpValLeuAsnGlyThrGluArgThrCysGlnAspAspLysAsnTrpAspGlu 2823
Db GGATATGTGTGAATGGCCTGAGAGGAGAACTGCCAGATGACAAACCTGGGATGAG 8536
Qy AspGluProIleCysIleProValAspCysSerSerProProValSerAlaAsnGlyGln 2843
Db GATGAGCCCATTTGCAATTTCTGTGACTGCAGTTCACTCCCTCAGTCTCAGCCAAATGGCCAG 8596
Qy ValArgGlyAspGluTrpThrPheGlnLysGluIleGluTrpThrCysAsnGluGlyPhe 2863
Db GTGAGAGAGAGCAGATACACATTCCAAAAGAGATTTGAATACACTTGCATGAAGGGTTC 8656
Qy LeuLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTrpSerGlyAlaThr 2883
Db TTGCTTGAAGAGAGCCAGAGTGGGTTTGTCTTGCCATGGAAGTTGGAGTGGGCCACT 8716
Qy ProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGlyValThrGlu 2903
Db CCCGACTGTGTGCTGTGAGATGTGCCACCCGCCCACTGCGCCAAATGGGGTGCACGAA 8776
Qy GlyLeuAspTrpGlyPheMetLysGluValThrPheHisCysHisGluGlyTrpIleLeu 2923
Db GGCTTGGACTATGGCTTCATGAAGAGATTAACATTCCTGTCAGAGGGCTACATCTTG 8836
Qy HisGlyAlaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAlaGluIleProLeu 2943
Db CAGGTGTCTCCAAACTCACCTGTGCTCAGTGCAGATGGCACTGGGATGCAGAGATTCCTC 8896
Qy CysLysProValAsnCysGlyProProGluAspLeuAlaHisGlyPheProAsnGlyPhe 2963
Db TGTAAACCAAGTCAACTGTGGACCTCTCAAGATCTTGCCCATGTTTCCCTAATGGTTTTT 8956
Qy SerPheIleHisGlyGlyHisIleGlnTrpGlnCysPheProGlyTrpLysLeuHisGly 2983
Db TCCTTTATTCATGGGGGCTATATACGATATCAGTCTTCTCTGGTTATTAAGCTCCATGGA 9016
Qy AsnSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerProSerCysLeu 3003
Db AATTCATCAAGAGGTGCTCTCTCAATGCTCTCTGGAGTGGCAGCTCACCTCTCTGCTG 9076
Qy ProCysArgCysSerThrProValIleGluTrpGlyThrValAsnGlyThrAspPheAsp 3023
Db CTTTGCAGATGTTCCACACCACTGTAATTAATGAACTGTCTAATGGGACAGATTTTGAC 9136

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Qy	4	ArgLeuAlaPheCysCysTyrGlyLeuAlaLeuValSerGlyTyrAlaThrPheGlnGln	23	Qy	362	CysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeu	381
Db	83	AGAATTTGGCGGGCTTCTGGGCTCTGGCGCTCGTTTGGGCTGGCGACCTTTCCAGCAG	142	Db	1157	TGCAGAGAGGGATACAGGGCATCTGGCCAGACCTGTGAAGTTGTCCACTGGCCCTGCCCTG	1216
Qy	24	MetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaProGlyAlaPro	43	Qy	382	LyseProProGluAanGlyTyrPheIleGlnAanThrCysAanAanHisPheAanAlaAla	401
Db	143	ATGTCCCGCTGCGCAATTTTCAGCTTCGCGCTCTTCCCGCAGACCGCGCGCGCGCC	202	Db	1217	AAGCCTCCCGAAATGGTTACTTATCCAAACACTTGCACCAACCACTTCAATGAGCC	1276
Qy	44	GlySerIleProAlaProAlaProGlyValSerGlyAlaAlaGlySerArgValGluArg	63	Qy	402	CysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeuCysLeu	421
Db	203	GGGAGTATCCCGCGCGCCCTCTCTGGCGCAGAGCGCGGAGCGAGTGAGCGG	262	Db	1277	TGTGGGCTCCGATCTCACCTGGATTTGATCTGTGGGAGCAGCATCATCTTATGTCTA	1336
Qy	64	LeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGluArgLeuGlu	83	Qy	422	ProAsnGlyLeuThrPheSerGlySerGlySerTyrCysArgValArgThrCysProHisLeu	441
Db	263	CTGGGCCAGCGCTTC-----CGCGTGGCGTCTGCGGAGCTCAGCGAGCGCTGGAG	316	Db	1337	CCCAATGGTTTGTGGTTCGGTTTCAGAGAGCTACTGCAGAGTAAGAACAATGTCTCATCTC	1396
Qy	84	LeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArgSerGluLeu	103	Qy	442	ArgGlnProLyseHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLyseThr	461
Db	317	CTTGTCTTCTGGTGGATATTCGTCCAGCGTGGGCGAAGTCAACTTCCGAGCGAGCTC	376	Db	1397	CGCCAGCCGAAACATGGCCCATCAGCTGTCTACAGGGGAAATGTTATATANGAACAA	1456
Qy	104	MetPheValArgLyseLeuSerAspPheProValValProThrAlaThrArgValAla	123	Qy	462	CysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLyseLeuThrCysGln	481
Db	377	ATGTTGGTCCGCAAGCTGCTGTCCGACTTCCCGTGGTGGCCAGCCGCGCGTGGCC	436	Db	1457	TGTTTGGTGGCTGTGATGAGGCTACAGGCTAGAGGCGAGTATAGCTTACTTGTCAA	1516
Qy	124	IleValThrPheSerSerLyseAsnTyrValValProArgValAspTyrIleSerThrArg	143	Qy	482	GlyAsnSerGlnThrAspGlyProGluProArgCysValGluArgHisCysSerThrPhe	501
Db	437	ATCGTGACTTCTCGTCCAGAGACTACGTGGTGGCGCGGTGATATCATCTCCACCCGC	496	Db	1517	GGAAACAGCCAGTGGGATGGCCAGAACCCCGGTGTGTGGAGCGCCACTGTTTCCACCTT	1576
Qy	144	ArgAlaArgGlnHisLyseCysAlaLeuLeuGlnGluIleProAlaIleSerTyrArg	163	Qy	502	GlnMetProLyseAspValIleIleSerProHisAanCysGlyLyseGlnProAlaLysePhe	521
Db	497	CGCGCGGCCACGACAGTGGCGCTGCTCTCCAGAGATCCCTGCCATCTCTCTACCGA	556	Db	1577	CAGATGCCAAAGATGTCATCATATCCCCCACAACCTGTGGCAGCAGCCAGCCAAATTT	1636
Qy	164	GlyGlyGlyThrTyrThrLyseGlyAlaPheGlnGlnAlaAlaGlnIleLeuLeuHisAla	183	Qy	522	GlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLyseGluMet	541
Db	557	GGTGGCGGACCTACACCGAGCGGCTTCCAGCAGCGCGCGCAATTTCTTCTCATGCT	616	Db	1637	GGGAGCATCTGTATGATGTTGCGGCCAGGGTTCAATTTATCTGGAGTCAAGAAATG	1696
Qy	184	ArgGluAsnSerThrLyseValValPheLeuIleThrAspGlyTyrSerAsnGlyGlyAsp	203	Qy	542	LeuArgCysThrThrSerGlyLyseTyrAsnValGlyValGlnAlaAlaValCysLyseAsp	561
Db	617	AGAGAAACTCACAAAAGTTGTTATTTCTCATCTAGTATGATATTCATGGGGAGAC	676	Db	1697	CTGAGATGTACCACTTCTGGAAAATGGAAATGCGAGTTTCAGGCGACCTGTGTGTAAGAC	1756
Qy	204	ProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePheThrPheGlyIle	223	Qy	562	ValGluAlaProGlnIleAanCysProLyseAspIleGluAlaLyseThrLeuGlnGln	581
Db	677	CCTAGACCAATTCAGCGCTCACTCGAGATTCAGAGTGGAGATCTTCCACTTTTGGCATA	736	Db	1757	GTGAGGCTCTCCAAATCACTGCTCTTAGGACATAGAGGCTTAGACTCTGGACAGCNA	1816
Qy	224	TyrGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLyseGluGluHisCys	243	Qy	582	AspSerAlaAsnValThrTrpGlnIleProThrAlaLyseAspAsnSerGlyGlyLyseVal	601
Db	737	TGGCAGGGAAACATTCGAGACTGATGACATGCGCTTCCACCCCAAGGAGGAGCACTGT	796	Db	1817	GATTCGCCAATGTTACTCTGGCAGATTCCAACAGCTAAAGACAACCTCTGGTGAAGAGTG	1876
Qy	244	TyrLeuLeuHisSerPheGluPheGluAlaLeuAlaArg-----ArgAlaLeuHis	261	Qy	602	SerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspValAla	621
Db	797	TACCTGTCTACACAGTTTTGAAGAAATTTGAGGCTTTAGTGGCCCTCTGTGCATATGTTAT	856	Db	1877	TCAGTCCACGTTTCATCCAGCTTTTCCACCCCACTTACCTTTTCCCAATTTGGAGATGTGCT	1936
Qy	262	GluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyrLeuCys	281	Qy	622	IleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIleLyse	641
Db	857	GTAGATCTACCTTCTGGGAGTTTATTCAGATGATATGGTCCACTGCTCATATCTTTGT	916	Db	1937	ATCGTATACACGGCACTGACCTATTCGGCAACCAAGCCAGCTGCATTTTCCATATCAAG	1996
Qy	282	AspGluGlyLyseAspCysAspArgMetGlySerCysLyseCysGlyThrHisThrGly	301	Qy	642	ValIleAspAlaGluProProValIleAspTyrCysArgSerProProProValGlnVal	661
Db	917	GATGAGGCAAGGACTGCTGTGACCGAATGGGAGCTGCANATGTGGGAAACACACAGGC	976	Db	1997	GTTATTTGATGACAGAACCACTCTCATAGACTGGTGCAGATCTCCACCTCCCGTCCAGGTC	2056
Qy	302	HisPheGluCysIleCysGluLyseGlyTyrTyrGlyLyseGlyLeuGlnTyrGluCysThr	321	Qy	662	SerGluLyseValHisAlaAlaSerTyrAspGluProGlnPheSerAspAanSerGlyAla	681
Db	977	CATTTTGTAGTCACTGTGTAAGAGGGGTATAACGGGAAGGCTCTGCAATGATGACTGCACA	1036	Db	2057	TCGGAGAGGTACATGCGCAAGCTGGGATGAGGCTCAGTTCTTCAGACACTCAGGTGCT	2116
Qy	322	AlaCysProSerGlyThrTyrLyseProGluGlySerProGlyGlyIleSerSerCysIle	341	Qy	682	GluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThrIle	701
Db	1037	GTTTGGCCCATCGGGACATACAAACCTGAAGGCTCACCGAGGAAATCAGCAGTTGCAAT	1096	Db	2117	GAATTTGTTTATTACAGAGTTCATACACAGAGAGCTTTTCCCTCAAGGGGAGACTATA	2176
Qy	342	ProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAspCysVal	361	Qy	702	ValGlnTyrThrAlaThrAspProSerGlyAanAanArgThrCysAspIleHisIleVal	721
Db				Db	2177	GTACAGATATACAGCCACTGACCCCTCAGGCAATTAACGACATGTGATATCATATTGTC	2236

QY 722 IleValSerProCysGluIleProPheThrProValAsnGlyAspPheIleCysThr 741
DB 2237 ATAAAGGTTCTCCCTGTGAATTCATTCACACTGTAAATGGGATTTTATGCACT 2296
QY 742 ProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPheThrGlu 761
DB 2297 CCAGATAATACTGGAGTCAACTGTACATTAACCTTGTCTGGAGGGCTATGATTTTCACAGAA 2356
QY 762 GlySerThrAspLysTyrCysAlaTyrGluAspGlyValTyrLysProThrTyrThr 781
DB 2357 GGGTCTACTACAAAGTATTTATGTGCTTATGAGATGGCGCTCTGGAAACCAACATATACC 2416
QY 782 ThrGluTyrProAspCysAlaLysLysArgPheAlaAsnHisGlyPheLysSerPheGlu 801
DB 2417 ACTGAATGGCCGAGCTGTCCAGTAAGCGTTTGTCAAAACACCGGGTTCAAGTCTCTTGAG 2476
QY 802 MetPheTyrLysAlaAlaArgCysAspAspThrAspLeuMetLysLysPheSerGluAla 821
DB 2477 ATGTTCTACAAAGCAGCTCGTTGTGATGACACAGATCTGATGAAGAAGTTTCTGAAGCA 2536
QY 822 PheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAspIleAsp 841
DB 2537 TTTGAGACGACCTCGGAAAAATGGTCCCATCATTTGTAGTATGATGACAGGACATTCAC 2596
QY 842 CysArgLeuGluLysLeuThrLysLysTyrCysLeuGluTyrAsnTyrAspTyrGlu 861
DB 2597 TGCAGACTGGAGAGAACCTTGACCAAAAAATATTCCTAGATATAATATGACTATGAA 2656
QY 862 AsnGlyPheAlaIleGlyProGlyGlyTyrGlyValAlaAlaAsnArgLeuAspTyrSerTyr 881
DB 2657 AATGGCTTTGCAATTTGTCAGGTGGCTGGGGTGCAGCTAATAGCTGGATTAATCTTAC 2716
QY 882 AspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLysSerSer 901
DB 2717 GATGACTTCTCGACACCTGTGCAAGAAACAGCCACAAAGCATCGGCAATGCCAAGTCTCTCA 2776
QY 902 ArgIleLysArgSerAlaProLeuSerAspTyrLysLysLeuIlePheAsnIleThr 921
DB 2777 CGGATTTAAAGAAGTGGCCCCATTCATCTGACTATATAAATTAAGTTAAATTTTAAACATCA 2836
QY 922 AlaSerValProLeuProAspGluArgAsnAspThrLeuGluTyrGluAsnGlnArg 941
DB 2837 GCTAGTGTGCCATTAACCGATGAAGAAGAAATGATACCTTCGATGGGAATACGACGA 2896
QY 942 LeuLeuGlnThrLeuGluThrIleThrAsnLysLeuLysArgThrLeuAsnLysAspPro 961
DB 2897 CTCTCTCAGACATTTGGAAACTATACAAATAAATCTGAAAGAGACTCTCTCAACAAGACCCC 2956
QY 962 MetTyrSerPheGlnLeuAlaSerGluIleLeuIleAlaAspSerAsnSerLeuGluThr 981
DB 2957 ATGTATTCCTTTTTCAGCTTGTATCAGAAATATCTATAGCCACAGCAATTCATTAGAAACA 3016
QY 982 LysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCysValAsn 1001
DB 3017 AAAAAGGCTTCCCTCTTCAGACACAGGCTCAGTGTGAGAGGGCGTATGTGTCAAT 3076
QY 1002 CysProLeuGlyThrTyrTyrAsnLeuGluHisPheThrCysGluSerCysArgIleGly 1021
DB 3077 TGCCCTTTGGGAACCTATTAATATCTGGAACATTTTCACTGTGAAAGCTGCCGGATCGGA 3136
QY 1022 SerTyrGlnAspGlnGluGlyGlnLeuGluCysLysLeuCysProSerGlyMetTyrThr 1041
DB 3137 TCTATCAAGATGAAGAGGGCACTTGAAGTGCAGCTTTTGCCCTCTGGGATGTACAG 3196
QY 1042 GluTyrIleHisSerArgAsnIleSerAspCysLysAlaGlnCysLysGlnGlyThrTyr 1061
DB 3197 GAATATATCAATTCAGAAACATCTCTGATTTGTAAGCTCAGTGTAAACCAAGGCCCTAC 3256
QY 1062 SerTyrSerGlyLeuGluThrCysGluSerCysProLeuGlyThrTyrGlnProLysPhe 1081
DB 3257 TCATACAGTGGACTTGAGACTTGTGAATCGTCCACTGGGCATTTATCAGGCCAAATTT 3316

QY 1082 GlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGlyValAlaVal 1101
DB 3317 GGTTCGCGAGCTGCTCTCTGTGTCAGAAAAACACCTCACTGTGAAAAAGAGGCCCTG 3376
QY 1102 AsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGlyLeuMet 1121
DB 3377 AACATTTCTGCATGTGGAGTTCTGTGTCCAGAGAAAAATCTCGCGTTCCTGGGTAAATG 3436
QY 1122 ProCysHisProCysProArgAspTyrTyrGlnProAsnAlaGlyLysAlaPheCysLeu 1141
DB 3437 CCCTGTCAACCATGTCTCGTGACTATTACCAACTAATGAGGAGGCCCTTCTGCGCTG 3496
QY 1142 AlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGluCysSer 1161
DB 3497 GCCTGTCCCTTTTATGAACTTACCCCATTCGTGTGTTCCAGATCCATCACAGAAATGTCA 3556
QY 1162 SerPheSerSerThrPheSerAlaAlaGluGluSerValValProProAlaSerLeuGly 1181
DB 3557 AGTTTATAGTTCAACTTCTCAGCGCAGAGAGAAAGTGTGTGCGCCCTCTCTCTTGGGA 3616
QY 1182 HisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPheAsnPro 1201
DB 3617 CATATTAAAGAGGCGCATGAATCAGCAGTCAGCAAGTCATGAATGCTTCTTTAACCCCT 3676
QY 1202 CysHisAsnSerGlyThrCysGlnGlnLeuGluValArgGlyTyrValCysLeuCysProLeu 1221
DB 3677 TGCACACATAGTGGAACTTCCAGCAACTTGGGGTGTGTTATGTTTCTCTGTCCACTT 3736
QY 1222 GlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuProCysLeu 1241
DB 3737 GGAATATACAGCTTTAAAGTGTGAAACAGACATCGATGAGTGCAGCCCACTGCTTGCCTC 3796
QY 1242 AsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSerGlyTyr 1261
DB 3797 AACAATGGAGTTTGTAAAGACCTAGTTTGGGGAATTCATTTGTGAGTGCCTCAGGTAC 3856
QY 1262 ThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerProCysLeuAsnLys 1281
DB 3857 ACAGTAAGCACTGTGAATTTGAACATCAATGAATGTCACTCATTCATTCATGTAANTCAG 3916
QY 1282 GlyIleCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPheValGly 1301
DB 3917 GCCACCTGTGTGGATGAATTAATTCATACAGTTGTAAATGTCCAGCCAGGATTTTCAGGC 3976
QY 1302 LeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAlaVal 1321
DB 3977 AAAAGGTGTGAAACAGGTATGTATCAACTCAGTGTGTTATTAATACCTTAATATGCAATC 4036
QY 1322 CysGluAspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGlyThrArg 1341
DB 4037 TGTGAGACACAGGTGTGGGGATTTCTGTGCAATGCCACCTGGATTTTGGGTACCGCA 4096
QY 1342 CysGlyLysAsnValAspGluCysLeuSerGlnProCysLysAsnGlyAlaThrCysLys 1361
DB 4097 TGTGGAAGAAACCTCGATGATGTCTCAGTCAGCATCGCAAAATGAGACTTACCTGTAAA 4156
QY 1362 AspGlyAlaAsnSerPheArgCysLeuCysAlaIleGlyPheThrGlySerHisCysGlu 1381
DB 4157 GACGGTGCCTAATAGCTTTCAGGTGCTGTGTGCAAGTGTGCAAGTTCACAGGATCACTGTGAA 4216
QY 1382 LeuAsnIleAsnGluCysGlnSerAsnProCysArgAsnGlnAlaThrCysValAspGlu 1401
DB 4217 TTGACATCATGAAATGTCACTCTATCCATGTAGAAATCAGGCCACCTGTGTGGATGAA 4276
QY 1402 LeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGluThrGlu 1421
DB 4277 TTAATATCATACAGTTGTAAATGTTCAGCCAGGATTTTCAGGCCAAAAGGTGTGAAACAGAA 4336
QY 1422 GlnSerThrGlyPheAsnLeuAspPheGluValSerGlyIleTyrGlyTyrValMetLeu 1441
DB 4337 CAGTCTACAGGCTTTTAACTGGATTTTGAAGTTTCTGGCATCTATGGAATATGTATGCTA 4396
QY 1442 AspGlyMetLeuProSerLeuHisAlaLeuThrCysThrPheThrMetLysSerSerAsp 1461

Db 4397 GATGGCATGCTCCCATCTCTCCATGCTCTAACTGTACCTTCTGGATGAATCTCTGAC 4456
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Db 4457 GACATGAACATATGGAACACCAATCTCTATGAGATTGATACGGCAGCACAATACCTTG 4516
QY 1482 LeuLeuThrAspTyrAsnGlyTyrValLeuTyrValAspGlyArgGluLysIleThrAsn 1501
Db 4517 CTCCTGACTGATTATAACGGGTGGTCTTTATGTGAATGGCAGGAAAGATAACAAAC 4576
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QY 1562 GluGlyPheSerProAlaGluSerPheValGlySerIleSerGlnLeuAsnLeuTyrAsp 1581
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QY 1602 LysGlyAsnValIleAlaTyrProAspPheLeuSerGlyIleValGlyLysValLysIle 1621
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QY 1622 AspSerLysSerIlePheCysSerAspCysProArgLeuGlyGlySerValProHisLeu 1641
Db 4937 GATTTCAAGACATATTTTGTCTGATTGCTGATCCACCGCTTGGAGGGTCAGTGCCTCATCTG 4996
QY 1642 ArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAspProGly 1661
Db 4997 AGACTGCACTGAAGATTAAACAGGTTCMAAGTCAATCTGTTCTGTGACCAAGGC 5056
QY 1662 PheGlnLeuValGlyAsnProValGlnTyrCysLeuAsnGlnGlyGlnTyrThrGlnPro 1681
Db 5057 TTCCAGCTGTGGGAACCTGTGTCAGTACTGTCTGAATCAAGGACAGTGGACACAACA 5116
QY 1682 LeuProHisCysGluArgIleSerCysGlyValProProProLeuGluAsnGlyPheHis 1701
Db 5117 CTCGCCCACTGTGAACGCATTCTGCTGGGGTGCACCTCTTTGGAGAAATGGCTTCCAT 5176
QY 1702 SerAlaAspAspPheTyrAlaGlySerThrValThrTyrGlnCysAsnAsnGlyTyrTyr 1721
Db 5177 TCAGCCGATGACTTCTATGCTGGCAGACAGTAACCTACAGTGCACAACATGGCTACTAT 5236
QY 1722 LeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTyrAsnGlyValSerPro 1741
Db 5237 CTATTGGGTGACTCAAGGATGTTCTGTACAGATAATGGGAGCTGGAAACGGCTTCAACA 5296
QY 1742 SerCysLeuAspValAspGluCysAlaValGlySerAspCysSerGluHisIleAspCys 1761
Db 5297 TCTCTGTAGATGTCGATGAGTGCAGTTGGATCAGATTGTAGTGCAGCATGCTCTTTCG 5356
QY 1762 LeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAspGlyLys 1781
Db 5357 CTGAAGTGAATGATCCATACATATTTTATGTGTCCACCCGTACACAGAGATGGGAAA 5416
QY 1782 AsnCysAlaGluProIleLysCysValAlaProGlyAsnProGluAsnGlyHisSerSer 1801
Db 5417 AACTGTGCAGAACCTATAAAATGTAAGGTCCAGGAAATCCGGAATAATGGCCACTCTCA 5476
QY 1802 GlyGluIleTyrThrValGlyAlaAlaValThrPheSerCysGlnGluGlyTyrGlnLeu 1821

Db 5477 GGTGAGATTATATACAGTAGGTCCGGAAGTCAACATTTTCTGTGAGGAAGATACCAAGTTG 5536
QY 1822 MetGlyValThrLysIleThrCysLeuGluSerGlyGluTyrAsnHisIleLeuIleProTyr 1841
Db 5537 ATGGGAGTAAACCAATATCAATGTTTGGAGTCTGGAGNATGGAAATCATCTAATACCATAT 5596
QY 1842 CysLysAlaValSerCysGlyLysProAlaIleProGluAsnGlyCysIleGluGluLeu 1861
Db 5597 TGTAAAGCTGTTTCATGTGTAAACCGGCTATTTCCAGAAAAATGTTGTCATTGAGGAGTTA 5656
QY 1862 AlaPheThrPheGlySerLysValThrTyrArgCysAsnLysGlyTyrThrLeuAlaGly 1881
Db 5657 GCATTTTACTTTTGGCAGCAAGTGCATATAGGTGTAAATAAGGATATATCTCTGGCCGGT 5716
QY 1882 AspLysGluSerSerCysLeuAlaAsnSerSerTyrSerHisSerProValCysGlu 1901
Db 5717 GATTAAGATCATCTCTGCTTGTCTACAGTCTTGGAGTCAATTTCCCTCTCTGTGTGAA 5776
QY 1902 ProValLysCysSerSerProGluAsnIleAsnAsnGlyLysTyrIleLeuSerGlyLeu 1921
Db 5777 CCAGTGAAGTGTCTAGTCCGGAATAATAATAATAATGAAAAATATATTTTGAAGTGGGCTT 5836
QY 1922 ThrTyrLeuSerThrAlaSerTyrSerCysAspThrGlyTyrSerLeuGlnGlyProSer 1941
Db 5837 ACCTACCTTTCTACTGTCATCATATTCATGCGATACAGGATACAGCTTTACAGGGCCCTTCC 5896
QY 1942 IleIleGluCysThrAlaSerGlyIleTyrAspArgAlaProProAlaCysHisLeuVal 1961
Db 5897 ATATTGAATGCACGGCTTCTGGCATCTGGACAGAGGCGCACCTGCTCTCACTCTGTC 5956
QY 1962 PheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPheThrPhe 1981
Db 5957 TTCTGTGGAGAACCACTGCCATCAAAAGATGCTGTCTATTACGGGGAATAAATCTTCACTTTC 6016
QY 1982 ArgAsnThrValThrTyrThrCysLysGluGlyTyrThrLeuAlaGlyLeuAspThrIle 2001
Db 6017 AGAAACACCGTCATTTACACTTGCAAAGAGGGCTATACTCTTGTGTGCTTTGACACCAT 6076
QY 2002 GluCysLeuAlaAspGlyLysTyrSerArgSerAspGlnGlnCysLeuAlaValSerCys 2021
Db 6077 GAATGCTGGCCGACCGCAAGTGGAGTAGAAGTGACCAAGTGCCTGGCTGTCTCTCTGT 6136
QY 2022 AspGluProProIleValAspHisAlaSerProGluThrAlaHisArgLeuPheGlyAsp 2041
Db 6137 GATGACCAACCATTTGTGGACCAACGCTCTCCAGAGACTGCCCATCGGCTTTTGGAGAC 6196
QY 2042 IleAlaPheTyrTyrCysSerAspGlyTyrSerLeuAlaAspAsnSerGlnLeuLeuCys 2061
Db 6197 ATTGCATTTCTACTACTGCTCTGATGTTACAGCTAGCAGACAAATTTCCAGCTTCTCTGC 6256
QY 2062 AsnAlaGlnGlyLysTyrValProProGluGlyGlnAspMetProArgCysIleAlaHis 2081
Db 6257 AATGCCACGCGCAAGTGGGTACCCCCAGAAAGGTCAAGACATGCCCGCTGTATAGCTCAT 6316
QY 2082 PheCysGluLysProProSerValSerTyrSerIleLeuGluSerValSerLysAlaLys 2101
Db 6317 TTCTGTGAAAAACCTCCATCGGTTCCTATAGCATCTTGGAAATCTGTGAGCAAGCAAAA 6376
QY 2102 PheAlaAlaGlySerValValSerPheLysCysMetGluGlyPheValLeuAsnThrSer 2121
Db 6377 TTTGCACTGGCTCAGTTGTGAGCTTTAATGCAATGGAGGCTTTGTACTGAACACCTCA 6436
QY 2122 AlaLysIleGluCysMetArgGlyGlyGlnTyrAsnProSerProMetSerIleGlnCys 2141
Db 6437 GCAAGATTGAATGATGATGAGGTGGGAGTGGACCCCTTCCCCCATGTCCATCCAGTGC 6496
QY 2142 IleProValArgCysGlyGluProProSerIleMetAsnGlyTyrAlaSerGlySerAsn 2161
Db 6497 ATCCCTGTGGGTGTGGAGAGCCACCAAGCATCATGAATGGCTATGCAAGTGAATCAAC 6556
QY 2162 TyrSerPheGlyAlaMetValAlaTyrSerCysAsnLysGlyPheTyrIleLysGlyGlu 2181
Db 6557 TACAGTTTGGAGCCATGTTGGCTTACAGCTGCACACAGGGGTTCTACATCAAGGGGAA 6616

QY 2182 LysLysSerThrCysGluAlaThrGlyGlnTrpSerSerProIleProThrCysHisPro 2201
DB 6617 AAGAAAGAGCACCCTGCGAAGCCACAGGCGAGTGGAGTAGTCTCTATACCGACGTCGCCACCG 6676
QY 2202 ValSerCysGlyGluProProLysValGluAenGlyPheLeuGluHisThrThrGlyArg 2221
DB 6677 GTATCTTGTGGTGAACCACTAAGGTTGAGATGGCTTTCTGGAGCATACAACCTGGCAG 6736
QY 2222 IlePheGluSerGluValArgTyrGlnCysAsnProGlyTyrLysSerValGlySerPro 2241
DB 6737 ATCTTTGAGAGTGAAGTGAAGTATCAGTGTACCCCGGCTATPAAGTCAGTCGGAAGTCT 6796
QY 2242 ValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeuMetCysValPro 2261
DB 6797 GTATTTGTCTGCGACAGCAATCGCCACTGCGCAGTGAATCCCTCTGTATGTGTCTCT 6856
QY 2262 LeuAspCysGlyLysProProIleGlnAenGlyPheMetLysGlyGluAenPheGlu 2281
DB 6857 CTCGACTGTGGAAACCTCCCGCATCCAGATGGCTTTCATGAAGGAGAAACTTTGAA 6916
QY 2282 ValGlySerLysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyAspSerSer 2301
DB 6917 GTAGGTCACAGGTTTCAGTTTCTGTATGAGGTTATGAGCTTGTGTGACAGTTCT 6976
QY 2302 TrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAla 2321
DB 6977 TCGACATGTGCAAAATCTGCGAAATGGAATGAAGTCAAAATCAAAAGTGCATGCGCTGCC 7036
QY 2322 LysCysProGluProProLeuLeuGluAenGluValLeuLysGluLeuThrThrGlu 2341
DB 7037 AGTGTGCCAGAGCGGCCCTCTTTGGAAACCACTAGTATTAAGGNGTTGACACCGAG 7096
QY 2342 ValGlyValValThrPheSerCysLysGluGlyHisValLeuGlnGlyProSerValLeu 2361
DB 7097 GTAGGATGTGACATTTCTTCTGTAAGAGGCGCATGTCTCTGCAAGGCCCTCTGTCTCTG 7156
QY 2362 LysCysLeuProSerGlnTrpAsnAspSerPheProValCysLysLysIleValLeuCys 2381
DB 7157 AAATGCTTGCATCCCGCAATGGAATGACTTTCTCCCTGTTTGTGAAGATGTCTCTTGT 7216
QY 2382 ThrProProLeuLeuSerPheGlyValProIleProSerSerAlaLeuHisPheGly 2401
DB 7217 ACCCCACCTCCCTAAATTTCTTTGTGTGTCCTCCCATCTCTTCTCTCTCTCTCTCTCTG 7276
QY 2402 SerThrValLysTyrSerCysValGlyGlyPhePheLeuArgGlyAsnSerThrThrLeu 2421
DB 7277 AGTACTGTCAAGTATTTCTGTGTAGTGGGTTTTCTTAAGAGGAAATTTCTACCCCTC 7336
QY 2422 CysGlnProAspGlyThrTrpSerSerProLeuProGluCysValProValGluCysPro 2441
DB 7337 TGCACACCTGATGGCACCTGGAGCTCTCCACTGCCAGAATGTGTTCAGTAGAATGTCCC 7396
QY 2442 GlnProGluGluLeuProAsnGlyIleIleAspValGlnGlyLeuAlaTyrLeuSerThr 2461
DB 7397 CAACCTTGAGGAATCCCAATGGAATCATTTGATGTGCAGGCTTGTCTATCTCAGCACA 7456
QY 2462 AlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeuCysGly 2481
DB 7457 GCTCTCTATACCTGCAAGCCAGGCTTTGAATTTGGTGGAAATATACTACCACCTTTGTGGA 7516
QY 2482 GluAsnGlyHisTrpLeuGlyGlyLysProThrCysLysAlaIleGluCysLeuLysPro 2501
DB 7517 GAAATGGTCACTGGCTTGGAGGAAACCAACATGTAAGCCCAATGAGTGCCTGGAACCC 7576
QY 2502 LysGluIleLeuAenGlyLysPheSerTyrThrAspLeuHisTyrGlyGlnThrValThr 2521
DB 7577 AAGGAGATTTGAATGGCAATTTCTCTTACCGGACTACACTATGACGACGCGTTACC 7636
QY 2522 TyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThr 2541
DB 7637 TACTCTTGCAACCGAGGCTTTGCGCTCGAAGGTCCTGAGTGCCTTTGAGAGACA 7696

QY 2542 GlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGlnPro 2561
DB 7697 GGTGATTTGGATGTAGATGCCCTCTTGCATATGCCATCCACTGTGATTTCCTCCCAACCC 7756
QY 2562 IleGluAenGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIleIleTyrSer 2581
DB 7757 ATTGAAATGGTTTTGTAGAGGTGCAGATTACAGCTATGTGTGCATAATCATCTACAGT 7816
QY 2582 CysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrp 2601
DB 7817 TGTCTCCCTGGGTTTCAGGTGGCTGTGTCATGTCATGCGACCTGTGAGAGTTCAGGATG 7876
QY 2602 SerSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIleAspPhe 2621
DB 7877 TCAAGTTCCATCCCAACATGTATGCCAATAGACTGTGGCCTCCCTCTCATATAGATTT 7936
QY 2622 GlyAspCysThrLysLeuLysAspAspGlnGlyTyrPheGluGlnGluAAspAspMetMet 2641
DB 7937 GGAGACTGTACTAAACTCAAGATGACCGGATATTTTCAGCAAGAAAGACGACATGATG 7996
QY 2642 GluValProTrpValThrProHisProProTrpHisLeuGlyAlaValAlaLysThrTrp 2661
DB 7997 GAAGTTCCATATGTGACTCTCTCCCTCTTATCATTTTGGGAGCAGTGGCTTAAACCTGG 8056
QY 2662 GluAsnThrLysGluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetVal 2681
DB 8057 GAAATACAAAGAGGCTCTCTGCTACACATTCATCAAACTTCTGTATGTGATGACATGGT 8116
QY 2682 SerTyrThrCysAsnProGlyTyrGluLeuLeuGlyAsnProValLeuIleCysGlnGlu 2701
DB 8117 TCATACACCTGTAACTCCAGGATATGAATCTTCTGGGAACCTGTGTCTGATCTGCAGAA 8176
QY 2702 AspGlyThrTrpAsnGlySerAlaProSerCysLysIleSerIleGluCysAspLeuProThr 2721
DB 8177 GATGGAACTTTGGATGGCAGTCACCATCTCTGCAATTTCAATTTGAATGTGATCTTGCAT 8236
QY 2722 AlaProGluAenGlyPheLeuArgPheThrGluThrSerMetGlySerAlaValGlnTyr 2741
DB 8237 GCTCTCGAAATGGCTTTTTCGCTTTTACAGAGACTAGCTGGAGTGTCTGTGAGTAT 8296
QY 2742 SerCysLysProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArg 2761
DB 8297 AGCTGTAAACCTCGACACATTTCTAGCAGGCTCTGACTTAAGCTTTGTCTAGAGAAATGA 8356
QY 2762 LysTrpSerGlyAlaSerProArgCysGluAlaIleSerCysLysLysProAsnProVal 2781
DB 8357 AAGTGGAGTGGTGCCTCCCAAGCTGTGAAGCCATTTTCATGCAAAAAGCCAAATCCAGTC 8416
QY 2782 MetAsnGlySerIleLysGlySerAsnTyrThrTyrLeuSerThrLeuTyrTyrGluCys 2801
DB 8417 ATGAATGGATCCCATCAAGGAAGCACTACACATCTGAGCAGCTGTGTACTATGAGTGT 8476
QY 2802 AspProGlyTyrValLeuAenGlyThrGluArgThrCysGlnAspAspLysAsnTrp 2821
DB 8477 GACCCCGATATGTGCTGAATGGCAGCTGAGAGAGAACATGCCAGGATGACAAAACTGG 8536
QY 2822 AspGluAspGluProIleCysIleProValAspCysSerSerProProValSerAlaAsn 2841
DB 8537 GATGAGATGAGGCCCATTTGCTCTCTGTGAGCTGCGAGTTTCCACCCAGTCTCAGCCAA 8596
QY 2842 GlyGlnValArgGlyAspGluTyrThrPheGlnLysGluIleGluTyrThrCysAsnGlu 2861
DB 8597 GGCAGGTGAGAGAGACGATACACATTCNAAAAGAGATTGAATACACTTGCATGCAATGA 8656
QY 2862 GlyPheLeuLeuGluGlyAlaArgSerArgValCysLeuAlaAsnGlySerTrpSerGly 2881
DB 8657 GGGTTCTTGTGAGGAGGAGCAGTGGTGTCTTGTGCAATGGAAGTTGGAGTGGAGTGA 8716
QY 2882 AlaThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGlyVal 2901
DB 8717 GCCACTCCCGACTGTGTGCTGTGATGTGCCATGTCACCCCGCACCACTGGCCCAATGGGGTG 8776
QY 2902 ThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGluGlyTyr 2921

Db	8777	ACGGAAGCGCTGGACTATGGCTTCAAGGAAGTAACATTTCACTGTCACGAGGCGTAC	8836
Qy	2922	IleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGlyAsnTrpAspAlaGluIle	2941
Db	8937	ATCTTGACCGGTGCTCAAAACTCACCTGTCACTGCAGATGGCACTGGGATGCAGATT	8996
Qy	2942	ProLeuCysLysProValAsnCysGlyProProGluAspLeuAlaHisGlyPheProAsn	2961
Db	8897	CCTCTGTAAACCACTCAACTGTGGACCTCTCTGAAGATCTTGCCCATGGTTTCCCTTAAT	8956
Qy	2962	GlyPheSerPheIleHisGlyGlyHisIleGlnTyrrGlnCysPheProGlyTyrrLysLeu	2981
Db	8957	GGTTTTTCTTTATTTCAATGGGGGCATATACAGTATCAGTGCCTTTCTGTTGTATAAGCTC	9016
Qy	2982	HisGlyAsnSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerProSer	3001
Db	9017	CATGGAAATTCATCAGAAGGTGCTCTCCATGCGCTCTGGAGTGGCAGCTACCTTCC	9076
Qy	3002	CysLeuProCysArgCysSerThrProValIleGluTyrrGlyThrValAsnGlyThrAsp	3021
Db	9077	TGCTGCTTGCAGATGTTCCACACCACTGAATTCGAATATGGAACCTGTCAATGGGACAGAT	9136
Qy	3022	PheAspCysGlyLysAlaAlaArgIleGlnCysPheLysGlyPheLysLeuLeuGlyLeu	3041
Db	9137	TTTGACTGTGGAAAGGCGAGCCGGATTCAGTGCCTTCAAGGCTTCAAGCTCTCTAGGACTT	9196
Qy	3042	SerGluIleThrCysGlyAlaAspGlyGlnTrpSerSerGlyPheProHisCysGluHis	3061
Db	9197	TCTGAAATACCTGTGAAGCCGATGGCCAGTGGAGCTCTGGGTTCCTCCCACTGTGAACAC	9256
Qy	3062	ThrSerCysGlySerLeuProMetIleProAsnAlaPheIleSerGluThrSerSerTrp	3081
Db	9257	ACTTCTTGGTGTTCTCTTCCAAATGATACCAATGCGTTTCATCAGTGAGACCAGCTCTGG	9316
Qy	3082	LysGluAsnValIleThrTyrrSerCysArgSerGlyTyrrValIleGlnGlySerSerAsp	3101
Db	9317	AAGGAAATATGATAAATCTTACAGCTGCAGGCTCGATATGTCTATACAAAGGCGTTCAGAT	9376
Qy	3102	LeuIleCysThrGluLysGlyValTrpSerGlnProTyrrProValCysGluProLeuSer	3121
Db	9377	CTGATTTGTACAGAAAGGGGTATGAGCCAGCTTATCAGTCTGTGAGCCCTTGTGCC	9436
Qy	3122	CysGlySerProProSerValAlaAsnAlaValAlaThrGlyGluAlaHisThrTyrrGlu	3141
Db	9437	TGTGGGTCCCACCCTCTGTGCCAATGCAGTGGCACTGGAGAGGCACACACCTATGAA	9496
Qy	3142	SerGluValLysLeuArgCysLeuGluGlyTyrrThrMetAspThrAspThrAspThrPhe	3161
Db	9497	AGTGAAGTGAACCTCAGATGCTCGGAAGGTATACGATGGATACAGATACAGATACATTCT	9556
Qy	3162	ThrCysGlnLysAspGlyArgTrpPheProGluArgIleSerCysSerProLysLysCys	3181
Db	9557	ACCTGTGAGAAAGATGTGTGGTCTCCCTGAGAGAATCTCTGTCAGTCTCTAAAATGT	9616
Qy	3182	ProLeuProGluAsnIleThrHisIleLeuValHisGlyAspAspPheSerValAsnArg	3201
Db	9617	CCTCTCCGGAAACATAAACATATATCTGTACATGGGACGATTTCACTGTGAATAGG	9676
Qy	3202	GlnValSerValSerCysAlaGluGlyTyrrThrPheGluGlyValAsnIleSerValCys	3221
Db	9677	CAAGTTTCTGTGTCAATGTCAGAAAGGATATACCTTTGAGGAGGTAAACATATCAGTATGT	9736
Qy	3222	GlnLeuAspGlyThrTrpGluProPheSerSerAspGluSerCysSerProValSerCys	3241
Db	9737	CAGCTTGATGGAACCTGGAGCCACCAATCTCCGATGAATCTTGCAGTCCAGTTTCTGT	9796
Qy	3242	GlyLysProGluSerProGluHisGlyPheValValGlySerLysTyrrThrPheGluSer	3261
Db	9797	GGGAAACCTGAAAGTCCAGAACATGGATTTGTGGTGGCAGTAATAATACACTTTGAAGC	9856
Qy	3262	ThrIleIleTyrrGlnCysGluProGlyTyrrGluLeuGluGlyAsnArgGluArgValCys	3281

9957	ACAAATTATTATTCAGTGTGAGCCTCGCTATGAACCTAGAGGGGAAACAGGGAAAGTGCTCTGC	9916
3282	GlnGluAsnArgGlnTrpSerGlyGlyValAlaIleCysLeuGluThrArgCysGluThr	3301
9917	CAGGAGAACAGACAGTGGAGTGGAGGGTGGCAATATGCAAAAGAGACACAGGTGTGAAACT	9976
3302	ProLeuGluPheLeuGlnGlyValAlaAspIleGluAsnArgThrThrGlyProAsnVal	3321
9977	CCACTTGAATTTCTCAATGGGAAGCTGCACATTGAAAAACAGACGACGTGGACCCACGCG	10036
3322	ValTyrSerCysAsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThrGlu	3341
10037	GTATATTCTGCAACAGAGGCTACAGTCTTTGAAGGGCCATCTGAGGACACATGACAGAA	10096
3342	AsnGlyThrTrpSerHisProValProLeuCysLysProAsnProCysProValProPhe	3361
10097	AAITGGAACTGGAGGCCACCCAGTCCCTCTCTGCNAACCAAAATCCATGGCCCTGTCTCTTT	10156
3362	ValIleProGluAsnAlaLeuLeuSerGlyLysGluPheTyrValAspGlnAsnValSer	3381
10157	GTGATTTCCGAGAAATGCTCTGCTGCTCGAAAGGAGTTTATGTGTGATCAGATGTGTCC	10216
3382	IleLysCysArgGluGlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAsnProAsp	3401
10217	ATCAAAATGTAGGGAAGGTTTTCTGCTGCAGGGCCACGGCATCATTTACCTGCACACCCGAC	10276
3402	GluThrTrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProProAlaHis	3421
10277	GAGACGTGGACACAGACAAGCGCAAAATGTGAAAAAATCTCAATGTGTCCACAGCTCAC	10336
3422	ValGluAsnAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyrSer	3441
10337	GTAGAAAAATGCAATTGCTCGAGGCGTACATTATCAATATGGAGACATGATCACTACTCA	10396
3442	CysTyrSerGlyTyrMetLeuGlnGlyPheLeuArgSerValCysLeuGluAsnGlyThr	3461
10397	TGTTACAGTGGATACATGTGGAGGGTTTCCGTAGAGAGTGTGTGTTAGAAATGTGAACA	10456
3462	TrpThrSerProIleCysArgAlaValCysArgPheProCysGlnAsnGlyGlyIle	3481
10457	TGGACATCACTCTATTTCGAGAGCTGTCTGTGATTTCCATGTGAGAAATGGGGCATC	10516
3482	CysGlnArgProAsnAlaCysSerCysProGluGlyTrpMetGlyArgLeuCysGluGlu	3501
10517	TGCCAAGGCCCAAAATGCTTTGTTCTGTCTCAGAGGGCTGGATGGGGCGCTCTGTGAAGAA	10576
3502	ProIleCysIleLeuProCysLeuAsnGlyGlyArgCysValAlaProTyrGlnCysAsp	3521
10577	CCAACTGCAATCTTCCCTGTCTGAACGGAGGTGCTGTGTGGCCCCCTTACAGTGTGAC	10636
3522	CysProProGlyTrpThrGlySerArgCysHisThrAlaValCysGlnSerProCysLeu	3541
10637	TGCCCGCTGGCTGGACGGGGTCTCGCTGTCTATACAGCTGTGTGGCAGTCTCCCTGCTTA	10696
3542	AsnGlyGlyLysCysValArgProAsnArgCysHisCysLeuSerSerTrpThrGlyHis	3561
10697	AAITGGTGGAAAAATGTGTAGACCAACCAACCAATGACTACTGTCTTTCTTCTTGTGGACGGACAT	10756
3562	AsnCysSerArgLysArgThrGlyPhe	3571
10757	AACTGTTCCAGAAAAAGGAGCACTGGGTTTT	10786
db		db

RESIST

AF206329	AF206329	11289 bp	mRNA	linear	ROD 15-NOV-2000
LOCUS	Mus musculus polydrom protein mRNA, complete cds.				
DEFINITION	AF206329				
ACCESSION	AF206329.1	GI:11177163			
VERSION					
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				

Db 461 GGCACCTGGAGCTGCTCTCTCTGTTGGAGAGTGGTCCAGGTGGGCAACCAACTTC 520
Qy 100 ArgSerGluLeuMetPheValArgIysLeuLeuSerAspPheProValProThrAla 119
Db 521 CTCACAGAGCTCAAGTTCGTGGCGCAAGCTGCTGTCGCACTCCCGCTGGTGTCCACGGCC 580
Qy 120 ThrArgValAlaIleValThrPheSerSerIysAsnTyrValValProArgValAspTyr 139
Db 581 ACGCTGTGGCCATCGTCACTCTCATCCAGAACAACAGTGGTGGCGCGGTGGATTAC 640
Qy 140 IleSerThrArgAlaArgGlnHisIysCysAlaLeuLeuLeuGlnGluProAla 159
Db 641 ATCTCCACGCGCGCGCACCAACACAAAGTGGCGCTACTCAGCGCGAGATCCCGGCC 700
Qy 160 IleSerTyrArgGlyGlyGlyThrTyrThrIysGlyAlaPheGlnAlaGlnIle 179
Db 701 ATCAGCTACCGCGGTGGTGGCACTATACCAAGGGCGCTTCAGCAAGCGCGCAAAATC 760
Qy 180 LeuLeuHisAlaArgGluAsnSerThrIysValValPheLeuIleThrAspGlyTyrSer 199
Db 761 CTTCCTCACTTAGAGAAAACCTCCACCAAGTCATATTTCTCATCAGCGCTATTTC 820
Qy 200 AsnGlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePhe 219
Db 821 AATGGCGGAGACCCAGACCTATTGCAGCATCGCTTGGGATTCGGAGTGGAGATCTTC 880
Qy 220 ThrPheGlyIleTyrGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProIys 239
Db 881 ACGTTCCGGATTTGGCAGGGGAATATCCGGGAATGCAATGATGATGCTTCCACCCCGAAG 940
Qy 240 GluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAla 259
Db 941 GAAGAACATGTGTACTGCTCCACAGTGTGAAGAAATTTAGAGCTTTAGCTCGCAGGGCG 1000
Qy 260 LeuHisGluAspLeuSerGlySerPheIleGlnAspAspMetValHisCysSerTyr 279
Db 1001 TTGCATGAAGATCTACTTCTGGAGTTTATCCAAAGAGGATATGCCCGCTGCTTTAT 1060
Qy 280 LeuCysAspGluGlyIysAspCysCysAspArgMetGlySerCysIysCysGlyThrHis 299
Db 1061 CTCCTGAGGCTGGGAAGACTGCTGTGACAGATGGCCAGCTGCAAAATGTGGGACACAC 1120
Qy 300 ThrGlyHisPheGluCysIleCysGluIysGlyTyrTyrGlyIysGlyLeuGlnTyrGlu 319
Db 1121 ACGGTCAATTTGAATGCATCTGTGAGAGGCTATTACGGGAAGTCTGCAGCATGAG 1180
Qy 320 CysThrAlaCysProSerGlyThrTyrIysProGluGlySerProGlyIysSerSer 339
Db 1181 TGCACAGCTTGGCCATCAGGACATATAAGCCGGAAGCTTCTCCAGGAGGATCAGCACC 1240
Qy 340 CysIleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAsp 359
Db 1241 TGCATCCCATGTCTCTGAGCTAAGCACACACTCCACCCTCGGAAGCACTTCCCTGAAGAC 1300
Qy 360 CysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysPro 379
Db 1301 TCGGTGTCGGAGAGGATACCAAGACTGTGCCAGACTGTGAGGTGTCCACTGTCTCT 1360
Qy 380 AlaLeuIysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsn 399
Db 1361 GCCCTGAAGCCTCTGAAAATGTTTTTTATACAAAACACTTGCAAAACCACTTCAAT 1420
Qy 400 AlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleIleLeu 419
Db 1421 GCCGCTGTGGGGTCCGATGTGCCCGGGCTTTGACCTTGTGGGAAGCAGCATCCATTG 1480
Qy 420 CysLeuProAsnGlyLeuTyrSerGlySerGluSerTyrCysArgValArgThrCysPro 439
Db 1481 TGTCAACCAATGGTTTGTGTCTGGGACAGAAAGCTTCTGCAGAGTGTGAGACGTGCC 1540
Qy 440 HisLeuArgGlnProIysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrIys 459

Db 1541 CACCTCGACACGCCCAACACGCGCACATCAGCTGCTCCACTCGCGGAATGTCTTACAAC 1600
Qy 460 ThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspIysLeuThr 479
Db 1601 ACCCTGTGTTGGTTTACCTGCAATGAAGGATACAGATTAGAAGGCGACATAGGCTTACC 1660
Qy 480 CysGlnGlyAsnSerGlnTyrAspGlyProGluProArgCysValGluArgHisCysSer 499
Db 1661 TGTCAAGGAATGCCAGTGGGATGGCCAGAGCCCGGTGTGTAGACGCCATTTGTGCC 1720
Qy 500 ThrPheGlnMetProIysAspValIleIleSerProHisAsnCysGlyIysGlnProAla 519
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Qy 520 IysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValIys 539
Db 1781 AGGCTGGGATGACCTGTGCTAAGCTGCCGCCAGGATACATTTTATCCGGGGTCAGA 1840
Qy 540 GluMetLeuArgCysThrThrSerGlyIysTyrAsnValGlyValGlnAlaAlaValCys 559
Db 1841 GAA---GTGAGATGTCCACATCTGGGAAGTGGAGTGGCCAAAGTTCAGACAGCTGTGTC 1897
Qy 560 IysAspValGluAlaProGlnIleAsnCysProIysAspIleGluAlaIysThrLeuGlu 579
Db 1898 AAGATGTGGAGGCTCCCAAAATCAGCTGTCCAAATGCAATTCAGGCAAGACTGGGAG 1957
Qy 580 GlnGlnAspSerAlaAsnValThrTyrGlnIleProThrAlaIysAspAsnSerGlyGlu 599
Db 1958 CAGCAGGACTCTGTGCTAATGTCACTGGCAAGTCCCAACAGCTAAAGCAACTCTGGTGA 2017
Qy 600 IysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp 619
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Qy 620 ValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHis 639
Db 2078 GTGGCCATCACCTACAGGCAACCGACTCATCCGGTAACCAAGCCAGCTGCACTTCTAC 2137
Qy 640 IleIysValIleAspAlaGluProProValIleAspTyrCysArgSerProProVal 659
Db 2138 ATTAAGGTGATTGATGTGGACCGCTGTCAAGATTGTGTGGCGATCTCCACCTCCAACT 2197
Qy 660 GlnValSerGluIysValHisAlaAlaSerTyrAspGluProGlnPheSerAspAsnSer 679
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Qy 680 GlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGlu 699
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Qy 700 ThrIleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHis 719
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Qy 720 IleValIleIysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIle 739
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Qy 740 CysThrProAspAsnThrGlyValAsnCysThrLeuThrCysLeuGluGlyTyrAspPhe 759
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Qy 760 ThrGluGlySerThrAspIysTyrTyrCysAlaTyrGluAspGlyValTyrIysProThr 779
Db 2498 ACGAAGGCTCACTGAGAGTACTACTGTGCTTTTGAAGATGTTATCTGAGAGACCCCA 2557
Qy 780 TyrThrThrGluTyrProAspCysAlaIysIysArgPheAlaAsnHisGlyPheIysSer 799
Db 2558 TACTCTACAGATGCCAGACTGTGCTATAAAGCGTTTTTGGCAACCATGTTTCAAGTCC 2617
Qy 800 PheGluMetPheTyrIysAlaAlaArgCysAspAspThrAspLeuMetIysIysPheSer 819
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QY 820 GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp 839
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QY 840 IleAspCysArgLeuGluGluAsnLeuThrLysLysTyxCysLeuGluTyrAsnTyrAsp 859
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QY 860 TyrGluAsnGlyPheAlaIleGlyProGlyGlyTyrGlyAlaAlaAsnArgLeuAspTyr 879
DB 2795 TATGAAAATGGCTTTGCAATTTGGACACGAGGCTGGGCTGCAGGCAACAGGCTGGATTAT 2854
QY 880 SerTyrAspAspPheLeuAspThrValGlnGluThrAlaThrSerIleGlyAsnAlaLys 899
DB 2855 TCTTACGATCACTTCCTGGATGTTGTACAGGAACAACCCACCGATGTGGGCAAGGCCAGA 2914
QY 900 SerSerArgIleLysArgSerAlaProLeuSerAspTyrLysIleLysLeuIlePheAsn 919
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QY 980 GluThrLysLysAlaSerProPheCysArgProGlySerValLeuArgGlyArgMetCys 999
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QY 1080 LysPheGlySerArgSerCysLeuSerCysProGluAsnThrSerThrValLysArgGly 1099
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QY 1100 AlaValAsnIleSerAlaCysGlyValProCysProGluGlyLysPheSerArgSerGly 1119
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QY 1140 CysLeuAlaCysProPheTyrGlyThrThrProPheAlaGlySerArgSerIleThrGlu 1159
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QY 1180 LeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePhe 1199
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QY 1200 AsnProCysHisAsnSerGlyThrCysGlnGlnLeuGlyArgGlyTyrValCysLeuCys 1219
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QY 1220 ProLeuGlyTyrThrGlyLeuLysCysGluThrAspIleAspGluCysSerProLeuPro 1239
DB 3875 CCACCTGGGATACACAGCTTAAAGTGTGAACAGATATTGATGAATGACGCTCTCTGC 3934
QY 1240 CysLeuAsnAsnGlyValCysLysAspLeuValGlyGluPheIleCysGluCysProSer 1259
DB 3935 TGCTCTAATGCTGGAAATTTGTAGAGACCAAGTTGGGGATTCACGTCGGAATGTTCTTG 3994
QY 1260 GlyTyrThrGlyGlnArgCysGluGluAsnIleAsnGluCysSerSerSerProCysLeu 1279
DB 3995 GGCTATTCAAGTCAAAATATGTGAAGAAATATATAATGAGTGTATCTCCAGCCCTTGCTTA 4054
QY 1280 AsnLysGlyLysCysValAspGlyValAlaGlyTyrArgCysThrCysValLysGlyPhe 1299
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QY 1300 ValGlyLeuHisCysGluThrGluValAsnGluCysGlnSerAsnProCysLeuAsnAsn 1319
DB 4115 ATGGGTGTCATCTGTGAACAGACGTCATGATGCAATGCAATGCAATGCAATGCAATG 4174
QY 1320 AlaValCysGluAspGlnValGlyGlyPheLeuCysLysCysProGlyPheLeuGly 1339
DB 4175 GCAATTTGTAAGACCAACAGTGGGGGCTTCTCATGCAAAATGCCACCCGCGATTTTGGGT 4234
QY 1340 ThrArgCysGlyLysValAspGluCysLeuSerGlnProCysLysAsnGlyValThr 1359
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QY 1360 CysLysAspGlyAlaAsnSerPheArgCysLeuCysAlaAlaGlyPheThrGlySerHis 1379
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QY 1400 AspGluLeuAsnSerTyrSerCysLysCysGlnProGlyPheSerGlyGlnArgCysGlu 1419
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5015 Db CTGAGTCGGGGAACGTTGATGATGGCCGATTTCTGTCGCGAATCAGCGGGAAGGTG 5074
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5075 Db AAGGTTGATTCCAGCAGCATGTTCTGCTCTGATGCTCGCTCTTAGAAGGATCCGTCGCT 5134
1640 QY HisLeuArgThrAlaSerGluAspLeuLysProGlySerLysValAsnLeuPheCysAsp 1659
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1720 QY TyrTyrLeuLeuGlyAspSerArgMetPheCysThrAspAsnGlySerTrpAsnGlyVal 1739
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5435 Db TCACCATCTGCTCGATGTCGATGAGTGCAGTGCAGTCCGCTCGGCTGATGAGCAGCCGCC 5494
1760 QY SerCysLeuAsnValAspGlySerTyrIleCysSerCysValProProTyrThrGlyAsp 1779
5495 Db TCCTGCTGTAACACCAACCGGATCTTACGTATGTTCTGTAACTTACCCACCATACACGGGAGAT 5554
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5915 Db TCGAGCTAGTGAAGTGTTCAGGCTGAGGACATAAATAACGCGCAATACATCTTAAGT 5974
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1960 QY LeuValPheCysGlyGluProProAlaIleLysAspAlaValIleThrGlyAsnAsnPhe 1979
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RESULT 6
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DEFINITION Sequence 3 from patent US 6656707.
ACCESSION AR435510
VERSION AR435510.1 GI:40198413
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11230)
AUTHORS Welch, A. A. and Elliott, G. S.
TITLE C3b/C4b complement receptor-like molecules and uses thereof
JOURNAL Patent: US 6656707-A 3 02-DEC-2003;
FEATURES Location/Qualifiers
source 1. 11230
/organism="unknown"
/mol_type="genomic DNA"

Alignment Scores:
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Score: 16707.00 Matches: 2915
Percent Similarity: 89.72% Conservative: 289
Best Local Similarity: 81.63% Mismatches: 361
Query Match: 83.65% Indels: 6
DB: 6 Gaps: 5

US-09-977-053-4 (1-3571) x AR435510 (1-11230)

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236 TTCCAGCGGTGGCCCTTCGCTCAACTTCAGCTTCGCGCTGTTCGCCGAGGCTCTCCG 295
41 GlyAlaProGlySerIleProAlaProAlaProGly--AspGluAlaGlySer 59
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100 ArgSerGluLeuMetPheValArgGlyLeuLeuSerAspPheProValProThrAla 119
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Qy	820	GluAlaPheGluThrThrLeuGlyLysMetValProSerPheCysSerAspAlaGluAsp	839	Qy	1180	LeuGlyHisIleLysLysArgHisGluIleSerSerGlnValPheHisGluCysPhePhe	1199
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Db	3410	GAATTTGGATCCCGAGCTGCTCTATGCTGATGCCAGAAACCAACACAGGTTGAAAGAGGA	3469	Db	4490	CTGCTAGATGGGTGTGTCACCAACCTTCAATGCGGTAAACCTGCGCATTTCTTGTGATGAATCC	4549
				Qy	1460	SerAspAspMetAsnTyrGlyThrProIleSerTyrAlaValAspAsnGlySerAspAsn	1479

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RESULT 7

AX375163 LOCUS 11230 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 3 from Patent WO0210388.
ACCESSION AX375163
VERSION AX375163.1 GI:19169917
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Welch, A.A. and Elliot, G.S.
TITLE C3b/c4b complement receptor-like molecules and uses thereof
JOURNAL Patent: WO 0210388-A 3 07-FEB-2002;

FEATURES		Amgen Inc. (US)		Location/Qualifiers	
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		/mol_type="unassigned DNA"		/db_xref="taxon:10090"	
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Alignment Scores:		0	Length:	11230	
Pred. No.:		16707.00	Matches:	2915	
Percent Similarity:		89.72%	Conservative:	289	
Best Local Similarity:		81.63%	Mismatches:	361	
Query Match:		83.63%	Indels:	6	
DB:		6	Gaps:	5	
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QY	1	MetTTPProArgLeuAlaPheCysGlyTrpGlyLeuAlaLeuValSerGlyTrpAlaThr	20		
DB	176	ATGTGGTCGGCGCTGGCCCTTTTGTGCTGGCTCTGGCACTGGTGGCGCTGGACCAAC	235		
QY	21	PheGlnGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro	40		
DB	236	TTCCAGCGGTGGCCCTTGGCTCACTTCAGCTTCGGCTGTTCCCGAGGCTCTCG	295		
QY	41	GlyAlaProGlySerIleProAlaProAlaProGly---AspGluAlaAlaGlySer	59		
DB	296	GGGGCTCTGGGCAGACTGGCGGTACTCCCGGCTCCAGTGGAGGAGGAGGAGGAGG	355		
QY	60	ArgValGluArgLeuGlyGlnAlaPheArgArgValArgLeuArgGluLeuSer	79		
DB	356	AAAGTGGAGCGCTGGCGCGCGGTTCGGAGCCGCTGGAGGAGGAGGAGGAGGAGG	415		
QY	80	GluArgLeuGluLeuValPheLeuValAspSerSerValGlyGluValAlaAsnPhe	99		
DB	416	GGCAGCTTGGAGCTGCTCTCTGCTGGAGAGTGTCCAGGCTGGCCCAACCACTTC	475		
QY	100	ArgSerGluLeuMetPheValArgLysLeuLeuSerAspPheProValProThrAla	119		
DB	476	CTCAACGAGCTCAAGTTCGTGGCAGAGCTGCTGTCGCACTTCCCGGTGGTGTCCAG	535		
QY	120	ThrArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyr	139		
DB	536	ACGGGTGGCGCATCGTCACTTCTCATCCAGAACACAGTGGTGGCGCGGTGGATAC	595		
QY	140	IleSerThrArgAlaArgGlnHisLysCysAlaLeuLeuLeuGlnGluIleProAla	159		
DB	596	ATCTCCACGCGCGCGGCACCAACACAGTGGCGCTCTCAGCGCGAGATCCGGCC	655		
QY	160	IleSerThrArgGlyGlyGlyThrThrLysGlyAlaPheGlnGlnAlaGlnIle	179		
DB	656	ATCACCTACCGCGTGGTGGCACTATACCAAGGGCGCTTCCAGCAAGCGCGCAATC	715		
QY	180	LeuLeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSer	199		
DB	716	CTTCGTCACTTAGAGAAACTCCCAAGTCATATTTCTCATCCGACGCTTATTC	775		
QY	200	AsnGlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePhe	219		
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DB	896	GAAGAACATTGTCTCTCCAGTTTGAAGATTTAGGCTTTAGCTGCGAGGGCG	955		
QY	260	LeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyr	279		
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DB	1016	CTCTGTGAGCTGGGAAAGACTGCTGTGACAGATGGCCAGCTGCAAAATGTGGACAC	1075		
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DB	1076	ACGGTCAATTGATGATCTGTGAGAGGCTTATACGGGAAAGGTCTGAGCATGAG	1135		
QY	320	CysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyLysSerSer	339		
DB	1136	TGCACAGCTTGGCCATCAGGACATATAAGCGGAGCTTCTCCAGAGGAATCAGCACC	1195		
QY	340	CysIleProCysProAspGluAsnHisThrSerProProGlySerThrSerProGluAsp	359		
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QY	400	AlaAlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeu	419		
DB	1376	GGCGCTGTGGGGTCCGATGTCGCGGCTTTGACCTTGTGGGAGCAGCATTCATTTG	1435		
QY	420	CysLeuProAsnGlyLeuTyrSerGlySerGluSerTyrCysArgValArgThrCysPro	439		
DB	1436	TGTCACCCATGTTTGTGHTCTGGGACAGAAAGCTTCTGCAGAGTGAGAACGTGCCC	1495		
QY	440	HisLeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLys	459		
DB	1496	CACCTCCGACAGCCCAACACAGCCACATCAGCTGCTCCACTCGGAAATGTCTACAAC	1555		
QY	460	ThrThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThr	479		
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QY	500	ThrPheGlnMetProLysAspValIleSerProHisAsnCysGlyLysGlnProAla	519		
DB	1676	ACCTTCCAGAGCCCAAGGCGTCATCTCTCCACCCAGCTGCGGCAAGCAGCCGCC	1735		
QY	520	LysPheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLys	539		
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QY	540	GluMetLeuArgCysThrSerGlyLysTyrAsnValGlyValGlnAlaAlaValCys	559		
DB	1796	GAA---GTGAGATGTCACATCTGGAGTGGAGTGGCCAAAGTTCAGACAGCTGTGTC	1852		
QY	560	LysAspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGlu	579		
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QY	580	GlnGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGlu	599		
DB	1913	CAGCAGGACTGTCTTAATGCCACTGGCAGTCCCAAGCTTAAGACCAACTCTGTGAA	1972		
QY	600	LysValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAsp	619		
DB	1973	AAAGTGTCACTCCAGTCCAGCCAGCTTTACCCCACTTACCTTCCCAATTTGAGAC	2032		
QY	620	ValAlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHis	639		
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QY 2300 SerSerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMet 2319
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QY 2400 PheGlySerThrValLysTyrSerCysValGlyPhePheLeuArgGlyAsnSerThr 2419
DB 7370 TTGGCAGTACTGTCAAGTATCTGTGTGTCGACGGGTTTTTCTTAAGAGCGATCCNACC 7429
QY 2420 ThrLeuCysGlnProAspGlyThrTrpSerSerProLeuProGluCysValProValGlu 2439
DB 7430 ATCTCTGCGAGCTGATAGCAGCTCGAGTTCTCCATTTGCCGAATGCGTTCGGTAGAA 7489
QY 2440 CysProGlnProGluGluLeuProAsnGlyIleIleAspValGlnGlyLeuAlaTyrLeu 2459
DB 7490 TGTCCCAACCTCAGAGATCCTCAACGGTATCATCCAGTACAGGGCTTGCCTATCTC 7549
QY 2460 SerThrAlaLeuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrLeu 2479

DB 7550 AGCACCAAGCTCTACACCTGCAGCCAGGCTTTGAGTTAGTGGCAATGCTACCAACCTC 7609
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QY 2520 ValThrTyrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeu 2539
DB 7730 ATCACATATTTTGTGACCGGGCTTCGGCTCGAAGGTCCCAATCCCTGACCTGTTTA 7789
QY 2540 GluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAspSerPro 2559
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QY 2560 GlnProIleGluAsnGlyPheValGluGlyAlaAspTyrSerTyrGlyAlaIleIle 2579
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QY 2580 TyrSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGlySer 2599
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QY 2600 GlyTrpSerSerSerIleProThrCysMetProIleAspCysGlyLeuProProHisIle 2619
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Db	8744	CGTGAAGGGTTCATACTGGNAGGAGCCAGGAGTCGTATCTGTCTTACCAATGGNAGTGG	8803
Qy	2880	SerGlyAlaThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAen	2899
Db	8804	AGTGGTGCCTCCAGCTGCATGCTGTGTAGATGCTCTGCCCCACCAACAGGTGCCAAT	8863
Qy	2900	GlyValThrGluGlyLeuAspTyrGlyPheMetLysGluValThrPheHisCysHisGlu	2919
Db	8864	GGGGTGGCAGATGGCTAGACTATGGGTTCAAGAAGGAGTAGTCGTCCACCTGTCTAGAG	8923
Qy	2920	GlyTyrIleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGlyAsnTtpAspAla	2939
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Qy	2940	GluIleProLeuCysLysProValAsnCysGlyProProGluAspLeuAlaHisGlyPhe	2959
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Db	9341	GAGCACGCTCAGTGGCGGCTCTCCCAACCATACCCAAACGCAATTGTCTTGGAGGGCAGC	9400
Qy	3080	SerTtpLysGluAsnValIleThrTyrSerCysArgSerGlyTyrValIleGlnGlySer	3099
Db	9401	CTTTCCGAGGACCAATGTGTAACTTACAGCTGCAGACCTGGCTACACCATGCAAGGTAGT	9460
Qy	3100	SerAspLeuIleCysThrGluLysGlyValTtpSerGlnProTyrProValCysGluPro	3119
Db	9461	TCGATCTGATTTGTACGGAAGGCGATATGAGCGCAGCTTACCCACCGTGTGAACCC	9520
Qy	3120	LeuSerCysGlySerProProSerValAlaAsnAlaValAlaThrGlyGluAlaHisThr	3139
Db	9521	CTGTCTGTGGACCCCCACCACTGTAGCCAAATGCAGTGCAGCGCAACAGGAGGCTCATACC	9580
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Db	9581	TATGAAGCAAGTGAACCTCAGGTCTCGGAAGGGTATGTGATGATTCGGATACAGAT	9640
Qy	3160	ThrPheThrCysGlnLysAspGlyArgTtpPheProGluArgIleSerCysSerProLys	3179
Db	9641	ACATTCACCTGCCAGCAAGATGGCCATATGGTCCCTGAAAGATACACCTGCAGTCTTAA	9700
Qy	3180	LysCysProLeuProGluAsnIleThrHisIleLeuValHisGlyAspAspPheSerVal	3199
Db	9701	AAATGCCCTGTGCCATCCAAATGACATGACATGATCGTCTTCAACGAGATGACTTCCAGGTG	9760
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Db	10601	GGTGTCTGTCAACGTCCAAATGCTGTCTCATGCCCCAGACGGCTGGAGTGGAGCTCTGT	10660
Qy	3500	GluGluProIleCysIleLeuProCysLeuAsnGlyGlyArgCysValAlaIleProTyrGln	3519
Db	10661	GAAGACCAATATGATATCTCCCTCTTGAATGGTGGGCGCTGTGTGGCCCCCTTATCAG	10720
Qy	3520	CysAspCysProProGlyTtpThrGlySerArgCysHisThrAlaValCysGlnSerPro	3539
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RESULT 9
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ACCESSION AK075235.1 GI:22761191
VERSION AK075235.1
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahari, K., Masuh, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
NEDO human cDNA sequencing project
JOURNAL Unpublished
TITILE 2 (bases 1 to 5421)
JOURNAL Isogai, T. and Otsuki, T.
REFERENCE Direct Submission
AUTHORS Isogai, T. and Otsuki, T.
TITILE Direct Submission
JOURNAL
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
FEATURES
Location/Qualifiers

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source

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CQDDKWDDEDPICIPVDRSSPPVANGQVRDVTYQKIEYTCNEGFLLEGASRV
CLANGWSGATDVPVRCATPGLANGVTEGLDYGMKEVTFHCEGYILHGAPKLT
CQSGNMDAIEPLCKFPVNGCPEDLAHGPNGFSPITGHGHIQYQFPYKLGHSRR
CLNSGWSGSSPSCLPFCRSTPIEVGTWNGTDFDQGAARIQCFKFKLGLSLITC
RADQWSGSPFCHESTCSGLPMIENAFSETSMKENVITYCSRGVYVIGSSDLIC
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CQDGRWPPERISCPKPCPLPENITHILVHGDDFSVKNQSVSCABGTFPEGVNIS
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ORIGIN

Alignment Scores:

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Percent Similarity:	97.56%	Conservative:	4
Best Local Similarity:	97.33%	Mismatches:	11
Query Match:	47.06%	Indels:	32
DB:	9	Gaps:	1

US-09-977-053-4 (1-3571) x AK075235 (1-5421)

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QY	1901	GluProValLysCysSerSerProGluAsnIleAsnAsnGlyLysTrpIleLeuSerGly	1920
DB	63	GAACCAAGTGAAGTGTCTAGTCGGGAAATATAAATAATAGAAATATATTTTGAAGTGGG	122
QY	1921	LeuThrTrpLeuSerThrAlaSerTrpSerCysAspThrGlyTrpSer	1936
DB	123	CITACCTACCTTTCTACTGCATCATATTATTCGATACAGGATACAGATACAG-ATGCGGTTTCG	181
QY	1936	-----	1936
DB	182	CCATTGTTGTCAGACTAGTCTCGAACTCTTGAGTCTCAAGCAATCCACCTGCTCAACCTC	241
QY	1937	-----LeuGlnGlyProSerIleIleGluCysThrAlaSerGly	1949
DB	242	CCAAAGTGTGGAATTTACAGCTTTACAGGCGCTTCCATTATTGAATGACACGCTTCTGCG	301
QY	1950	IleTrpAspArgAlaProProAlaCysHisLeuValPheCysGlyGluProProAlaIle	1969

DB	302	ATCTGGGCAAAAGCCGCCCTGCTCACCTGCTGCTCTTCTGTGGAGAACCACTGCGATC	361
QY	1970	LysAspAlaValIleThrGlyAsnAsnPheThrPheArgAsnThrValThrTrpTrpCys	1989
DB	362	AAAGATGCTGTCATTAACGGGGAATAACTTCACTTTTCAGGACACACCGCTCACTTACACTTGC	421
QY	1990	LysGluGlyTrpThrIleuAlaGlyLeuAspThrIleGluCysLeuAlaAspGlyLysTrp	2009
DB	422	AAAGAAGGCTTACTCTTGTCTGCTCTTGACACCATTTGAATGCTGCGCCGACGCAAGTGG	481
QY	2010	SerArgSerAspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAspHis	2029
DB	482	AGTAGAGTACACAGAGTGCCTGCTGCTCTGTGATAGACCACTTGTGGACCAAC	541
QY	2030	AlaSerProGluThrAlaHisArgLeuPheGlyAspIleAlaPheTrpTrpCysSerAsp	2049
DB	542	GCCTCTCCAGAGTCTGCCCATCGGCTCTTTGGAGACATTTGCATCTTACTACTCTCTGAT	601
QY	2050	GlyTrpSerLeuAlaAspAsnSerGlnLeuLeuCysAsnAlaGlnGlyLysTrpValPro	2069
DB	602	GGTTACAGCTTAGCAGACAATTCACAGCTTCTTGCATATGCCCGAGGCAAGTGGTACCC	661
QY	2070	ProGluGlyGlnAspMetProArgCysIleAlaHisPheCysGluLysProProSerVal	2089
DB	662	CCAGAGGTCACAGACATGCCCCGTTGTATAGTCACTTTCTGTGAANAACCTCCATCGGTT	721
QY	2090	SerTrpSerIleLeuGluSerValSerTrpAlaLysPheAlaAlaGlySerValSer	2109
DB	722	TCCTATGATCATCTTGGATCTGTGAGCAAGCAAAATTTGCAGCTGGCTCAGTTGTGAGC	781
QY	2110	PheLysCysMetGluGlyPheValLeuAsnThrSerAlaLysIleGluCysMetArgGly	2129
DB	782	TTTAAATGCATGGAAGGCTTTGTACTGAACACCTCAGCAAGATTAATGTATGAGAGGT	841
QY	2130	GlyGlnTrpAsnProSerProMetSerIleGlnCysIleProValArgCysGlyGluPro	2149
DB	842	GGGAGTGAACCCCTTCCCCATGTCATCCAGTGCATCCCTGTGCGGTGTGAGAGCCA	901
QY	2150	ProSerIleMetAsnGlyTrpAlaSerGlySerAsnTrpSerPheGlyAlaMetValAla	2169
DB	902	CCAAGCATCATGATGGCTATGCAAGTGCATCAACTACAGTTTGTGAGCATGGTGGCT	961
QY	2170	TrpSerCysAsnLysGlyPheTrpIleLysGlyLysLysSerThrCysGluAlaThr	2189
DB	962	TACAGCTGCACAAAGGGGTTTACATCAAGAGGGAAGAGAGAGACCTCCGAGAGCCCTCA	1021
QY	2190	GlyGlnTrpSerSerProIleProThrCysHisProValSerCysGlyGluProProLys	2209
DB	1022	GGGAGTGGAGTAGTCTTATACGACGTGCCACCCCGTATCTTGTGTGAACCACTTAAG	1081
QY	2210	ValGluAsnGlyPheLeuGluHisThrThrGlyArgIlePheGluSerGluValArgTrp	2229
DB	1082	GTTGAGATGGCTTTCTGGAGGACATCAACTGGCAGGATCTTTTGAGAGTGAAGTGAAT	1141
QY	2230	GlnCysAsnProGlyTrpLysSerValGlySerProValPheValCysGlnAlaAsnArg	2249
DB	1142	CAGTGAACCCGGGCTATAGCCAGTCGGAAGTCTCTGTTTGTGTGCCATGCAATCGC	1201
QY	2250	HisTrpHisSerGluSerProLeuMetCysValProLeuAspCysGlyLysProProPro	2269
DB	1202	CACGGCACAGTGAATCCCTCTGATGTGGGTTCTCTGACCTGTGGAANAACCTCCCGC	1261
QY	2270	IleGluAsnGlyPheMetLysGlyGluAsnPheGluValGlySerLysValGlnPhePhe	2289
DB	1262	ATCCGAATGGCTTATGAAGAGGAAAACTTTGAAGTAGGGTCCCAAGGTTTCAAGTTTTC	1321
QY	2290	CysAsnGluGlyTrpGluLeuValGlyAspSerSerTrpThrCysGlnLysSerGlyLys	2309
DB	1322	TGTAATGAGGGTATGAGCTTGTGTGTGACAGTCTTGTGACATGTCTGAGAAATCTGGCAA	1381
QY	2310	TrpAsnLysLysSerAsnProLysCysMetProAlaLysCysProGluProProLeuLeu	2329

1382	Db	TGGAAATGAAGAGTCAAATCCAAAGTCGANGCCTGCCAAGTGCCCGAGAGCGCGCCCTCTTG	1441
2330	Qy	GluAsnGlnLeuValLeuLysGluLeuThrThrGluValGlyValValThrPheSerCys	2349
1442	Db	GAATAACCCAGCTAGTATTAAAGGAGTTGACACCGAGGTAGGAGTTGTGACATTTCTCGT	1501
2350	Qy	LysGluGlyHisValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnGlnTrp	2369
1502	Db	AAAGAGGGCATGTCTCTGCAAGGCCCTCTGTCTCTGAAATGCTTGGCATCCGAGCAATGG	1561
2370	Qy	AsnAspSerPheProValCysLeuValLeuCysThrProProLeuLeuLeuSerPhe	2389
1562	Db	AATGACTCTTTTCCCTGTGTTGAAAGATTGTTCTTTGTATCCCCACCTCCCTTAATTTCTCTT	1621
2390	Qy	GlyValProIleProSerSerAlaLeuHisPheGlySerThrValLysIleThrCysVal	2409
1622	Db	GGTGTCCCATCTCTTCTTCTGCTCTTCATTTTGGAGTACTGTCAAGTATTCTTGTGTA	1681
2410	Qy	GlyGlyPhePheLeuArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSer	2429
1682	Db	GGTGGGTTTTTCTTAAGAGGAAATCTTACCACCCCTCTGCCAACCTGATGGCACCTGGAGC	1741
2430	Qy	SerProLeuProGluCysValProValGluCysProGlnProGluGluIleProAsnGly	2449
1742	Db	TCTCCACTGCGCAGAAATGTGTTCCAGTAGAAATGTCCCAACCTGAGGAAATCCCCAAATGGA	1801
2450	Qy	IleIleAspValGlnGlyLeuAlaIleLeuSerThrAlaLeuIleThrCysLysProGly	2469
1802	Db	ATCATTTGATGTGGAGGCTTGCCTTCTCTGACGACAGCTCTCTATATCTGCGAGCCAGGC	1861
2470	Qy	PheGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGly	2489
1862	Db	TTTGAAATTTGGTGGCAATATCTACCACCTTTGTGGAGAAAAATGGTCACTGGCTTTGGAGGA	1921
2490	Qy	LysProThrCysLysAlaIleGluCysLeuLysProLysGluIleLeuAsnGlyLysPhe	2509
1922	Db	AAACCAACATGTAAGGCCATTGAGTGCTGAAACCCCAAGGAGATTTTGAATGGCAAAATTC	1981
2510	Qy	SerTyrThrAspLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArg	2529
1982	Db	TCTTTACAGGACCTACACTATGGACAGACCGTTACTCTCTTGCAACCGAGGCTTTGGG	2041
2530	Qy	LeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAspTrpAspValAspAlaPro	2549
2042	Db	CTCGAAGTCCCGAGTGCCTTGACCTGTTTAGAGACAGGTGATTTGGATGTAGATGCCCCA	2101
2550	Qy	SerCysAsnAlaIleHisCysAspSerProGlnProIleGluAsnGlyPheValGluGly	2569
2102	Db	TCTTTGCAATGTCATCCACTGTGTATTCGCCACAAACCCCATTTGAAATGGTTTTGTAGAAGGT	2161
2570	Qy	AlaAspTyrSerTyrGlyAlaIleIleIleTyrSerCysPheProGlyPheGlnValAla	2589
2162	Db	GCAGATTACAGCTATGGTGCCATTAATCATCTACAGTTGCTTCCCTCGGTTTCAGTGCGCT	2221
2590	Qy	GlyHisAlaMetGlnThrCysGluGluSerGlyTrpSerSerSerIleProThrCysMet	2609
2222	Db	GGTCATGCCATGCAGACCTGTGAGAGGTCAGATGGTCAAGTTCCATCCCAACATGATGATG	2281
2610	Qy	ProIleAspCysGlyLeuProProHisIleAspPheGlyAspCysThrLysLeuLysAsp	2629
2282	Db	CCAATAGACTGTGGCCCTCCCTCCTCATATAGATTTTGGAGAGCTGTACTAAACTCAAGAT	2341
2630	Qy	AspGlnGlyTyrPheGluGlnGluAspAspMetMetGluValProTyrValThrProHis	2649
2342	Db	GACCAGGAGTATTTTGTAGCAGAGAAGACGACATGATGGAGTTCCATATGTGACTCTCTCAC	2401
2650	Qy	ProProTyrHisLeuGlyAlaValAlaLysThrTrpGluAsnThrLysGluSerProAla	2669
2402	Db	CCTCCTTATCATTTTGGAGCAGTGGCTTAAACCTGGGAAAAATACAAGGAGTCTCTCTGCT	2461
2670	Qy	ThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProGlyTyr	2689
2462	Db	ACACATTTCAACAACTTTCTGTATGTGACCAATGTTTTCATACCTGTAAATCCAGGATAT	2521

Qy	2690	GlulLeuLeuGlyAenProValLeuLeuLeuCysGlnGluAaspGlyThrTrpAenGlySerAla	2709
Db	2522	GAACTTCTGGGGAACCCCTGTGCTGATCTGCAGAGATGGAACTAGGAATGGCAGTGCA	2581
Qy	2710	ProSerCysIleSerIleGluCysAasPleuProThrAlaProGluAenGlyPheLeuArg	2729
Db	2582	CCATCTCGCATTTCAATTGAATGTGACTTGCCCTACTGCTCTGAAATGGCTTTTGGGT	2641
Qy	2730	PheThrGluThrSerMetGlySerAlaValGlnTyrSerCysIysProGlyHisIleLeu	2749
Db	2642	TTTACAGAGACTAGCATGGGAAGTGTGTGCAGTATAGCTGTAAACCTGGACACATCTA	2701
Qy	2750	AlaGlySerAspLeuArgLeuCysLeuGluAenArgIysTrpSerGlyAlaSerProArg	2769
Db	2702	GTGGGCTCTGGCTTTAAGGCTTTGTCTAGAGAAATAGAAGTGGAGTGTGCTCTCCCAAGC	2761
Qy	2770	CysGluAlaIleSerCysIysLysProAasnProValMetAasnGlySerIleLysGlySer	2789
Db	2762	TGTGAGGCCATTTCAATGCAAAAGGCCAAATCCAGTCATGAATGGATCCATCAAGGAAGC	2821
Qy	2790	AsnTyrThrTyrLeuSerThrLeuTyrTyrGluCysAaspProGlyTyrValLeuAasnGly	2809
Db	2822	AACTACACATACCTGAGCAGCTTGTACTATGAGTGTGACCCCGCATATGTCTGAATGGC	2881
Qy	2810	ThrGluArgArgThrCysGlnAaspAspLysAsnTrpAaspGluAaspGluProIleCysIle	2829
Db	2882	ACTGAGGGAGAACATGCCAGATGACAAAACTGGGATGGAGATGAGCCCATTTGCATT	2941
Qy	2830	ProValAaspCysSerSerProProValSerAlaAasnGlyGlnValArgGlyAspGluTyr	2849
Db	2942	CCTGTGACCGCAGTTCAACCCCACTCTACGCCCAATGGCCAGGTGAGAGAGACGAGTAC	3001
Qy	2850	ThrPheGlnIysGluIleGluTyrThrCysAasnGluGlyPheLeuLeuGluGlyAlaArg	2869
Db	3002	ACATTCCAAAAGAGATTGAATACACTTGCAATGAAGGGTCTTTGCTTGGAGGGAGCCAGG	3061
Qy	2870	SerArgValCysLeuAlaAasnGlySerTrpSerGlyAlaThrProAaspCysValProVal	2889
Db	3062	AGTCGGGTGTGCTTGCCCAATGAGTTGGAGTGGAGGCCACTCCCGCATGTGTGCCCTGTC	3121
Qy	2890	ArgCysAlaThrProProGlnLeuAlaAasnGlyValThrGluGluLeuAaspTyrGlyPhe	2909
Db	3122	AGATGTGCCACCCCGCCACAACTGGCCCAATGGGGTGACGGAAGGCCCTGGACATATGGCTTC	3181
Qy	2910	MetIysGluValThrPheHisCysHisGluGlyTyrIleLeuHisGlyAlaProLysLeu	2929
Db	3182	ATGAAGGAGTAACTTCCTACTGTACAGGGCTACATCTTGCACGGTGTCTCCAAACTC	3241
Qy	2930	ThrCysGlnSerAaspGlyAsnTrpAaspAlaGluIleProLeuCysIysProValAasnCys	2949
Db	3242	ACCTGTCAGTCAAGTGGCAACTGGGATGACAGAGATTCCTCTCTGTAACCAAGTCAACTGT	3301
Qy	2950	GlyProProGluAaspLeuAlaHisGlyPheProAasnGlyPheSerPheIleHisGlyGly	2969
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Qy	2970	HisIleGlnTyrGlnCysPheProGlyTyrIlysLeuHisGlyAasnSerSerArgArgCys	2989
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Qy	2990	LeuSerAasnGlySerTrpSerGlySerSerProSerCysLeuProCysArgCysSerThr	3009
Db	3422	CTCTCCAAATGGCTCCTGGAGTGGCAGCTACCTTTCCTGCTGCCCTTTTCAGATGTTTCACA	3481
Qy	3010	ProValIleGluTyrGlyThrValAasnGlyThrAaspPheAaspCysGlyLysAlaAlaArg	3029
Db	3482	CCAGTAATTGAATAGNACTGTCTAATGGACAGATTTTGACTGTGGAAAGCGACCCCG	3541
Qy	3030	IleGlnCysPheIysGlyPheLysLeuLeuGlyLeuSerGluIleThrCysGluAlaAasp	3049
Db	3542	ATTCAAGTCTTCAAGGCTTCAAGCTCTAGGACTTTCTGAATCACTCTGTGAAGCCGAT	3601

QY 3050 GlyGlnTrpSerSerGlyPheProHisCysGluHisThrSerCysGlySerLeuProMet 3069
DB 3602 GGCAGTGGAGCTCTGGGTTCGCCCACTGTGAACACACTCTCTGTGGTGTCTCTTCCAAATG 3661
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AX350821
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DEFINITION Sequence 21 from Patent WO0179294.
ACCESSION AX350821
VERSION AX350821.1 GI:18616296
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Taupier,R.J., Vernet,C.A., Fernandes,E., Shimkets,R.A.,
Majumder,K., Padigaru,M., Colman,S.D., Zerhusen,B.D., Spytek,K.A.,
Burgess,C.B. and Liu,X.
TITLE Novel human proteins, polynucleotides encoding them and methods of
using the same
JOURNAL Patent: WO 0179294-A 21 25-OCT-2001;
Curagen Corporation (US)
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Location/Qualifiers
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ORIGIN
Alignment Scores:
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Best Local Similarity: 78.60% Mismatches: 5
Query Match: 42.19% Indels: 412
DB: 6 Gaps: 3

US-09-977-053-4 (1-3571) x AX350821 (1-6153)
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VERSION BX537918.1 GI:31873946
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4701)
AUTHORS Koehler, K., Bever, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pobo, G., Han, M. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686110142) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cDNA/>.

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ORIGIN

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Best Local Similarity: 99.72% Mismatches: 2
Query Match: 40.84% Indels: 0
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US-09-977-053-4 (1-3571) x HSM806032 (1-4701)

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DB	661	GAAAGGCACTGCTTCAAGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	720
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DB	721	GACTCTTCCCTGTTGTAAAGATGTTCTTGTGTACCCCACTCTCCCTAAATTTCTTTGGT	780
QY	2391	ValProIleProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCysValGly	2410
DB	781	GTCCCATTTCTTCTTCTGCTCTTCAATTTTGGAGTACTGTCAAGTATTCTTGTGTAGGT	840
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DEFINITION Sequence 15810 from Patent EP1074617.
ACCESSION AX880905
VERSION AX880905.1 GI:40035641
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1.
AUTHORS Ota, T., Iwagai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 15810 07-FEB-2001;
Research Association for Biotechnology (JP)
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LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD158659
ACCESSION BD158659
VERSION BD158659.1 GI:27864417
KEYWORDS JP 2002191363-A/13502.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 5124)
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 13502 09-JUL-2002;
HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/13502
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KENICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof PH Key
Location/Qualifiers (119) . . (4066) .

FT CDS
source Location/Qualifiers
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Score: 7537.00 Matches: 1347
Percent Similarity: 99.63% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 5
Query Match: 37.74% Indels: 0
DB: 6 Gaps: 0

US-09-977-053-4 (1-3571) x BD158659 (1-5124)

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415 SerSerIleLeuCysLeuProAsnGlyLeuTrpSerGlySerGluSerThrCysArg 434
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RESULT 14

AK027870

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

JOURNAL

COMMENT

FEATURES

AK027870 5124 bp mRNA linear PRI 01-AUG-2002
 Homo sapiens cDNA FLJ14964 fig. clone PLACE4000581, moderately
 similar to FIBROBLASTIN 1 PRECURSOR.

AK027870.1 GI:14042858
 oligo capping; file (full insert sequence).
 Homo sapiens (human)

Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Isoqai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
 Nishikawa, T., Nagai, K., Sugano, S., Aotsuka, S., Yoshikawa, Y.,
 Matsumura, H., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J.,
 Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuno, Y. and Sasaki, N.
 NEDO human cDNA sequencing project
 Unpublished

2 (bases 1 to 5124)
 Isoqai, T. and Otsuki, T.
 Direct Submission

Submitted (10-MAY-2001) Takao Isoqai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kibarasu, Chiba 292-0812, Japan
 (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology; cDNA library construction;
 5'- & 3'-end one pass sequencing and clone selection; Helix
 Research Institute (supported by Japan key technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.

Location/Qualifiers

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CDS

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 5124
 Score: 7537.00 Matches: 1347
 Percent Similarity: 99.63% Conservative: 1
 Best Local Similarity: 99.56% Mismatches: 5
 Query Match: 37.74% Indels: 0
 DB: 9 Gaps: 0

US-09-977-053-4 (1-3571) x AK027870 (1-5124)

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Griffin, J.A., Kallick, D.A., Tribouley, C.M., Yue, H., Nguyen, D.B.,
 Tang, Y.T., Lal, P., Policky, J.L., Azimzai, Y., Lu, D.A., Graul, R.,
 Yao, M.G., Burford, N., Hafalia, A.J., Baughn, M.R., Bandman, O.,
 Patterson, C., Yang, J., Xu, Y., Warren, B.A., Ding, L. and
 Sanjanwalla, M.S.
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QY 2444 uGluIleProAsnGlyIleAspValGlnGlyLeuAlaIleuLeuSerThrAlaLeuTy 2464
DB 721 GGAATATCCCAATGGAATCATTTGATGTGCAAGGCTTGGCTATCTCAGCACAGCTCTTA 780
QY 2464 rThrCysLYsProGlyPheGluLeuValGlyAsnThrThrLeuCysGlyGluAsnGl 2484
DB 781 TACCTGCAAGCAGGCTTTGAAATGTGTGGAAATACTACACCCCTTTGTGGAGAAATGG 840
QY 2484 yHisTrpLeuGlyLYsProThrCysLYsAlaIleGluCysLeuLYsProLYsGluI 2504
DB 841 TCACCTGGCTTGGAGBAACCAACATGTAAAGCCATTGATGCTGCAACCCAGGAGAT 900
QY 2504 eLeuAsnGlyLYsPheSerTYrThrAspLeuHisTYrGlyGlnThrValTYrSerCy 2524
DB 901 TTTGAATGGCAAAATCTCTTACACGACCCTACACTATGGACAGACCGCTTACCTCTTG 960
QY 2524 eAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAspPr 2544
DB 961 CAACCGAGGCTTTGGCTCGAAGGTCCTGAGTGGCTTGACCTGTTTAGACACAGGTGATG 1020
QY 2544 pAspValAspAlaProSerCysAsnAlaIleHisCysAspSerProGlnProIleGluAs 2564
DB 1021 GGATGTAGATGCCCATCTTGCAATGCCATCCACTGTGATTCGCCACACCCATGAAAA 1080
QY 2564 nGlyPheValGluGlyAlaAspTYrSerTYrGlyAlaIleIleIleTYrSerCysPhePr 2584
DB 1081 TGGTTTTGTAGAAGGTGACAGATTACAGCTATGCTGTCATATGTCATAATCATCTACAGTTGCTTCC 1140
QY 2584 oGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrpSerSerSe 2604
DB 1141 TGGGTTTCAGGTGGCTGTGTCATGCCATGCCAGCTGTGGAAGAGTCAGGATGTCAAGTTC 1200
QY 2604 rIleProThrCysMetProIleAspCysGlyLeuProProHisIleAspPheGlyAspCy 2624
DB 1201 CATCCCAACATGTATGCCAATAGACTGTGGCTCCCTCCCTCATATAGATTTTGGAGACTG 1260
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DB 1381 AAAGGAGTCTCTGCTACACATTCATCAAACTTTCTGTATGTGTACCATGGTTTCATACAC 1440
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QY 2744 sProGlyHisIleLeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArgLYsTrpSe 2764
DB 1621 ACCTGGACACATTTAGCAGGCTCTGACTTAAGGCTTTGTCTAGAGAAATAGAAAGTGGAG 1680
QY 2764 rGlyAlaSerProArgCysGluAlaIleSerCysLYsLYsProAsnProValMetAsnGl 2784
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QY 2824 pGluProIleCysIleProValAspCysSerSerProProValSerAlaAsnGlyGlnVa 2844
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QY 2964 rPheIleHisGlyGlyHisIleGlnTYrGlnCysPheProGlyTYrLYsLeuHisGlyAs 2984
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QY 2984 nSerSerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerProSerCysLeuPr 3004
DB 2341 TTCATCAAGAGGTGCTCTCCAAATGGCTCTCTGGAGTGGCAGCTCAGCTTCTCTGCTGCC 2400
QY 3004 oCysArgCysSerThrProValIleGluTYrGlyThrValAsnGlyThrAspPheAspCy 3024
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Alignment Scores:

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 Best Local Similarity: 99.12% Mismatches: 10
 Query Match: 34.80% Indels: 1
 DB: 6 Gaps: 0

US-09-977-053-4 (1-3571) x BD127948 (1-4088)

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Qy	2349	CysLysGluGlyHisValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnGln	2368
Db	61	TGTAAGAAGGCGCATGCTCGCAAGGCCCTCTGTCTGAAATGCTTGCCATCCAGCA	120
Qy	2369	TrpAsnAspSerPheProValCysLysIleValLeuCysThrProProLeuIleSer	2388
Db	121	TGGAATGACTCTTTCCCTGTTTGAAGATGTTCTTTGTACCCACCTCCCTTAATTTCC	180
Qy	2389	PheGlyValProIleProSerSerAlaLeuHisPheGlySerThrValLysTyrSerCys	2408
Db	181	TTTGGTGTCCCATCTCTCTCTGCTCTTCAATTTGGAAGTACTGTCAAGTATCTGT	240
Qy	2409	ValGlyGlyPhePheLeuArgLysAsnSerThrThrLeuCysGlnProAspGlyThrTrp	2428
Db	241	GTAGTGGGTTTTTCTTAAGAGGAAATCTACCAACCTCTGCCAACCTGTATGGCACCTGG	300
Qy	2429	SerSerProLeuProGluCysValProValGluCysProGlnProGluGluIleProAsn	2448
Db	301	AGCTCTCCACTGCCAGAAATGTTTCAGTAGAATGTCCCCAACCTGAGGAAATCCCCAAT	360
Qy	2449	GlyIleIleAspValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyrThrCysLysPro	2468
Db	361	GGAATCATGTATGTGCAAGGCTTGCCCTATCTCAGCAGACGCTCTCTATACCTGCAGGCA	420
Qy	2469	GlyPheGluLeuValGlyAsnThrThrThrLeuCysGlyGluAsnGlyHisTrpLeuGly	2488
Db	421	GGCTTTGAAATGGTGGGAAATACTACCAACCTTTGTGGAGAAATGGTCACTGGCTTGG	480
Qy	2489	GlyLysProThrCysLysAlaIleGluCysLysLeuLysProLysGluIleLeuAsnGlyLys	2508
Db	481	GGAAACCAACATGATTAAGCCATTTAGTGCTTGAAACCCAAAGGAGATTTTGAATGGCAAA	540
Qy	2509	PheSerTyrThrAspLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPhe	2528
Db	541	TTCTCTACACGGACCTACATATGGACAGACCGTTACTTACTCTTGCACCGAGGCTTT	600
Qy	2529	ArgLeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAspTrpAspValAspAla	2548
Db	601	CGGCTCGAAGGTCCAGTGCCCTTGACCTGTTTATAGACAGAGTGATTTGGGATGTAGATGCC	660
Qy	2549	ProSerCysAsnAlaIleHisCysAspSerProGlnProIleGluAsnGlyPheValGlu	2568
Db	661	CCATCTGCAATGCCATCCATGTAATCCCCACCAACCATTTGAATGGTTTGTAGNA	720
Qy	2569	GlyAlaAspTyrSerTyrGlyAlaIleIleTyrSerCysPhePheProGlyPheGlnVal	2588
Db	721	GGTGCAGATTACAGCTATGGTGGCCATATCATCTACAGTTGCTTCCCTGGGTTTCAGGTG	780
Qy	2589	AlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrpSerSerSerIleProThrCys	2608
Db	781	GCTGGTCATGTCATGCAGACCTGTGAAGAGTCAGGATGGTCAAGTTCCATCCCAATGT	840
Qy	2609	MetProIleAspCysGlyLeuProProIleAspPheGlyAspCysThrLysLeuLys	2628
Db	841	ATGCCAATAGACTGTGGCTTCCCTCTCATATAGATTTTGGAGACTGTACTTAACCTCAAA	900
Qy	2629	AspAspGlnGlyTyrPheGluGlnGluAspAspMetMetGluValProTyrValThrPro	2648
Db	901	GATGACCAAGGATATTTTGGACGAGAACGACATGATGGAAATTTCCATATGTGACTCT	960
Qy	2649	HisProProTyrHisLeuGlyAlaValAlaLysThrTrpGluAsnThrLysGluSerPro	2668
Db	961	CACCTCTCTATCATTTTGGAGAGCAGCGCTAAACCTGGGAAATATCAAGAGAGTCTCT	1020
Qy	2669	AlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProGly	2688
Db	1021	GCTACACATTCATCAAACTTCTGTATGTATGACCATGTTTTCATACACCTGTATTCAGGA	1080
Qy	2689	TyrGluLeuLeuGlyAsnProValLeuIleCysGlnGluAspGlyThrTrpAsnGlySer	2708
Db	1081	TATGAACCTTCTGGGAGAACCTGTGTGATCTGCCAGGAAGATGGAATCTGGAATGGCAGT	1140
Qy	2709	AlaProSerCysIleSerIleGluCysAspLeuProThrAlaProGluAsnGlyPheLeu	2728
Db	1141	GCACCATCTCGATTTCAATTAATGATGTGCTTACTGTCTCTGCTGCTGCTGCTGCTGCT	1200
Qy	2729	ArgPheThrGluThrSerMetGlySerAlaValGlnTyrSerCysLysProGlyHisIle	2748
Db	1201	CGTTTACAGAGACTAGCATGGAAGTGTCTGTGCAATATAGCTGTAAACCTGGACACAT	1260
Qy	2749	LeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArgLysTrpSerGlyAlaSerPro	2768
Db	1261	CTAGCAGGCTCTGACTTAAGGCTTTGTCTAGAGAATAGAAAGTGGAGTGTGCTGCCCA	1320
Qy	2769	ArgCysGluAlaIleSerCysLysLysProAsnProValMetAsnGlySerIleLysGly	2788
Db	1321	CGCTGTGAAGCCATTTTCATGCANAAAGCCAAATCCAGTCATGAATGGATCCATCAAGGA	1380
Qy	2789	SerAsnTyrThrTyrLeuSerThrLeuTyrTyrGluCysAspProGlyTyrValLeuAsn	2808
Db	1381	AGCACTACATACATACCTGAGCAGCTGTGTACTATGATGTGTGCTGCTGCTGCTGCTGCT	1440
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Db	1441	GGCACTGAGAGAGAGCAATGCCAGATGACAA-NACTGGATGAGGATGAGGCCCATTTGC	1499
Qy	2829	IleProValAspCysSerSerProProValSerAlaAsnGlyGlnValArgGlyAspGlu	2848
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Qy	2849	TyrThrPheGlnLysGluIleGluTyrThrCysAsnGluGlyPheLeuLeuGluGlyAla	2868
Db	1560	TACATTTCCAAAGAGATTTGAATACACTTGCATGAGGGTTCTTGTCTGAGGGAGCC	1619
Qy	2869	ArgSerArgValCysLeuAlaAsnGlySerTrpSerGlyAlaThrProAspCysValPro	2888
Db	1620	AGGAGTGGGTTTGTCTTGGCAATGGAGTTGGAGTGGAGCCATCTCCGACCTGTGTGCT	1679
Qy	2889	ValArgCysAlaThrProProGlnLeuAlaAsnGlyValThrGluGlyLeuAspTyrGly	2908
Db	1680	GTGAGATGTGCCACCCGCCCAACTGGCCCAATGGGGTGACGGAGGCTTGACATATGCT	1739
Qy	2909	PheMetLysGluValThrPheHisCysHisGluGlyTyrIleLeuHisGlyAlaProLys	2928
Db	1740	TTGATGAGGAGTAACATTCATCTCATGAGGCTACATCTTGCACGGTCTCCCAAA	1799
Qy	2929	LeuThrCysGlnSerAspGlyAsnTrpAspAlaGluIleProLeuCysLysProValAsn	2948
Db	1800	CTCACCTGTGAGTCAGATGGCAACTGGGATGAGAGATTCCTCTCTGTAACACAGTCAAC	1859
Qy	2949	CysGlyProProGluAspLeuAlaHisGlyPheProAsnGlyPheSerPheIleHisGly	2968
Db	1860	TGTGACCTCTGAGATGATTTGCCCAATGGTTTCCCTAATGGTTTCTTTATTCATGGG	1919
Qy	2969	GlyHisIleGlnTyrGlnCysPheProGlyTyrLysLeuHisGlyAsnSerSerArgArg	2988
Db	1920	GGCCATATACAGTATCAGTCTGCTTCTCTGTTATAGCTCCATGGAAATTCATCAAGAGG	1979
Qy	2989	CysLeuSerAsnGlySerTrpSerGlySerProSerCysLeuProCysArgCysSer	3008
Db	1980	TGCTCTCCAAATGGCTCTGGAGTGGCAGCTCACCTCTCTGCTGCTGCTGCTGCTGCT	2039

QY	3009	ThrProValIleGluTyrGlyThrValAsnGlyThrAspPheAspCysGlyLysAlaala	3028	Db	3120	CTGTCTCAAAAGGAGTTTATGTTGATCAGAAATGTCATCAAAATGTAGGAAAGCTTTT	3179
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QY	3029	ArgIleGlnCysPheLysGlyPheLysLeuLeuGlyLeuSerGluIleThrCysGluAla	3048	Db	3180	CTGCTGACGGGCCACCGCATCATTTACCTGCAACCCGACGAGCGTGGACACAGCAAGC	3239
Db	2100	CGGATTCAGTGTCTTCAAAAGGCTTCAAGCTCTCTAGGACTTTCTGAATATCACTGTGAAGCC	2159	QY	3409	AlaLysCysGluLysIleSerCysGlyProProAlaHisValGluAsnAlaIleAlaArg	3428
QY	3049	AspGlyGlnTrpSerSerGlyPheProHisCysGluHisThrSerCysGlySerLeuPro	3068	Db	3240	GCCAAATGTGMAAAATCTCATTTGGTCCACAGCTCAGCTAGAAAATGCAATTCCTCGA	3299
Db	2160	GATGGCCAGTGGAGCTCTGGGTCTCCCACTGTAACACACTCTTGTGGTCTCTTTCCA	2219	QY	3429	GlyValHisTyrGlnTyrGlyAspMetIleThrTyrSerCysTyrSerGlyTyrMetLeu	3448
QY	3069	MetIleProAsnAlaPheIleSerGluThrSerSerTrpLysGluAsnValIleThrTyr	3088	Db	3300	GGGTACATATTAATATGGAGACATGATCACTACTCATGTTACAGTGGATACATGTTG	3359
Db	2220	ATGATACCAATGGCTTCATCAGTGAGACACGCTCTTGGAAAGGAATGTGATTAACCTAC	2279	QY	3449	GluGlyPheLeuArgSerValCysLeuGluAsnGlyThrTrrThrSerProProIleCys	3468
QY	3089	SerCysArgSerGlyTyrValIleGlnLysSerSerAspLeuIleCysThrGluLysGly	3108	Db	3360	GAGGGTTTCACAGAGGAGTGTGTTTGAATAATGGAACATGACATCACTCTTATTTGC	3419
Db	2280	AGCTGCAGGTCTGGATATGTCATCAACAGGCAGTTTCAGATCTGAGTGTGTACAGAGAAAGG	2339	QY	3469	ArgAlaValCysArgPheProCysGlnAsnGlyGlyIleCysGlnArgProAsnAlaCys	3488
QY	3109	ValTrpSerGlnProTyrProValCysGluProLeuSerCysGlySerProProSerVal	3128	Db	3420	AGACTGTCTGTGATTTCCATGTTCAGATGGGGGCATCTGCCAACGCCCAATGCTTGT	3479
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QY	3149	LeuGluGlyTyrThrMetAspThrAspThrPheThrCysGlnLysAspGlyArg	3168	Db	3540	CTGAACGGAGGTCTGCTGTGTGGCCCTTACCAAGTGTGACTGCCGCCCTGGTGGACGGG	3599
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QY	3169	TrpPheProGluArgIleSerCysSerProLysLysCysProLeuProGluAsnIleThr	3188	Db	3600	TCTCGCTGTCTATGACAGCTGTGTCAGTCTCCCTGCTTAATGTGGAAATGTGTAGA	3659
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Db	2580	CATATACCTGTATCATGGGAGCATTTTCAGTGTGTGATAGGCAGTTTCTGTCTCATGTGCA	2639	QY	3569	ThrGlyPhe	3571
QY	3209	GluGlyTyrThrPheGluGlyValAsnIleSerValCysGlnLeuAspGlyThrTrpGlu	3228	Db	3720	ACTGGGTTTT	3728
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QY	3249	HisGlyPheValValGlySerLysTyrThrPheGluSerThrIleIleTyrGlnCysGlu	3268	DEFINITION	Homo sapiens cDNA FLJ90753 fis, clone PLACE3000213, weakly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR.		
Db	2760	CATGGATTTGTGGTGGCAGTAAATATACACCTTTGAAGACACATATTTATCATGTGTAG	2819	ACCESSION	AK075234		
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Db	2940	AAAGCTGACATTTGAACAGGACGACCTGGACCCCAACCTGGTATATTTCTTCAACAGAGGC	2999	AUTHORS	Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Sato, H., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.		
QY	3329	TyrSerLeuGluGlyProSerGluAlaHisCysThrGluAsnGlyThrTrpSerHisPro	3348	TITLE	NEDO human cDNA sequencing project		
Db	3000	TACAGTCTTGAAGGGCCATCTGAGGCACACTGCACAGAAAATGGAACCTGGAGCCACCCA	3059	JOURNAL	Unpublished		
QY	3349	ValProLeuCysLysProAsnProCysProValProPheValIleProGluAsnAlaLeu	3368	REFERENCE	2 (bases 1 to 4088)		
Db	3060	GTCCCTCTCTGCAAAACCAATTCATGCCCTTCTTGTGTGATTCGCCGAGAAATGCTCTG	3119	AUTHORS	Isogai, T. and Otsuki, T.		
QY	3369	LeuSerGluLysGluPheTyrValAspGlnAsnValSerIleLysCysArgGluGlyPhe	3388	TITLE	Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction:		

Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center, cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
Location/Qualifiers

FEATURES

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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 4088
Score: 6950.00 Matches: 1232
Percent Similarity: 99.20% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 10
Query Match: 34.80% Indels: 1
DB: 9 Gaps: 0

US-09-977-053-4 (1-3571) x AK075234 (1-4088)

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QY 2349 CysLysGluGlyHisValLeuGlnGlyProSerValLeuLysCysLeuProSerGlnGln 2368
DB 61 TGTAAAGAGGCGATGCTCTGACAGGCCCTCTGCTGGAATGCTTGCCATCCAGCAA 120
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ACCESSION AL832416
VERSION AL832416.1 GI:21732980
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AL158158/c

LOCUS

DEFINITION

complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AL158158 194835 bp DNA linear PRI 05-APR-2001
Human DNA sequence from clone RP11-4271L11 on chromosome 9q31.2-32,
complete sequence.

AL158158

AL158158.14 GI:135559997

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 194835)

Williams, S.

Direct Submission

JOURNAL

Submitted (05-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquy@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

COMMENT

On April 6, 2001 this sequence version replaced gi:12733508.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Swi:
 SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; information on the WORMPEP
 database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
 Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr9>
 RP11-427L11 is from the library RP11-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6
 This sequence is the entire insert of clone RP11-427L11.

FEATURES

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 misc_feature
 complement(9886..10119)
 /note="match: GSS: Em:B53125"
 misc_feature
 complement(9897..10091)
 /note="match: STS: Em:HSAL08WE1"
 misc_feature
 complement(9907..10123)
 /note="match: GSS: Em:B17453"
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 9932..9967
 /note="18 copies 2 mer ta 100t conserved"
 repeat_region
 9973..10105
 /note="AluJ repeat: matches 1..133 of consensus"
 repeat_region
 10133..10392
 /note="AluSx repeat: matches 38..299 of consensus"
 misc_feature
 10183..10319
 /note="match: GSS: Em:AQ782105"
 repeat_region
 10404..10492
 /note="MER5B repeat: matches 7..97 of consensus"
 misc_feature
 10992..11078
 /note="match: GSS: Em:AQ544271"
 repeat_region
 11354..11653
 /note="AluSx repeat: matches 1..300 of consensus"
 repeat_region
 11742..12929
 /note="Tigger3b repeat: matches 2..1231 of consensus"
 repeat_region
 12987..13146
 /note="MIR repeat: matches 89..248 of consensus"
 repeat_region
 13153..13468
 /note="AluSx repeat: matches 1..312 of consensus"
 repeat_region
 13678..13848
 /note="L2 repeat: matches 2537..2703 of consensus"
 repeat_region
 14394..14609
 /note="MIR repeat: matches 12..257 of consensus"
 misc_feature
 15816..15902
 /note="match: GSS: Em:B46502"
 repeat_region
 15900..15947
 /note="24 copies 2 mer aa 79t conserved"
 repeat_region
 16257..16558
 /note="AluSg repeat: matches 1..302 of consensus"
 repeat_region
 16956..17220
 /note="AluSg repeat: matches 38..304 of consensus"
 repeat_region
 17415..17488
 /note="37 copies 2 mer aa 71t conserved"
 repeat_region
 18552..18845
 /note="AluSg repeat: matches 1..293 of consensus"


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repeat_region 19629..19689
misc_feature /note="L2 repeat: matches 2685..2743 of consensus"
repeat_region 19779..21330
misc_feature /note="Cpg Island"
repeat_region 21481..21679
misc_feature /evidence=not experimental
repeat_region 22591..22818
misc_feature /note="MIR repeat: matches 48..262 of consensus"
repeat_region 22591..22818
misc_feature /note="MIR repeat: matches 23..258 of consensus"
misc_feature complement (23067..23458)
misc_feature /notes="match: GSS: Em:B43385"
repeat_region complement (23074..23458)
misc_feature /notes="match: GSS: Em:B43132"
repeat_region 23731..23893
misc_feature /note="MER50 repeat: matches 17..180 of consensus"
repeat_region 24008..24365
misc_feature /note="match: GSS: Em:AQ088039"
repeat_region 24107..24196
misc_feature /note="MIR repeat: matches 105..202 of consensus"
repeat_region 24953..25091
misc_feature /note="L1MB8 repeat: matches 6145..6287 of consensus"
repeat_region 25184..25589
misc_feature /note="MER50 repeat: matches 1..436 of consensus"
repeat_region 25620..25718
misc_feature /note="MER50 repeat: matches 640..734 of consensus"
repeat_region 25839..25991
misc_feature /note="L1MB1 repeat: matches 5347..6036 of consensus"
repeat_region 27326..27430
misc_feature /note="L1MB6 repeat: matches 4066..4176 of consensus"
repeat_region 27431..27740
misc_feature /note="AluSp/q repeat: matches 174..260 of consensus"
repeat_region 27741..28086
misc_feature /note="L1MBx repeat: matches 1..310 of consensus"
repeat_region 28087..28226
misc_feature /note="L1MB6 repeat: matches 4176..4455 of consensus"
repeat_region 28087..28226
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Alignment Scores:
Pred. No.: 0 Length: 194835
Score: 6218.00 Matches: 1228
Percent Similarity: 49.74% Conservative: 1
Best Local Similarity: 49.70% Mismatches: 2
Query Match: 31.13% Indels: 1242
DB: 9 Gaps: 2

US-09-977-053-4 (1-3571) x AL158158 (1-194835)
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Db 176047 TATACTTCTGCTGCTTGTACACATTGATGCTGCGCCGACGCAAGTGGAGTAGAAGT 175988
Qy 2013 AspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAspHisAlaSerPro 2032
Db 175987 GACCAGCAGTCCGCTGCTCTCTGTGATGAGCCACCCATTGTGGACCGCTCTCCA 175928
Qy 2033 GluThrAlaHisArgLeuPheGlyAspIleAlaPheTyrCysSerAspGlyTyrSer 2052
Db 175927 GAGACTGCCCATCGGCTCTTGGAGACATTGCTTACTACTCTCTGATGGTTACAGC 175868
Qy 2053 LeuAlaAspAsnSerGlnLeuLeuCysAsnAlaGlnGlyLysTrpValProProGluGly 2072
Db 175867 CTAGCAGACAAATCCCGACTTCTCTGCAATGCCCGGCGCAAGTGGGTACCCCGAGAGGT 175808
Qy 2073 GlnAspMetProArgCysValIleAlaHisPheCysGluLysProProSerValSerTyrSer 2092
Db 175807 CAAGCATGCCCGCTGTATAGTCTCATTTCTGTGAAMAACTCCATCGGTTCTCTATAGC 175748
Qy 2093 IleLeuGluSerValSerLysAlaLysPheAlaAlaGlySerValValSerPheLysCys 2112

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Db 175687 ATGGAAGGCTTTGTACTGAAACACCTCAGCAAAAGATTGAATGATGAGAGGTTGGGCGAGTGG 175628
Qy 2133 AsnProSerProMetSerIleGlnCysIleProValArgCysGlyGluProProSerIle 2152
Db 175627 AACCTTCCCATGTCATCCAGTGCATCCCTGTGCGGTGTGGAGAGCCACCAAGCATC 175568
Qy 2153 MetAsnGlyTyrAlaSerGlySerAsnTyrSerPheGlyAlaMetValAlaTyrSerCys 2172
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Qy 2173 AsnLysGlyPheTyrIleLysGlyGluLysLysSerThrCysGluAlaThrGlyClnTrp 2192
Db 175507 AACAGGGGTTTACATCAACGAGGGAAGAAAGAGACCTCCGAGGCCACAGGGCGAGTGG 175448
Qy 2193 SerSerProIleProThrCysHisProValSerCysGlyGluProProLysValGluAsn 2212
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Qy 2213 GlyPheLeuGlu----- 2216
Db 175387 GGCTTCTCGA-GGTAAGAGACCAATTAGCAAAATGCTGTGCTTTTGTACAGGGGCC 175329
Qy 2216 ----- 2216
Db 175328 ATAATAAATAAATAAACAACAATAAATTGAGTCCAAACACTGCCAAAGTTCACTAAGGC 175269
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Qy 2216 ----- 2216
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Qy 2216 ----- 2216

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Qy	2489	GlyLysProThrCysLysAlaIleGluCysLeuLysProLysGluLeuLeuAsnGlyLys	2508
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Qy	2509	PheSerTyrThrAspLeuHisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPhe	2528
Db	172388	TTCTCTTACACGGACCTACACTATGGACAGACCGTTACTACTCTTTGCAACCGAGGCTTT	172329
Qy	2529	ArgLeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAspTyrAspValAspAla	2548
Db	172328	CGGCTCGAAGTCCCAAGTGCCTTGACCTGTGTTAGAGACAGGTGATGGAGTGTAGATGCC	172269
Qy	2549	ProSerCysAsnAlaIleHisCysAspSerProGlnProIleGluAsnGlyPheValGlu	2568
Db	172268	CCATCTTGCAATGCCATCCACTGCTGATTTCCCCACAAACCATTGAAATGGTTTTCTAGAA	172209
Qy	2569	GlyAlaAspTyrSerTyrGlyAlaIleIleIleTyrSerCysPheProGlyPheGlnVal	2588
Db	172208	GSTGCAGATTACAGCTATGGTGCCATAATCATCTACAGTTGCTTCCCTGGGTTTCAGGTG	172149
Qy	2589	AlaGlyHisAlaMetGlnThrCysGluGluSerGlyTyrSerSerSerIleProThrCys	2608
Db	172148	GCTGGTCATGCCATGCAGACCTGTGAGAGTCAGATGTCGAAGTTCATCCCAACATGT	172089
Qy	2609	MetProIleAspCysGlyLeuProProHisIleAspPheGlyAspCysThrLysLeuLys	2628
Db	172088	ATGCCAATAGACTGTGGCTCCCTCCCTCATATAGATTTTGAGACTGTACTAAACTCAA	172029
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Db	172028	GATGACCAGGGATATTTTGGACAGAAGACGACATGATGGGAAGTTCATATATGTGACTCT	171969
Qy	2649	HisProProTyrHisLeuGlyAlaValAlaIleTyrThrTyrGluAsnThrLysGluSerPro	2668
Db	171968	CACCTCTCTTATCATTTCTGGGAGCAGTGCTAAACCTGGGAAAATACAAAGAGTCTCT	171909
Qy	2669	AlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProGly	2688
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Qy	2749	LeuAlaGlySerAspLeuArgLeuCysLeuGluAsnArgLysTyrSerGlyAlaSerPro	2768
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Db	171428	ATTCTGTGGACTCGATTTACCCCCAGTCTCAGCCCAATGCCAGGTGAGGAGACCGAG	171369
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AX050034
LOCUS AX050034 3706 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 47 from Patent WO0071710.
ACCESSION AX050034
VERSION AX050034.1 GI:12226407
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Denefle, P., Rosier-Montus, M.P., Arnould-Reguigne, I., Prades, C. and Clepet, C.
TITLE Expression products of genes involved in diseases related to cholesterol metabolism
JOURNAL Patent: WO 0071710-A 47 30-NOV-2000;
Aventis Pharma S.A. (FR)
FEATURES Location/Qualifiers
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Score: 99.72% Conservative: 0
Percent Similarity: 99.72% Mismatches: 3
Best Local Similarity: 30.26% Indels: 0
Query Match: 6 Gaps: 0
DB: 6
US-09-977-053-4 (1-3571) x AX050034 (1-3706)

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2526 ArgGlyPheArgLeuGluGlyProSerAlaLeuThrCysLeuGluThrGlyAspTrpAsp 2545
62 CGAGGCTTTCCGNCGAGAGTCCAGTGCCTTGACCTGTGTAGAGACAGGTGATGGGAT 121
2546 ValAspAlaProSerCysAsnAlaIleHisCysAspSerProGlnProIleGluAsnGly 2565
122 GTAGATGGCCCATCTTGCATATGCCATCCACTGTGATTTCCCAACCCATGGAATGGT 181
2566 PheValGluGlyAlaAspTyrSerTyrGlyValAlaIleIleTyrSerCysPheProGly 2585
182 TTTGTAGAGAGTGCAGATACACTATAGTGTGCCATATCATCTACAGTTCCTCCCTGGG 241
2586 PheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSerGlyTrpSerSerIle 2605
242 TTTTCAGGTGGCTGGTCAATGCAGACCTGTGAAGAGTCAGGATGGTCAAGTTCATC 301
2606 ProThrCysMetProIleAspCysGlyLeuProProHisIleAspPheGlyAspCysThr 2625
302 CCAACATGATATGCCAATAGACTGTGGCTCCCTCCTCATATAGATTTTGGAGACTGTACT 361
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422 GTGACTCCTCACCTCTCTATATCTTTGGAGCAGTGGCTAAACCTGGGAAATACAAAG 481
2666 GluSerProAlaThrHisSerSerAsnPheLeuTyrGlyThrMetValSerTyrThrCys 2685
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2946 ProValAsnCysGlyProProGluAspLeuAlaHisGlyPheProAsnGlyPheSerPhe 2965
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2966 IleHisGlyGlyHisIleGlnTyrGlnCysPheProGlyTyrLysLeuHisGlyAsnSer 2985
1382 ATTCATGGGGCCCATATACAGTATCAGTCTTCTTCTGGTATATAGCTCATGGAATTCAT 1441
2986 SerArgArgCysLeuSerAsnGlySerTrpSerGlySerSerProSerCysLeuProCys 3005
1442 TCAAGAGGTGCTCTCCATGGCTCTGGAGTGGCAGCTCACCTTCTGCTGCTGCTTGC 1501
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1502 AGATGTTTCCACACCCAGTAATATGAATATGGAACTGTCTCAATGGGACAGATTTTGACTGTGA 1561
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 DB 2402 CTCATGGGAAGCTGACATTGAAACAGAGCAGCTGAGCCCAACGTGGTATATCTCTGC 2461
 QY 3326 AsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThrGluAsnGlyThrTrp 3345
 DB 2462 AACAGAGGCTACAGTCTTGGAGGGCCATCTGAGGCACACCTGCACAGAAATGGACCTGG 2521
 QY 3346 SerHisProValProLeuCysLysProAsnProCysProValProPheValIleProGlu 3365
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RESULT 22

AC096906

LOCUS

DEFINITION Rattus norvegicus clone CH230-11319, *** SEQUENCING IN PROGRESS

AC096906 266868 bp DNA linear HTG 10-MAY-2003

Rattus norvegicus clone CH230-11319, *** SEQUENCING IN PROGRESS

***, 3 unordered pieces.

AC096906

GI:30522617

HTG: HTGS_DRAFT; HTGS_ENRICHED.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 266868)

REFERENCE

AUTHORS

Muzny, D., Marie, E., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, P., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. I., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenschwari, L., Loulseghe, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemeloh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L. L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Sneed, A., Sodergren, E., Song, X. Z., Sorrelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, S., Yen, J., Yoon, L., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G., and Gibbs, R. A.

TITLE

JOURNAL

Unpublished

2 (bases 1 to 266868)

REFERENCE

AUTHORS

TITLE

JOURNAL

Direct Submission

Submitted (02-OCT-2001)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 266868)

REFERENCE

AUTHORS

TITLE

JOURNAL

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

COMMENT

On May 10, 2003 this sequence version replaced gi:23267390.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GGN7
 Center clone name: CH230-11319
 ----- Summary Statistics

Assembly program: Atlas 3.0;
 Consensus quality: 223096 bases at least Q40
 Consensus quality: 226986 bases at least Q30
 Consensus quality: 229938 bases at least Q20
 Estimated insert size: 232899; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 259563: contig of 259563 bp in length
 * 259564 259663: gap of unknown length
 * 259664 261157: contig of 1494 bp in length
 * 261158 261257: gap of unknown length
 * 261258 266868: contig of 5611 bp in length.

FEATURES

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 misc_feature
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 /note="wgs contig"
 misc_feature
 222699..222742
 /note="clone_boundary
 clone_end:r7
 site:ECORI
 end_sequence:BH262152"

ORIGIN

Alignment Scores:
 Pred. No.: 4,53e-273 Length: 266868
 Score: 5142.50 Matches: 1060
 Percent Similarity: 40.61% Conservative: 127
 Best Local Similarity: 36.26% Mismatches: 215
 Query Match: 25.75% Indels: 1523
 DB: 2 Gaps: 14

US-09-977-053-4 (1-3571) x AC096906 (1-266868)

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 ||| |||||::: ::|||

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 Qy 1877 -----TyrThrLeuAlaGlyAspLysGlu 1884
 Db 113215 CCGCTTTGTGGGGCGTGGCTCGTATTATTCTAGTACTGGGAAGTGGTGAAGCAG 113274
 Qy 1885 SerSerCysLeuAlaAsnSerSerTyrSerHisSerProValCysGluProValLys 1904
 Db 113275 -----GTTAGCAGATCTCCGAGACTCACCAGTAAGCCAGCTGCT-ATGCTGCA 113324
 Qy 1905 CysSerSerProGluAsnLeuAsnAsnGlyLys----- 1915
 Db 113325 TATTGAGTCCAGCAAAATAAAACAACAACAACAACAACAACAACAACAACAACA 113384
 Qy 1916 -----TyrIleLeuSerGlyLeuThrTyrLeu 1924
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 Qy 1925 SerThrAlaSerTyrSerCysAspThrGlyTyr-SerLeuGlnGly----- 1939
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 Db 113625 ATTAAATCATTTTACATAAGTTCAATATTC-----AGTTGCTAAATA 113669
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Thu May 13 07:11:09 2004

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Db	116609	CGTTCCGGTGGAAATGTCCTCCCACTCGAGGATCCTCAACCGCATCATCTGTCGAAG	116668	Db	117686	TGTGTTGTCATAGCAGTGTGACTCCGGCTATGTCTCAATGGCCTGAGAAAGGACATG	117745
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Db	116849	GTATGACAAACCACTACATCTCTTTGTGACCGAGGCTTCGGCTCGAAGTCCCAATC	116908	Db	117926	CAATGGAGTTGGAGTGTACCACTCCACGCTGTGCTGTGTGTGTGTGTGTGTGTGTGT	117985
Qy	2535	aLeuThrCysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHi	2555	Qy	2895	oGlnLeuAlaAsnGlyValThrGluGlyLeuAspTrpGlyPheMetLysGluValThrPh	2915
Db	116909	CCTGACCTGTGTAGACAGAGTAACCTGGGATATGGATATGGATATGGATATGGATATG	116968	Db	117986	ACAGTGGCAATGGGTGCACAGATGCGCTAGACTATGGGTTCAGAAAGAAAGTAACATT	118045
Qy	2555	sCysAspSerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTrpSerTrpGl	2575	Qy	2915	eHisCysHisGluGlyTrpIleLeuHisGlyAlaProLysLeuThrCysGlnSerAspGl	2935
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Qy	2575	yAlaIleIleIleTrpSerCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnTh	2595	Qy	2935	yAenTrpAspAlaGluIleProLeuCysLysProValAsnGlyProProGluAspLe	2955
Db	117029	CGCCATGATTTATCTATAGCTTTTCCTCCGGGTTTCAGGTGTGTGGCGATGCCATGCA	117088	Db	118106	GACTTGGATGCAAGAGTTCCCATCTGTAAACCGCTACCTGTGTGTGTGTGTGTGTGTGT	118165
Qy	2595	rCysGluGluSerGlyTrpSerSerIleProThrCysMetProIleAspCysGlyLe	2615	Qy	2955	uAlaHisGlyPheProAsnGlyPheSerPheIleHisGlyGlyHisIleGlnTrpGlnCy	2975
Db	117089	CTGCGAAGAGACGGGTGTGTCAAGCTCCAGCCCGACGCTGTGTATCCATAGACTGCGGTCT	117148	Db	118166	TCCCCAGGGCTTCCCTAATGGCTTTCTTTTTCATGGGGGCCACATACAGTACCAATG	118225
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Qy	2635	uGlnGluAspAspMetGluValProTrpValThrProHisProProTrpHisLeuGl	2655	Qy	2995	pSerGlySerSerProSerCysLeuProCysArgCysSerThrProValIleGluTrpGl	3015
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Db	117446	TGAATGTGATTTGCCCTGCTCCGAAATATGGCTTCTACATTTTACAGACTACTAT	117505	Db	118523	CATCAAGGGTAGCCCTTCAGAGGACACGTTGGTAACCTTACAGCTGCAGACCTGCTCAT	118582
Qy	2735	tGlySerAlaValGlnTrpSerCysLysProGlyHisIleLeuAlaGlySerAspLeuAr	2755	Qy	3095	lIleGlnGlySerSerAspLeuIleCysThrGluLysGlyValTrpSerGlnProTrpPr	3115
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RESULT 23
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LOCUS
DEFINITION
AL929406 152909 bp DNA linear ROD 01-JUN-2003
Mouse DNA sequence from clone RP23-332H16 on chromosome 4, complete
sequence.
ACCESSION AL929406
VERSION AL929406
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (31-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Jun 2, 2003 this sequence version replaced gi:31076167.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
EMBL, EMBL; SW., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6.

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ORIGIN
Alignment Scores:
Pred. No.: 2.78e-270 Length: 152909
Score: 5086.50 Matches: 1008
Percent Similarity: 45.60% Conservative: 117
Best Local Similarity: 40.86% Mismatches: 183
Query Match: 25.47% Indels: 1160
DB: 13
Gaps: 13
US-09-977-053-4 (1-3571) x AL929406 (1-152909)

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Db	144647			143568	TTCTGCATTATAGTAGCCTATAGATAAGGCCTTTGTAGCCATATCTTAGCCATAAATGTG	143509
QY	2013	AspGlnGlnCysLeuAlaValSerCysAspGluProProIleValAspHisAlaSerPro	2032	2216	-----	2216
Db	144587			143508	AAATTAGAGTGAGCCAAATTTTGATGAAATTCATTTTGTCTTTTATAAAGTTTCATGGCTG	143449
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Db	144527	GAGACTGCTCACAGGCTCTTTGGAGACACGGGTTTTTACTACTGTGCGATGGTTACAGC	144468	143448	AATGGAACTAAATAGATAATTTATTTGTACTCTGATTTTAAAGTGAGATAAGAGGTGCAGTT	143389
QY	2053	LeuAlaAspAsnSerGlnLeuLeuCysAsnAlaGlnGlyLysTrpValProGluGly	2072	2216	-----	2216
Db	144467	CTGGCTGATAATTTCCAGCTCATCTGCAATGCCAGGGAACTGGGTTTCCCCCGCGGC	144408	143388	TTTGCAATTCCTCGTTCAAGATATCTAAAGTAATCTCACCATGGTGAGCCCAATTTGTTAAG	143329
QY	2073	GlnAspMetProArgCysIleAlaHisPheCysGluLysProProSerValSerTyrSer	2092	2216	-----	2216
Db	144407			143328	TGTGATACAAATGTGGTCTGCTCCACCCTAAAGTGTCTTCCCACTAAGTGTGTGCGGAAG	143269
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QY	2173	AsnLysGlyPheTyrIleLysGlyLysLysSerThrCysGluAlaThrGlyGlnTrp	2192	2216	-----	2216
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QY	2193	SerSerProIleProThrCysHisProValSerCysGlyGluProProLysValGluAsn	2212	2216	-----	2216
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Db	143868	AGAAATACTCAAGTCTACACAGTGTGTACTGGATAAAATGGATCAAGATAATTAAGAA	143809	142788	ATCTGTGTGTACTGCGCTTCAACTCACCAGATCTGTGTAGATCGTGTATCTTATCTGT	142729
QY	2216	-----	2216	2216	-----	2216
Db	143808	ACCTTACAATATACATCTTTTCAAGTCTTATTTATGCGTATAGGTATGGCCTGCACA	143749	142728	GTCCCTGATCTTATTTTCTCTGTGGGTTCATAGAGTTTCTACAGAGGAATGACCT	142669
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				2217	-----HisThrGlyArgIlePheGlu	2224

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Qy	2265	GlyLysProProProlleGlnaGlnPheMetLysGlyGluAsnPheGluValGlySer	2284
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Qy	2285	LysValGlnPhePheCysAsnGluGlyTyrGluLeuValGlyLysSerSerTrpThrCys	2304
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Qy	2305	GlnLysSerGlyLysTrpAsnLysLysSerAsnProLysCysMetProAlaLysCysPro	2324
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Qy	2365	ProSerGlnGlnTrpAsnAspSerPheProValCysLysIleValLeuCysThrProPro	2384
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Qy	2445	GluIleProAsnGlyIleIleAspValGlnGlyLeuAlaTyrLeuSerThrAlaLeuTyr	2464
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Marwaha, R., Chen, A. J., Chang, S. C., Gerstin, E. H., Peralta, C. H., David, M. H. and Lewis, S. A.
Molecules for disease detection and treatment
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5409.5	25.3	3009	29	AY405592	AY405592 Pan trogl
3	5048	25.3	3127	14	CB548140	CB548140 AMGNNUC:C
4	4803.5	24.0	3288	29	AY405593	AY405593 Mus muscu
5	4781	23.9	3171	11	BC030816	BC030816 Homo sapi
6	4350	21.8	2809	13	BQ832212	BQ832212 C82 AF702
7	3955	19.8	2736	11	AK052699	AK052699 Mus muscu
8	2865.5	14.3	2053	11	AK014693	AK014693 Mus muscu
9	2023.5	10.1	3242	11	AK035333	AK035333 Mus muscu
10	1793	9.0	3307	11	AK052463	AK052463 Mus muscu
11	1690	8.5	906	13	EX390270	EX390270 BX390270
12	1658.5	8.3	1201	13	EX392777	EX392777 BX392777
13	1629.5	8.2	918	14	CD515150	CD515150 AGENCOURT
14	1549	7.8	881	13	EX314119	EX314119 BX431419
15	1470.5	7.4	1201	13	EX356254	EX356254 BX356254
16	1407.5	7.0	1201	13	EX356253	EX356253 BX356253
17	1405.5	7.0	6030	29	AY407073	AY407073 Homo sapi
18	1386.5	6.9	5901	29	AY407075	AY407075 Mus muscu
19	1385	6.9	748	13	EX093982	EX093982 BX093982
20	1382	6.9	769	12	BG534331	BG534331 602553560
21	1362	6.8	940	14	CF407643	CF407643 CH38049 F
22	1359	6.8	738	9	AL706149	AL706149 DKF2686E
23	1319	6.6	839	14	CF409971	CF409971 CH38063 H
24	1304	6.5	801	9	AU137280	AU137280 AU137280
25	1295	6.5	756	12	BG620159	BG620159 602618422
26	1247.5	6.2	3496	11	BC032550	BC032550 Homo sapi
27	1236.5	6.2	792	14	CD109768	CD109768 AGENCOURT
28	1207	6.0	619	13	BU072726	BU072726 in19C07 Y
29	1192	6.0	670	14	CB268566	CB268566 1007472 H
30	1188	5.9	829	13	BG434540	BG434540 602506592
31	1176.5	5.9	701	13	BU929100	BU929100 AGENCOURT
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33	1128	5.6	626	12	BG535782	BG535782 602563911
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35	1124.5	5.6	3348	11	AK003072	AK003072 Mus muscu
36	1113	5.6	900	13	EX454462	EX454462 BX454462
37	1102	5.5	926	13	BQ899350	BQ899350 AGENCOURT
38	1076	5.4	674	29	AG123704	AG123704 Pan trogl
39	1072	5.4	613	10	BE082811	BE082811 RC2-BT064
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41	1057.5	5.3	3809	11	BC032548	BC032548 Homo sapi
42	1050	5.3	2408	11	AK087058	AK087058 Mus muscu
43	1046	5.2	9330	11	AK090118	AK090118 Mus muscu
44	1039.5	5.2	2019	11	BC047729	BC047729 Homo sapi
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46	1027.5	5.1	1035	12	BG621817	BG621817 602619678
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56	990	5.0	673	10	BB542219	BB542219 BB542219
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62	969.5	4.9	656	13	BY714190	BY714190 BY714190

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65	956	4.8	543	14	CD693738	CD693738 EST10261
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78	908	4.5	606	14	CD766382	CD766382 AGENCOURT
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LOCUS	Homo sapiens HCM2275 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	genomic survey sequence.				
ACCESSION	AY405591.1	GI:39761565			
VERSION	GSS.				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 3288)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,				
	Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,P., Murphy,B.,				
	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,				
	Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous				
	gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PubMed	14671302				
REFERENCE	2 (bases 1 to 3288)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,				
	Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,P., Murphy,B.,				
	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,				
	Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,				
	Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering				
	them based on alignment.				

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Alignment Scores:	
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Best Local Similarity:	90.33% Mismatches: 87
Query Match:	27.08% Indels: 19
DB:	29 Gaps: 1
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Qy	41 GlyAlaProGlySerIleProAlaProAlaProGlyAspGluAlaAlaGlySerArg 60
Db	121 NNN 180
Qy	61 ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu 80
Db	181 NNN 240
Qy	81 ArgLeuGluLeuValPheLeuValAspAspSerSerValGlyGluValAsnPheArg 100
Db	241 CCCTGGAGCTTGTCTTCTTGTGGATGATTCGTCCAGCGTGGCGGAGTCAACTTCGC 300
Qy	101 SerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAlaThr 120
Db	301 AGCGAGCTCATGTCGTCCGCAAGCTGTCTCCGACTTCCCGTGGTGGCCACGGCCAG 360
Qy	121 ArgValAlaIleValThrPheSerSerLysAenTyrValValProArgValAspTyrIle 140
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Qy	141 SerThrArgArgAlaArgGlnHisLysCysAlaLeuLeuGlnGluLeuProAlaIle 160
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Qy	161 SerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIleLeu 180
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VERSION AY405592.1
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 3009)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3009)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3288)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 3288)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 /mol_type="genomic DNA"
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 Score: 84.74% Conservative: 76
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 Query Match: 24.05% Indels: 33
 DB: 29 Gaps: 5
 US-09-977-053-4 (1-3571) x AY405593 (1-3288)

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 VERSION BC030816.1 GI:21411218

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3171)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 37 ROW: 9 Column: 23
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, GenomScan gene prediction, Similarity but not identity
 to protein

This clone has the following problem: retained intron.

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source Location/Qualifiers

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Percent Similarity: 100.00% Conservatives: 0

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Qy 281 CysAspGluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThr 300
Db 1178 TGTGATGAAGCAAGACTGCTGTGACCAATGGGAGCTGCAAAATGTGGGACACACACA 1237
Qy 301 GlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGluCys 320
Db 1238 GGCCATTTTGAAGTCATCTGTGAAAGGGTATTACGGGAAGGCTCGCAGATATGATGC 1297
Qy 321 ThrAlaCysProSerGlyThrTyrLysProGluLysProGlySerProGlyIleSerSerCys 340
Db 1298 ACAGCTGCCCATCGGGACATACAAACCTGAAGGCTCACAGGAGGAATCAGCAGTTGC 1357
Qy 341 IleProCysProAspGluAsnHisThrSerProGlySerThrSerProLysAspCys 360
Db 1358 ATTCCATGTCTGATGAATAATCACACCTCTCCACCTGGGAAGCACATCCCTCGAGACTGT 1417
Qy 361 ValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeuValHisCysProAla 380
Db 1418 GTCTCAGAGAGGGATACAGGGCATCTGGCCAGACCTGTGTAACCTGTCCACTCGCTCGCC 1477

Qy 381 LeuLysProProGluAsnGlyTyrPheIleGlnAsnThrCysAsnAsnHisPheAsnAla 400
Db 1478 CTGAAGCCTCCCGAAAAATGGTTACTTTATCCAAAAACACTTGCACAAACCACTTCAATGCA 1537
Qy 401 AlaCysGlyValArgCysHisProGlyPheAspLeuValGlySerSerIleLeuLeuCys 420
Db 1538 GCTGTGGGGTCCGATGTCACTCTGATTGATCTTGTGGGAAGCAGCATCATCTTATGT 1597
Qy 421 LeuProAsnGlyLeuTrpSerGlySerGluSerTyrCysArgValArgThrCysProHis 440
Db 1598 CTACCAATGGTTTGTGGTCCGGTTTCAGAGAGCTACTGCAGAGTAAGAACAATGCTCTCAT 1657
Qy 441 LeuArgGlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyrLysThr 460
Db 1658 CTCGCCACCGCAAAATGCGCCACATCAGCTGTCTTACAGGGAAATGTTATATAGACA 1717
Qy 461 ThrCysLeuValAlaCysAspGluGlyTyrArgLeuGluGlySerAspLysLeuThrCys 480
Db 1718 ACATGTTTGGTTGCTGTGTATGAGGTACAGCTAGAGGCGATGATTAAGCTTACTTGT 1777
Qy 481 GlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThr 500
Db 1778 CAAGGAAACAGCCAGTGGGATGGCCAGAAACCCCGGTGTGTGGAGCGCCACTGTTCACC 1837
Qy 501 PheGlnMetProLysAspValIleSerProHisAsnCysGlyLysGlnProAlaLys 520
Db 1838 TTTTCAGATGCCCAAGATGTCTATCATATCCCCCAACCTGTGGCAAGCAGCCAGCCAA 1897
Qy 521 PheGlyThrIleCysTyrValSerCysArgGlnGlyPheIleLeuSerGlyValLysGlu 540
Db 1898 TTTGGAGCATCTGCTATGTAAAGTTCGCCCAAGGGTTTCATTTATCTGGAGTCAAGAA 1957
Qy 541 MetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGlnAlaAlaValCysLys 560
Db 1958 ATGCTGAGATGTACCACTTCGAAAAATGGAATGTCCGAGTTTCAGGAGCTGTGTGATA 2017
Qy 561 AspValGluAlaProGlnIleAsnCysProLysAspIleGluAlaLysThrLeuGluGln 580
Db 2018 GACGTGGAGGCTCTCNAATCAACTGTCTTAAGACATAGAGCTAAGACTCTGGAAACAG 2077
Qy 581 GlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAspAsnSerGlyGluLys 600
Db 2078 CAAGATTCGCCAATGTACTTGGCAGATTCCACAGCTTAAGACAACTCTGTGTGAAG 2137
Qy 601 ValSerValHisValHisProAlaPheThrProProTyrLeuPheProIleGlyAspVal 620
Db 2138 GTGTCACTCCAGCTTCATCCAGCTTCACCCCACTTACCTTTTCCCAATGGAGATGT 2197
Qy 621 AlaIleValTyrThrAlaThrAspLeuSerGlyAsnGlnAlaSerCysIlePheHisIle 640
Db 2198 GCTATCGTATACACGGCAACTGACCTATCCGGCAACCGCAGCTGCATTTTCCATATC 2257
Qy 641 LysValIleAspAlaGluProProValIleAspTyrCysArgSerProProValGln 660
Db 2258 AAGGTTATGTAGCAGAACCACTGTCTATAGACTGGTGCAGATCTCCACCTCCGTCAG 2317
Qy 661 ValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPheSerAspAsnSerGly 680
Db 2318 GTCTCGGAAGGTACATGCGCAAGCTGGATGAGCCTCAGTTCTCTCAGACAACTCAGGG 2377
Qy 681 AlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPheProGlnGlyGluThr 700
Db 2378 GCTGAATTTGGTCATTTACCAAGATCATACAGGAGACTCTTTTCCCTCAGGGGAGACT 2437
Qy 701 IleValGlnTyrThrAlaThrAspProSerGlyAsnAsnArgThrCysAspIleHisIle 720
Db 2438 ATAGTACAGTATACAGCCACTGACCCCTCAGGCCAATAACAGGCATGTGATATCCATAT 2497
Qy 721 ValIleLysGlySerProCysGluIleProPheThrProValAsnGlyAspPheIleCys 740
Db 2498 GTCATAAAGGTTCTCCCTGTGAATTCATTTACACCTGTAAATGGGGATTTTATATGC 2557

QY 1978 AsnPheThrPheArgAsnThrValThrTyThrCysLysGluGlyTyThrLeuAlaGly 1997
DB 722 AACTTTCACTTTTGGGAACACAGTGTCTTACACATCAAGAGGGGTACACCCCTTCTGCG 781
QY 1998 LeuAspThrIleGluCysLeuAlaAspGlyLysTrpSerArgSerAspGlnClnCysLeu 2017
DB 782 CTTGACACATCTGATGACAGGCAACCGCAATGGAATTCAGTAACACCAAGTGCCTG 841
QY 2018 AlaValSerCysAspGluProProIleValAlaPheHisAlaSerProGluThrAlaHisArg 2037
DB 842 GCTGTCTCTGTGACGAGCCCAATGTGGACCAAGCCCTCTCCAGAGACTGCTCACAGG 901
QY 2038 LeuPheGlyAspIleAlaPheTyThrCysSerAspGlyTyThrSerLeuAlaAspAsnSer 2057
DB 902 CTCCTTGGAGACACCGCGTTTACTACTGTGCGGATGGTTACAGCTCGGCTGATAAATTC 961
QY 2058 GlnLeuLeuCysAsnAlaGlnGlyLysTrpValProGluGlyGlnAspMetProArg 2077
DB 962 CAGCTCATCTGCATGCCAGGGGAACCTGGTTCCCTCGCGGGCCAGGCTGTGCGCGC 1021
QY 2078 CysIleAlaHisPheCysGluLysProProSerValSerTyThrSerIleLeuGluSerVal 2097
DB 1022 TGCATAGCTCACTCTGTGAAAAACCCCATCTGTCTTCTACAGCATCTTGGAAATCTGTG 1081
QY 2098 SerLysAlaLysPheAlaGlySerValValSerPheLysCysMetGluGlyPheVal 2117
DB 1082 AGCAAGCAAAAGTTTGCAGCTGGCTCGGTAGTACGCTTCAAGTGTATGGAGGGTTTGTG 1141
QY 2118 LeuAsnThrSerAlaLysIleGluCysMetArgGlyGlyGlnTrpAsnProSerProMet 2137
DB 1142 CTGAACACCTCAGCGAAGATTGAATGCTTGAGAGGTGGAGGTGAGGCGCTTCTCCCTC 1201
QY 2138 SerIleGlnCysIleProValArgCysGlyGluProProSerIleMetAsnGlyTyAla 2157
DB 1202 TGGTCCAGTGATCCCGGTGCGTGGAGAGCCCTCCAAAGCATGCCAAATGGCTACCG 1261
QY 2158 SerGlySerAsnTyThrPheGlyAlaMetValAlaTyThrSerCysAsnLysGlyPheTy 2177
DB 1262 AGTGGGACAACTACAGTTTGGGGCCGTGGTGGCTTACAGCTGCCCAAGGGATTCTAT 1321
QY 2178 IleLysGlyGluLysLysSerThrCysGluAlaThrGlyGlnTrpSerProIlePro 2197
DB 1322 ATCAAGGGGGAGAGAGAGACAGTGTGAGGCCACAGACAGTGGAGTAAACCCACGCC 1381
QY 2198 ThrCysHisProValSerCysGlyGluProProLysValGluAsnGlyPheLeuGluHis 2217
DB 1382 ACCTGCCATCTGTGTCTGTAAACGAGCCACTAAGGTGGAGAACCGCTTCTCGAGCAC 1441
QY 2218 ThrThrGlyArgIlePheGluSerGluValAlaArgTyThrGlnCysAsnProGlyTyThrLysSer 2237
DB 1442 ACCACTGGCAGGACCTTTGAGAGCGAAGCAAGGTTCAGTGTCAACCCAGGCTATTAAGGCA 1501
QY 2238 ValGlySerProValPheValCysGlnAlaAsnArgHisTrpHisSerGluSerProLeu 2257
DB 1502 GCCGAGTCTGTGTGTGTTCGACAGCCATCCCACTGGCAAGCAGCAGCCCTCTG 1561
QY 2258 MetCysValProLeuAspCysGlyLysProProIleGlnAsnGlyPheMetLysGly 2277
DB 1562 TCTGCAACCCCTCTCACTGTGGGAAACCCCTCCATTCAGAAATGGCTTTTGAAGCA 1621
QY 2278 GluAsnPheGluValGlySerLysValGlnPhePheCysAsnGluGlyTyThrLeuVal 2297
DB 1622 GAAAGCTTTGAAGTAGGTGTCAGGTTCAGTTGTCTGTAATGAGGGATATGAGTCTGTT 1681
QY 2298 GlyAspSerSerTrpThrCysGlnLysSerGlyLysTrpAsnLysLysSerAsnProLys 2317
DB 1682 GGTGATAATTTCTTGACTTTCAGAAATCTGGCAATGAGGTAAAGCAAGCCCGAG 1741
QY 2318 CysMetProAlaLysCysProGluProProLeuLeuGluAsnGlnLeuValLysGlu 2337
DB 1742 TGTGTCCCAACCAAGTGTGAGAGGCTCTCTCTCTAGAAAACCAAGCTGTATTAAGGAA 1801
QY 2338 LeuThrThrGluValGlyValThrPheSerCysLysGluGlyHisValLeuGlnGly 2357

DB 1802 TTAGCTTCCGAGGTAGGAGTGTATGACCATTTCTCTGTAAGAGGGCATGCTTTCGAAGGC 1861
QY 2358 ProSerValLeuLysCysLeuProSerGlnGlnTrpAsnAspSerPheProValCysLys 2377
DB 1862 CCTCTGTCTCTGAAGTGTTCCTCCGCGCAATGGAATGGTTCCTTCTTATTTGTAAG 1921
QY 2378 IleValLeuCysThrProProLeuLysSerPheGlyValProIleProSerSerAla 2397
DB 1922 ATGGTCTTGTCTCCCTCGCTCTCTTGAATTCCTTGGCGTCCCTCGCTTCTCCGGTCT 1981
QY 2398 LeuHisPheGlySerThrValLysTyThrCysValGlyGlyPhePheLeuArgGlyAsn 2417
DB 1982 CTTTCAATTTGGCAGTACTGTCAAGTATCTGTGTGTGCGAGCGGTTCCTTAAGAGGAGT 2041
QY 2418 SerThrThrLeuCysGlnProAspGlyThrTrpSerSerProLeuProGluCysValPro 2437
DB 2042 CCACCATCTCTGCCAGGTGATAGCACTGGAGTTCCTCATTCGCCGAATGCGTTCCG 2101
QY 2438 ValGluCysProGlnProGluGluIleProAsnGlyIleIleAspValGlnGlyLeuAla 2457
DB 2102 GTAGAATGTCCCAACCTGAGGAGATCTCTCAACGGTATCATCCAGTACAGAGGCTTGC 2161
QY 2458 TyrLeuSerThrAlaLeuTyThrCysLysProGlyPheGluLeuValGlyAsnThrThr 2477
DB 2162 TATCTCAGCACCACTCTACACCTGCAAGCGGCTTTAGTTAGTGGGCAATGCTACC 2221
QY 2478 ThrLeuCysGlyGluAsnGlyHisTrpLeuGlyGlyLysProThrCysLysAlaIleGlu 2497
DB 2222 ACCCTCTGTGGGAAATGGCCAGTGGCTGGAGGAAACCAATGTGCAAAACCCATTGAA 2281
QY 2498 CysLeuLysProLysGluIleLeuAsnGlyLysPheSerTyThrAspLeuHisTyThrGly 2517
DB 2282 TGCCAGAGCCCAAGAGATTTTAAATGGCCAAATTCCTCTCTCGTAGAGCTTTCAGTAGGA 2341
QY 2518 GlnThrValThrTyThrSerCysAsnArgGlyPheArgLeuGluGlyProSerAlaLeuThr 2537
DB 2342 CAACCATCACATCTTTTGTGACCGGGCTTCCGGCTCGAAGGTCCTCCAAATCCCTGACC 2401
QY 2538 CysLeuGluThrGlyAspTrpAspValAspAlaProSerCysAsnAlaIleHisCysAsp 2557
DB 2402 TGTTTAGAGACAGGTGACTGGGATATGGATCCCTCTCTGTGATGCCATCCACTCGAGT 2461
QY 2558 SerProGlnProIleGluAsnGlyPheValGluGlyAlaAspTyThrTyThrGlyAlaIle 2577
DB 2462 GACCCACAGCCCATTTGAAATGGTTTCTAGAGGTGGGATTCAGATACGATGCGCATG 2521
QY 2578 IleIleTyThrCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGlu 2597
DB 2522 ATCATCTATAGTGTCTTCCCTGGGTTTCAAGTGTCTGTGTCATGCCATGCCAGCTGTGAA 2581
QY 2598 GluSerGlyTyTrpSerSerIleProThrCysMetProIleAspCysGlyLeuProPro 2617
DB 2582 GAGTCGGGATGTCAAGCTCCAGCCCACTGTGTACCATAGACTGCGGTCTCCCTCCT 2641
QY 2618 HisIleAspPheGlyAspCysThrLysLeuLysAspAspGlnGlyTyThrGluGlnGlu 2637
DB 2642 CACATAGACTTTGGTGACTGTACTAAGTCAGAGATGGCCAGGACATTTTGTATCAAGAA 2701
QY 2638 AspAspMetGluValProTyThrProHisProProTyThrHisLeuGlyAlaVal 2657
DB 2702 GATGACATGATGGAAGTCCCATATCTGGCT-----CACCTCAACATTTTGGAGCAACA 2755
QY 2658 AlaLysThrTrpGluAsnThrLysGluSerProAlaThr 2670
DB 2756 GCTAAGGCTTGGAAAAATACAAAGGAGTGGCTGCTCT 2794

RESULT 7

AK052699

LOCUS

DEFINITION

AK052699 2736 bp mRNA linear HTC 20-SEP-2003
Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
library, clone:D630026K16 product:polydomain protein, full insert
sequence.

Qy 3010 ProValIleGluTyrGlyThrValAsnGlyThrAspPheAspCysGlyValAlaAlaArg 3029
 Db 123 CCCATTCATCAACGGGAACCATCAACCAATGATTTGGGATGTGGAAAGACGGTCCAG 182
 Qy 3030 IleGlnCysPheIleGlyPheLeuLeuGlyLeuSerGluIleThrCysGluAlaAsp 3049
 Db 183 ATTGAGTCTCTCAAGGGCTTCAGCTGCTTGAGACTTCTGAAATCACTGTGATGCCAAT 242
 Qy 3050 GlyGlnTrpSerSerGlyPheProHisCysGluHisThrSerCysGlySerLeuProMet 3069
 Db 243 GGCCAAATGTCGTGAC--GTCCCACTGTGTGAGCAGCTCAGTGGCGGCTCTCCCAACC 299
 Qy 3070 IleProAsnAlaPheIleSerGluThrSerSerTrpLysGluAsnValIleThrTyrSer 3089
 Db 300 ATACCCAAACGCAATTTGCTTTGAGGCGACGCTTCGAGGAGCAATGTGGTAATCTACAGC 359
 Qy 3090 CysArgSerGlyTyrValIleGlnGlySerAspLeuIleCysThrGluLysGlyVal 3109
 Db 360 TGCAGACTGGCTACCATGCAAGTAGTTCAGATCTGATTTGTACGGAAAGCGGATA 419
 Qy 3110 TrpSerGlnProTyrProValCysGluProLeuSerCysGlySerProSerValAla 3129
 Db 420 TGGAGCCAGCTTACCCAAAGGTGGAACCCCTGCTGTGGACCCCAACCACTGTAGCC 479
 Qy 3130 AsnAlaValAlaThrGlyGluAlaHisThrTyrGluSerGluValLysLeuArgCysLeu 3149
 Db 480 AATGCAAGTGGCAACAGGAGAGGCTCATACCTATGAAGCAAGTGAATCTCAAGTGTCTG 539
 Qy 3150 GluGlyTyrThrMetAspThrAspThrPheThrCysGlnLysAspGlyArgTrp 3169
 Db 540 GAAGGTATGTGATGATTCGGATACAGATACATTCACCTGCGACAGATGGCCATTTGG 599
 Qy 3170 PheProGluArgIleSerCysSerProLysCysProLeuProGluAsnIleThrHis 3189
 Db 600 GTCCCTGGAAGAAATCACCTGCAGTCTCTAAATAATGCTGTGCCATCCCAACATGACAC 659
 Qy 3190 IleLeuValHisGlyAspAspPheSerValAsnArgGlnValSerValSerCysAlaGlu 3209
 Db 660 ATACGTTTTTACCGAGATGACTTCCAGGTGAACAGACAAAGTTTCTGTGTCATGTGCGAA 719
 Qy 3210 GlyTyrThrPheGluGlyValAsnIleSerValCysGlnLeuAspGlyThrTrpGluPro 3229
 Db 720 GGGTTTACCCAGAGAGTGAATCTGGTCAACATGCCAGCCGCGATACATGGGAGCCA 779
 Qy 3230 PropheSerAspGluSerCysSerProValSerCysGlyLysProGluSerProGluHis 3249
 Db 780 CCATTTCTTGATGATTCCTGTATCCAGTGTGTTGGGCGATCCTGAAAGCCAGCGCAT 839
 Qy 3250 GlyPheValValCysSerLysTyrThrPheGluSerThrIleIleTyrGlnCysGluPro 3269
 Db 840 GGCCTCGTGGTGGCAATGAACAGCAGCTTTGGAAGCACCATTGTTTACAGTGTGACCT 899
 Qy 3270 GlyTyrGluLeuGluGlyValAsnArgGluArgValCysGlnLeuAsnArgGlnTrpSerGly 3289
 Db 900 GGCCTACAAATTAGAGGGGACAGGGAAACGAACTGCGAGAGACAGACAGTGGAGTGA 959
 Qy 3290 GlyValAlaIleCysLysGluThrArgCysGluThrProLeuGluPheLeuAsnGlyLys 3309
 Db 960 GAGGTGGCAGTGTGCAGAGAGAACAGATGTGAGACTCCAGCTGAGTTTCCCAATGGGAAG 1019
 Qy 3310 AlaAspIleGluAsnArgThrThrGlyProAsnValValTyrSerCysAsnArgGlyTyr 3329
 Db 1020 GCTGTCTGGAAAACCAACCATCTGAGCCAGCCCTTCTGTTTCTGTCTCAGAGAGGCTAC 1079
 Qy 3330 SerLeuGluGlyProSerGluAlaHisCysThrGluAsnGlyThrTrpSerHisProVal 3349
 Db 1080 ACCCTGGAAGGTGCCCCGAGGCGACACTGCACTGCAAAATGGAACTGGAAATCACTGACT 1139
 Qy 3350 ProLeuCysLysProAsnProCysProValProPheValIleProGluAsnAlaLeuLeu 3369
 Db 1140 CCCCTCTGCAACCAATCCATCCCTGCTCTTTGTTGATCTCTGAGAAGCCGCTCTT 1199
 Qy 3370 SerGluLysGluPheTyrValAspGlnAsnValSerIleLysCysArgGluGlyPheLeu 3389

Db 1200 TCTGAAAAGAGTTTATGTGCACCAAGATGATCTATCAAGTGCAGGGAAGGCTTCTCTG 1259
 Qy 3390 LeuGlnGlyHisGlyIleIleThrCysAsnProAspGluThrTrpThrGlnThrSerAla 3409
 Db 1260 CTCAAGGCAATGTTGTATCATCAGCTGCAGCCCTGACGAGACATGACGACCAATGCC 1319
 Qy 3410 LysCysGluLysIleSerCysGlyProProAlaHisValGluAsnAlaIleAlaArgGly 3429
 Db 1320 AGATGTGAAAATAATCTCTGTGGTCTCCAAATGCGTAGAGAAATGCAATCTCTCGAGA 1379
 Qy 3430 ValHisTyrGlnTyrGlyAspMetIleThrTyrSerCysTyrSerGlyTyrMetLeuGlu 3449
 Db 1380 GTGATACCAAGTATGGGACATATACCTACTCTCTGTACAGTGGCTACATGCTAGAA 1439
 Qy 3450 GlyPheLeuArgSerValCysLeuGluAsnGlyThrThrSerProProIleCysArg 3469
 Db 1440 GGTTCCTCGGAGTGTTCCTAGAAAATGCAATGGACACCATCTCTCTGTGTTCGAGA 1499
 Qy 3470 AlaValCysArgPheProCysGlnAsnGlyGlyIleCysGlnArgProAsnAlaCysSer 3489
 Db 1500 GCTGTCTGTGCGTTCCTCCATGTCAGAAATGAGGTGTCTGTCAACGTCCTCAATGCTCTCA 1559
 Qy 3490 CysProGluGlyTrpMetGlyArgLeuCysGluGluProIleCysIleLeuProCysLeu 3509
 Db 1560 TGCCAGACGGCTGATGGAGCTCTCTGTGAGAGCCATATGATATCTCTCTCTCTTTG 1619
 Qy 3510 AsnGlyGlyArgCysValAlaProTyrGlnCysAspCysProProGlyTrpThrGlySer 3529
 Db 1620 AATGCTGGCGCTGTGTGCGCTTATCAGTGTGATGCTGCCACACAGCTGGAGTGGTCC 1679
 Qy 3530 ArgCysHisThrAlaValCysGlnSerProCysLeuAsnGlyGlyLysCysValArgPro 3549
 Db 1680 CGCTGTCTATACAGCTACTTGTTCAGTCCCTCTCTTAAATGGCGGAAATGCATAGACCA 1739
 Qy 3550 AsnArgCysHisCysLeuSerSerTrpThrGlyHisAsnCysSerArgLysArgArgThr 3569
 Db 1740 AACCATGCCATGCTCTCTCAGCTGGACAGACATGATGTTCCAGGAAAGAGAGGCC 1799
 Qy 3570 Gly 3570
 Db 1800 GGG 1802
 RESULT 9
 AK035333 3242 bp mRNA linear HTC 18-SEP-2003
 LOCUS Mus musculus adult male urinary bladder cDNA, RIKEN full-length
 DEFINITION enriched library, clone:9530018121 product:polydomain protein, full
 insert sequence.
 ACCESSION AK035333
 VERSION AK035333.1 GI:26330611
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Db	546	TTCCAGCCCGTGGCCCTTCCTGCTCAACTTCAGCTTCGCCCTGTGTTCCTCCGAGCGCTCTCCG	605
Qy	41	GLyAlaProGlySerIleProAlaapProAlaProGly---AspGluAlaAlaGlySer	59
Db	606	GGGGCTCTGGGCACACTGGCGGTHACTTCCTCCGCTCCAGTGGAGGAGGACAGAGGAGC	665
Qy	60	ArgValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSer	79
Db	666	AAAGTGGAGCGCTTGGCGCGCGCTTCGGAGCCGCTGCGGCGACTGCGGAGCTCAGC	725
Qy	80	GluArgLeuGluLeuValPheLeuValAspAspSerSerSerValGlyGluValAspPhe	99
Db	726	GGCAGCCTTGGAGCTCGTCTTCCTGGTGGACGAGCTGTCACGCTGGGCGCCAAACCACTTC	785
Qy	100	ArgSerGluLeuMetPheValArgLysLeuLeuSerAspPheProValValProThrAla	119
Db	786	CTCAACGAGCTCAAGTTCTGTGGCCAGCTGCTGCCACTTCCCGCTGGTGTCTCCAGGCC	845
Qy	120	ThrArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyr	139
Db	846	ACGCGTGTGGCCATCGTCACCTTCTCATCAAGAACCAACGTGGTGGCGCGCTGGAATTAC	905
Qy	140	IleSerThrArgArgAlaArgGlnHisLysCysAlaIleLeuLeuGlnGluIleProAla	159
Db	906	ATCTCCACCAAGCCGCGGCGCAACAACACAGTGCCTACTTCAGCCCGAGATCCCGGCC	965
Qy	160	IleSerTyrArgGlyGlyGlyThrTyrThrLysGlyAlaPheGlnGlnAlaAlaGlnIle	179
Db	966	ATCACTTACCCTGGTGGTGGACCTTATCCAGGCGCCCTTCCAGCAGCCGCGCAATC	1025
Qy	180	LeuLeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSer	199
Db	1026	CTTCGTCACCTAGAGAAACTCCACCAAGTGCATATTTCTCATCACCGAGCGCTATTCC	1085
Qy	200	AsnGlyGlyAspProArgProIleAlaAlaSerLeuArgAspSerGlyValGluIlePhe	219
Db	1086	AATGGCGGAGACCCAGACCTATTTCGAGCATTCGCTTCGGATTTCCGAGTGGAGATCTTC	1145
Qy	220	ThrPheGlyIleTyrGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLys	239
Db	1146	ACGTTTCGGGATTTGGCAGGGGATATTCGGGACTGAATGACATGGCTTCCACCCGAG	1205
Qy	240	GluGluHisCysTyrLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAla	259
Db	1206	GAAGAACATTTGTACCTGCTCCAAGTTTGAAGAAATTGAGGCTTTAGCTCGCAGGGCG	1265
Qy	260	LeuHisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTyr	279
Db	1266	TTGCATCAAGATCTACCTCTCTGGAGTATTATCCAGAGATATGGCCCCCTGCTCTTAT	1325
Qy	280	LeuCysAspGluGlyLysAspCysAspArgMetGlySerCysLysCysGlyThrHis	299
Db	1326	CTCTGTGAGGCTGGGAAGAATCTCTGTGACAGAAATGGCCAGCTGCAAATGTGGACACAC	1385
Qy	300	ThrGlyHisPheGluCysIleCysGluLysGlyTyrTyrGlyLysGlyLeuGlnTyrGlu	319
Db	1386	ACGGCTCAATTTGAATGCATCTGTGAGAGGGCTATTACGGGAAAGGCTTCGACGATGAG	1445
Qy	320	CysThrAlaCysProSerGlyThrTyrLysProGluGlySerProGlyGlyIleSerSer	339
Db	1446	TGCACAGCTTTGCCCATCAGGGACATATAAGCCGAGAGCTTCTCCAGGAGGAATCAGCAC	1505
Qy	340	CysIleProCysProAspGluAsnHisThrSerProGlySerThrSerProGluAsp	359
Db	1506	TGCATCCATGTCTGTGACGTAAAGCAACCTCCCACTCGAAGCACTTCCCTGTGAGAC	1565
Qy	360	CysValCysArgGluGlyTyrArgAlaSerGlyGlnThrCysGluLeu-----	375
Db	1566	TGCGTGTGCCGAGAGGGATACAGAGATCTGGCCAGACCTGTGAGGG-TAAGCACCTTAC	1624
Qy	375	-----	375
Db	1625	TGCTCCCAATGGGATCTAGAAAGCTGATCTTGATCTCTGTGGTGCAGAGTGTGGTGGTGG	1684


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Qy 376 -----ValHisCysProAlaLeuLysProProGluAsn 386
Db 2765 TTTTGTCTCTCTCTGAATGTTAGTTGCTCCACTGCTCCCTGAGCCTCTGAAAT 2824
Qy 387 GLYTYRPhelLeuGlnAsnThrCysAsnAsnHisPheAsnAlaAlaCysGlyValArgCys 406
Db 2825 GTTATTTTATACAAACACCTTCGAAACCACTTCATGTCGCTGTGGGTCCGATGT 2884
Qy 407 HisProGlyPheAspLeuValGlySerSerlleLeuLeuCysLeuProAsnGlyLeuTrp 426
Db 2885 CGCCCGGCTTTGACCTTGTGGAGCAGCATCCATCTTGTGTGTCACACCCCAATGTTGTGG 2944
Qy 427 SerGlySerGluSerTyCysArg 434
Db 2945 TCTGGACAGAAAGCTTCTGCAGA 2968

RESULT 11
BX390270 906 bp mRNA linear EST 08-MAY-2003
LOCUS BX390270 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS01010YG21 5-PRIME, mRNA sequence.
ACCESSION BX390270
VERSION BX390270.1 GI:30463533
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4991.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG0252E09 CS02373 1&cluster=4991.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAG0252E09_CS02373_1.
FEATURES
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS01010YG21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 7 45e-125 Length: 906
Score: 1690.00 Matches: 294
Percent Similarity: 98.04% Conservative: 1
Best Local Similarity: 97.67% Indels: 6
Query Match: 8.46% Gaps: 0
DB: 13

US-09-977-053-4 (1-3571) x BX390270 (1-906)

Qy 243 CysTyRLeuHisSerPheGluPheGluAlaLeuAlaArgAlaLeuHisGlu 262
Db 2 TGTACCTGCTACACAGTTTTCAGAAATTTAGGCTTTAGCTCGCGGCAATGTCATGAA 61
Qy 263 AspLeuProSerGlySerPheLeuGlnAspAspMetValHisCysSerTyRLeuCysAsp 282

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Db 62 GATCTACCTTCTGGAGTTTATTTCAGATGATATGGTCCATGCTCATATCTTTGTGAT 121
Qy 283 GluGlyLysAspCysCysAspArgMetGlySerCysLysCysGlyThrHisThrGlyHis 302
Db 122 GAAGGCAAGGAGCTGCTGTGACCGAATGGAGAGCTGCAAAATGTGGACACACACAGGCCAT 181
Qy 303 PheGluCyslleCysGluLysGlyTyRTrpGlyLysGlyLeuGlnTyRgluCysThrAla 322
Db 182 TTTTGATGTCATCTGTGAAAAGGGGTATTACGGENAAGGTCTGACGATGATGAATGCACAGCT 241
Qy 323 CysProSerGlyThrTyRLeuSerProGluGlySerProGlyGlyLysSerCysIlePro 342
Db 242 TGCCCATCGGGACATACAACTGAGGCTCACAGAGGAAATCAGCAGTTGTCATCCA 301
Qy 343 CysProAspGluAsnHisThrSerProGlySerThrSerProGluAspCysValCys 362
Db 302 TGTCTGTATGAAATACACACCTCTCCCTGGAAGCACATCCCTGGAAGACTGTGTCTGC 361
Qy 363 ArgGluGlyTyRArgAlaSerGlyGlnThrCysGluLeuValHisCysProAlaLeuLys 382
Db 362 AGAGAGGGATACAGGGCATCTGGCCAGACCTGTGAACCTTGTCCACTGCCCTGCCCTGAAG 421
Qy 383 ProProGluAsnGlyTyR-PheIleGlnAsnThrCysAsnAsnHisPheAsnAlaAlaCys 402
Db 422 CCTCCCGAATATGTTACTTTATCCAAACACTTGCACACACCATCTCAATGCAGCCTGT 481
Qy 403 GlyValArgCysHisProGlyPheAspLeuValGlySerSerlleLeuLeuCysLeuPro 422
Db 482 GGGGTCCGATGTCACCTGGATTGATCTTGTGGGAAGCAGCATCATCTTATGCTTACCC 541
Qy 423 AsnGlyLeuTrpSerGlySerGluSerTyCysArgValArgThrCysProHisLeuArg 442
Db 542 AATGTTTGTGTCCAGTTCAGAGACTACTGCAGAGTAAGAACATGTCTCTCATCTCCGC 601
Qy 443 GlnProLysHisGlyHisIleSerCysSerThrArgGluMetLeuTyRlysThrCys 462
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Qy 463 LeuValAlaCysAspGluGlyTyRArgLeuGluGlySerAspLysLeuThrCysGlnGly 482
Db 662 TTGGTTGCTGTGATGAAAGGTACAGACTAGAAAGCAGTCATAAGCTTACTTGTCTAAGGA 721
Qy 483 AsnSerGlnTrpAspGlyProGluProArgCysValGluArgHisCysSerThrPheGln 502
Db 722 AACAGCCAGTGGGATGGGCCAGAACCCCGTGTGTGGAGCCACTGTTCACCTTTCAG 781
Qy 503 MetProLysAspValIleIleSerProHisAsnCysGlyLysGlnProAlaLysPheGly 522
Db 782 ATGCCCAAGATGTCATCATATTCCCCCACTGTGGCAGCAGCCAGCAAAATTTGGG 841
Qy 523 ThrIleCysTyRValSerCysArgGlnGlyPheIleLeuSerGlyValLysGluMetLeu 542
Db 842 ACGATCTGCTATGATGTTGGCCCAAGGTTCCATTTTATTTTGGAGTCAAGGAATGCTG 901
Qy 543 Arg 543
Db 902 AGA 904

RESULT 12
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LOCUS BX439277 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YML1
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX439277
VERSION BX439277.1 GI:30773765
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

```


TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4989.r For
more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/Cluster.cgi?seq=CS00E009AG06P1cluster=4989.r. Contact :
Ceng Liang Email : liang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Farakav Avenue Genoscope sequence ID : CS00E009AG06P1.

FRATTURE

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FEATURES
LOCATION/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0DR09Ym11"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched, into
double-strand cDNA was digested with Not I and cloned, into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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ORIGIN

Alignment Scores:		
Pred. No.:	4.25e-122	Length: 1201
Score:	1659.50	Matches: 327
Percent Similarity:	90.63%	Conservative: 2
Best Local Similarity:	90.08%	Mismatches: 24
Query Match:	8.30%	Indels: 15
DR:	13	Gaps: 4

US-09-977-053-4 {1-3571} x BX439277 {1-1201}

3003	QY	LeuProCysArgCysSer----	ThrProValIleGluTyrGlyThrValAsnGlyThrAsp	3021
		::::		
45	DB	GTACCGCTCGGGAATCCCGGGATCCAGTAAATTGAATATGGAACCTGTCAATGGGACAGAT	104	
3022	QY	PheAspCysGlyValAlaAlaAArgIleGlnCysPheLysGlyPheLysLeuLeuGlyLeu	3041	
105	DB	TTTGACTGTGGAAAGGCAGCCCGGATTCAGTGTCTTCAAGGCTTCAGCTCTCTAGGACTT	164	
3042	QY	SerGluIleThrCysGluAlaAspGlyGlnTrpSerSerGlyPheProHisCysGluHis	3061	
165	DB	TCTGAAATCACCTGTGAAGCCGATGGCCAGTGGAGCTCTGGGTTCCTCCCACTGTGAACAC	224	
3062	QY	ThrSerCysGlySerLeuProMetIleProAsnAlaPheIleSerGluThrSerSerTrp	3081	
225	DB	ACTTCTTGTTGTTCTCTTCCAAATCATACCAATGCGTTTCATCATGAGAGACAGCTCTTGG	284	
3082	QY	LysGluAsnValIleThrTyrSerCysArgSerGlyTyrValIleGlnGlySerSerAsp	3101	
285	DB	AAGGAAATGTGATAACTTACAGCTGCAGGTCTGGATATGTCATACAGGCGTTCAGAT	344	
3102	QY	LeuIleCysThrGlnLysGlyValTrpSerGlnProTyrProValCysGluProLeuSer	3121	
345	DB	CTGATTGTGTACAGAGAAAGGGGTATGGAGCCAGCTTATCCAGTCTGTGAGCCCTTGTC	404	
3122	QY	CysGlySerProProSerValAlaAsnAlaValAlaThrGlyGluAlaHisThrTyrGlu	3141	
405	DB	TGTGGGTCCCCACCGCTGTGCGCAATGCAAGTGGCACTGGAGAGGCACACACCTATGAA	464	
3142	QY	SerGluValLysLeuArgCysLeuGluGlyTyrThrMetAspThrAspThrAspThrPhe	3161	
465	DB	AGTGAGGTGAAACTCAGATGTCTGGAGGGTTATACGATGGATACAGATACAGATACATTC	524	
3162	QY	ThrCysGlnLysAspGlyArgTrpPheProGluArgIleSerCysSerProLysLysCys	3181	

FEATURES

http://image.nlm.gov
Plate: NDAM482 row: e column: 11
High quality sequence stop: 729.
Location/Qualifiers

525	Db	ACCTGTCAGAAAGATGGTCGCTGGTTCCTCGAGAGAAATCTCTCGCAGTCTCTAAAAATGT	584
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585	Db	CCTCTCCCGGAAAAACATACACATATACTACTTGTTCATGGCGACGATTTTCAGTGTGAATAGG	644
3202	QY	GlnValSerValSerCysAlaGluGlyTyrThrPheGluGlyValAsnIleSerValCys	3221
645	Db	CAAGTTTCTGTGTGTCATGTCGAAAGGGGTATACCTTTTGAGGGAGCTTAAACATATCAGTATGT	704
3222	QY	GlnLeuaspGlyThrTrpGluProProPheSerAspGluSerCysSerProValSerCys	3241
705	Db	CAGCTTGATGGAACTCGGGAGCCACCATCTCTCGATGAATCTTTCGAGTCGAGTTTCTGT	764
3242	QY	GlyLysProGluSerProGluHisGlyPheValValGlySerLysTyrThrPheGluSer	3261
765	Db	GGGAACCTGAAAGTCCAGNACATGATGTTGTGTGGCAGTAAATACACCTTTGAAAGC	824
3262	QY	ThrIleIleTyrGlnCysGluProGlyTyrGluLeuGluGlyAsnArgGluArgValCys	3281
825	Db	ACAATTATTATTCAGTGTGAGCTGGCTGCTATGAACTAGAGGGGACACGGGAACGTGTCTGC	884
3282	QY	GlnGluAsnArgGlnTrpSerGlyGlyValAlaIleCysLysGluThrArgCysGluThr	3301
885	Db	CAGGAGAACAGACAGTGGAGTGGAGGGGTGGCAATGATGCAAGAGACACCGTGTGAAT-	943
3302	QY	ProLeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArgThrThrGlyProAsnVal	3321
944	Db	CCACTTGAAATTTCTCAATGGGAACCT-GACATTTAAACACAGGMS-ACTGGACCMAC-GTG	1000
3322	QY	ValTyrSerCysAsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThrGlu	3341
1001	Db	GTATATTCTTCGAMAGAGG---YACAGTCTTGAAGGSCA-TCTGAGGMMAYK---SACAGA	1053
3342	QY	AsnGlyThrTrpSer-----HisProValProLeuCysLysPro	3354
1054	Db	NATGGAACTGGGCMCCCTTCCTCCYTTCAACCAAAWCTGCTCTTTTGTTCGGA	1113
3355	QY	AsnProCys	3357
1114	Db	WGBYTTGT	1122
RESULT 13			
CD515150			
LOCUS		918 bp	mRNA linear EST 06-JUN-2003
DEFINITION		AGENCOURT 14365556 NIH MGC 181	homo sapiens cDNA clone
ACCESSION		IMAGE:30398026 5'	mRNA sequence.
VERSION		CD515150	
KEYWORDS		CD515150.1	GI:31446868
SOURCE			EST.
ORGANISM			Homo sapiens (human)
REFERENCE			Homo sapiens
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL			NIH (bases 1 to 918)
COMMENT			1. (bases 1 to 918) National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cga@b3-r@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp DNA Sequencing by: The I.M.A.G.E. Consortium (LNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: NDAM482 row: e column: 11 High quality sequence stop: 729. Location/Qualifiers
FEATURES			


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source
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/db_xref="taxon:9606"
/clone="IMAGE:30398026"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="NIH MGC 181"
/clone_lib="NIH MGC 181"
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-AT primed and directionally
cloned [EcoRV site is destroyed upon cloning]. Average
insert size 1.42 Kb. Library was constructed by
(invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 5,618-120 Length: 918
Score: 1629.50 Matches: 295
Percent Similarity: 97.69% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 2
Query Match: 8.16% Indels: 6
DB: 14 Gaps: 1

US-09-977-053-4 (1-3571) x CD515150 (1-918)

QY 3263 llelletyrGlnCysGluProGlyTyrGluLeuGluGlyAsnArgGluArgValCysGln 3282
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QY 3283 GluAsnArgGlnTrpSerGlyGlyValAlaIleCysLysGluThrArgCysGluThrPro 3302
DB 62 GAGAACACACAGTGGAGTGGAGGGTGGCAATATGCAAAAGAGACACAGGTGTGAAACTCCA 121

QY 3303 LeuGluPheLeuAsnGlyLysAlaIleGluAsnArgThrThrGlyProAsnValVal 3322
DB 122 CTGTGAATTTCTCAATGGGAAGTGCATTTGAAACAGGAGCACTGGACCCACAGTGGTA 181

QY 3323 TyrSerCysAsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThrGluAsn 3342
DB 182 TATTCCTGCAACAGAGGCTACAGTCTTGAAGGGCCATCTGAGGCACACTGCACAGAAAT 241

QY 3343 GlyThrTrpSerHisProValProLeuCysLysProAsnProCysProValProPheVal 3362
DB 242 CGAATCTGGAGCACCCAGTCCCTCTCTGCAAAACCAATCCATGCCCTGTCTCTTTGTG 301

QY 3363 IleProGluAsnAlaLeuLeuSerGluLysGluPheTyrValAspGlnAsnValSerIle 3382
DB 302 ATTCGAGAGATGCTCTGCTGTCTGAAAGGAGTTTATGTGTATCAGAAATGTGTCCATC 361

QY 3383 LysCysArgGluGlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAsnProAspGlu 3402
DB 362 AAATGTAGGAAGTGTCTGTCTGTCAGGGCCACGGCATCATTAACCTGCAACCCGACGAG 421

QY 3403 ThrTrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProPheAlaHisVal 3422
DB 422 ACGTGACACACAGACGCGCAAAATGTGAAATAATCTCATGTGTGTCCACAGCTACAGTA 481

QY 3423 GluAsnAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyrSerCys 3442
DB 482 GAAATATCAATTTGCTCGAGCGGTACATATCATATATGAGACATGATCACTACTCATGT 541

QY 3443 TyrSerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGlyThrTrp 3462
DB 542 TACAGTGGATACATGTTGGAGGGTTTCTCTGAGGAGTGTGTTTGTAGAAATGGAACATGG 601

QY 3463 ThrSerProPheIleCysArgAlaValCysArgPheProCysGlnAsnGlyGlyIleCys 3482
DB 602 ACATCACTCTCTATTGTCAGAGCTGTCTGTGATTTCCATGTGCAATGCGGCGCATCTCC 661

QY 3483 GlnArgProAsnAlaCysSerCysProGluGlyTyrMetGlyArgLeuCysGluGluPro 3502
DB 662 CAACGCCCAATGCTTTGTTCTGTCCAGAGGGCTGTGATGGGCGGCTCTGTGTAGAGACAC 720

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QY 3503 lleCysIleLeuProCysLeuAsnGlyGlyArgCysValAla-ProTyrGlnCysAspCys 3522
DB 721 ATCTGCAATTTCTCCCTGTCTGAACGAGGTCGTGTGTGGCCCTTACCAGTGTGACTG 780

QY 3522 sPro-ProGlyTrpThrGlySerArgCysHisThrAlaValCysGlnSerProCysLeuA 3542
DB 781 CCGGCTCTGGCTGGAGCGGGTCTCGCTGTCTATACAGCTGTGTCCAGTCTCCCTGCTTAA 840

QY 3542 snGly-GlyLysCysValArgPro-AsnArgCysHisCysLeu---SerSerTrpThrGln 3560
DB 841 ATGTGGGGAATGTGTAAAGACCAAAACCGATGTCACTGGTCTTTTCTTCTTGGACGGG 900

QY 3560 Y 3560
DB 901 G 901

RESULT 14
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LOCUS BX431419 Homo sapiens PLACENTA Homo sapiens cDNA clone CS00E009YML1
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX431419
VERSION BX431419.1 GI:30775023
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 881)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4989.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG0132D02_CS01164_1&cluster=4989.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0BAG0132D02_CS01164_1.
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1,568-113 Length: 881
Score: 1549.00 Matches: 281
Percent Similarity: 96.56% Conservative: 0
Best Local Similarity: 96.56% Mismatches: 10
Query Match: 7.76% Indels: 4
DB: 13 Gaps: 0

US-09-977-053-4 (1-3571) x BX431419 (1-881)

QY 3267 CysGluProGlyTyrGluLeuGluGlyAsnArgGluArgValCysGlnGluAsnArgGln 3286
DB 10 TGTGAGCTGGCTT-GAATAGA-GGGACAGGAGAGTGTCTGTCCAGGAGACAGACAG 67

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3287 TrpSerGlyValAlaIleCysLysGluThrArgCysGluThrProLeuGluPheLeu 3306
 68 TGGAGTGGAGGGTGGCATATGCAAGAGACAGAGTGTGAATCTCCTGATTTCTC 127
 3307 AsnGlyLysAlaAspIleGluAsnArgThrThrGlyProAsnValValTyrSerCysAsn 3326
 128 AATGGAAAGCTGACATTGAAACAGGACGACGTGGACCAACGCTGATATCTCTGCAAC 187
 3327 ArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThrGluAsnGlyThrTyrSer 3346
 188 AGAGGCTACAGTCTTGAAGGGCCATCTGAGGCACTGACAGAAATGGAACCTGGAGC 247
 3347 HisProValProLeuCysLysProAsnProCysProValProPheValIleProGluAsn 3366
 248 CACCCAGTCCCTCTGCAACCAATCAATGCGCTGTTCTTTGTGATTCGAGAT 307
 3367 AlaLeuLeuSerGluLysGluPheTyrValAspGlnAsnValSerLeuLysCysArgGlu 3386
 308 GCTCTGCTGCTGAAAGAGTATTTATGTTGATCAGATGTGTCATCAATGAGGAA 367
 3387 GlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAsnProAspGluThrTyrThrGln 3406
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 3407 ThrSerAlaLysCysGluLysIleSerCysGlyProProAlaHisValGluAsnAlaIle 3426
 428 ACAGGCCCAATGTGAAAATATCTATGTGTCCACAGCTCAGTAGAATGCAAT 487
 3427 AlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyrSerCysTyrSerGlyTyr 3446
 488 GCTCGAGGCGTACATTTATCAATATGAGACATGATCACCTACTCATGTTACAGTGATAC 547
 3447 MetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGlyThrTyrThrSerProPro 3466
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 608 ATTTCAGAGCTGTCTGTGATTTTCATGTCAGATGGGGCATCTGCCAACCCCAAT 667
 3487 AlaCysSerCysProGluGlyTyrMetGlyArgLeuCysGluGluProIleCysIleLeu 3506
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 3507 ProCysLeuAsnGlyGlyArgCysValAlaProTyrGlnCysAspCysProProGlyTyr 3526
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 3527 ThrGlySerArgCysHisThrAlaValCysGlnSerProCysLeuAsnGlyGlyLysCys 3546
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 3547 ValArgProAsnArgCysHisCysLeuSerSer 3557
 846 GGTAGGACCAACGATGTCATCTGTTCTTCT 878
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 clone CS0D1010Y21 5-PRIME, mRNA sequence.
 ACCESSION BX356254
 VERSION BX356254.1 GI:30380055
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)

COMMENT

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4991.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1010AD101Q1&cluster=4991.r. Contact :
 Peng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1010AD101Q1.
 Location/Qualifiers

FEATURES

source

1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1010Y21"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with NotI and cloned into the NotI and EcoRV
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: Length: 1201
 Pred. No.: 5,64e-107 Matches: 295
 Score: 1470.50
 Percent Similarity: 93.99% Conservative: 2
 Best Local Similarity: 93.35% Mismatches: 18
 Query Match: 7.36% Indels: 5
 DB: 13 Gaps: 0
 US-09-977-053-4 (1-3571) x BX356254 (1-1201)
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 DB 102 ATGTGGCTCGCTGGCTTTGTTGCTGGGGTCTGGCGCTGTTTCGGGCTGGCGGACC 161
 QY 21 PheGlnMetSerProSerArgAsnPheSerPheArgLeuPheProGluThrAlaPro 40
 DB 162 TTTTCAGCAGATGTCCTCGCTGGCGCAATTTTCAGCTTTCGCTTTCCTCCGAGACCGCGGCC 221
 QY 41 GlyValProGlySerIleProAlaProProAlaProGlyAspGluAlaAlaGlySerArg 60
 DB 222 GGGGCCCCCGGAGTATCCCCGCGCCCGCTCTCTGGCAGCAGCGCGGGGAGCAGA 281
 QY 61 ValGluArgLeuGlyGlnAlaPheArgArgValArgLeuLeuArgGluLeuSerGlu 80
 DB 282 ATGGAGCGGCTGGCGCAGGCGTTCCGCGACGCGTGGCTGCTGGGAGCTCAACGAG 341
 QY 81 ArgLeuGluLeuValPheLeuValAspAspSerSerSerValGlyGluValAsnPheArg 100
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 QY 101 SerGluLeuMetPheValArgLysLeuLeuSerSerPheProValValProThrAlaThr 120
 DB 402 AGCGAGCTCATGTCTGTCGCAAGTCTGTCCGACTTCCCGTGGTGGCCCGCGCCACG 461
 QY 121 ArgValAlaIleValThrPheSerSerLysAsnTyrValValProArgValAspTyrIle 140
 DB 462 CGCGTGGCCATCGTGACCTTCTCGTCCAAAACCTACGCTGGTGGCGCGCTCGATTACATC 521
 QY 141 SerThrArgAlaAlaArgGlnHisLysCysAlaLeuLeuGlnGluIleProAlaIle 160
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 QY 161 SerTyrArgGlyGlyThrTyrThrLysGlyValAlaPheGlnGlnAlaAlaGlnIleLeu 180
 DB 581 TCCTACCGAGGTGGCGACCTACACCAAGGCGCCTTCCAGCAAGCGCGCCAAATTTCT 640
 QY 181 LeuHisAlaArgGluAsnSerThrLysValValPheLeuIleThrAspGlyTyrSerAsn 200


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641 CTTTCATGCTAGAGAAACTCAACAAAGTTGATTTCTCATCTAGTGATGATATCCAAAT 700
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QY -PheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThrProLysG 240
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QY uGluHisCysTrpLeuLeuHisSerPheGluGluPheGluAlaLeuAlaArgAlaLe 260
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QY uHisGluAspLeuProSerGlySerPheIleGlnAspAspMetValHisCysSerTrp 280
Db GCATGAAGATCTACCTCTCGGAGTTTATTCARATGATATGTTCCACTGCTCATATCT 940
QY uCysAspGluGlyLysAspCysAspArgMetGlySerCysLysCysGlyThrHisTh 300
Db TTGTGATGAAGAAA-GACTGCTGTGACCGAATKGGAGSTG-GMAATGKGGRMWACAC 998
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RESULT 16
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LOCUS BX356253 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1010YG21 3-PRIME, mRNA sequence.
ACCESSION BX356253
VERSION BX356253.1 GI:30378038
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLES 1 (bases 1 to 1201)
L1.W.B., Gruber,C., Jessee,J., and Polayes,D.
FULL-LENGTH cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4991.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1010AD11NP1&cluster=4991.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1010AD11NP1.
FEATURES
Location/Qualifiers
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/clone="CS0D1010YG21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 6 58e-102 Length: 1201
Score: 1407.50 Matches: 298
Percent Similarity: 89.18% Conservative: 7

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Best Local Similarity: 87.13% Mismatches: 30
Query Match: 7.05% Indels: 14
DB: 13 Gaps: 4
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Db 1002 TQKCCCTCCT---TCCTTTCCAAAT---GAGATGTGCTATCGWTACACGCMACCTACCTATC 949
QY 630 SerGlyAsnGlnAlaSerCysIlePheHisIleLysValIleAspAlaGluProProVal 649
Db 948 CCG---AACCAGCCGCGGCGCATTCATATTAAGGTTATGTT-GCAGAACACACCTGTC 893
QY 650 IleAspTrpCysArgSerProProValGlnValSerGluLysValHisAlaAlaSer 669
Db 892 WTAGATGTGTGAGATCTCCACCTCCGTCAGTTCTCGAGAAAGGTACATGCGCAAGC 833
QY 670 TrpAspGluProGlnPheSerAspAsnSerGlyAlaGluLeuValIleThrArgSerHis 689
Db 832 TGGAT-GAGCCTCAGTTCTCAGACCACTCAGGGGCTGAATT-GTCATTACAGAGTCAT 775
QY 690 ThrGlnGlyAspLeuPheProGlnGlyGluThrIleValGlnTrpThrAlaThrAspPro 709
Db 774 ACACAGGAGM-CTTTTCCCTCAGGAG-ACATAGTACAGTATACAGCCTGACCCC 717
QY 710 SerGlyAsnAsnArgThrCysAspIleHisIleValIleLysGlySerProCysGluIle 729
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QY 750 ThrLeuThrCysLeuGluGlyTrpAspPheThrGluGlySerThrAspLysTrpCys 769
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Db 537 GCTTATGAAGATGGGCTCTGGAAACCAACATATACCACTGAATGGCCAGACTGTGCCAA 478
QY 790 LysArgPheAlaAsnHisGlyPheLysSerPheGluMetPheTrpLysAlaAlaArgCys 809
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QY 810 AspAspThrAspLeuMetLysLysPheSerGluAlaPheGluThrThrLeuGlyLysMet 829
Db 417 GATGACACAGATCTGATGAAGAAGTTTCTGAAGCAATTTGAGAGTTCCTGGGGAAGAG 358
QY 830 ValProSerPheCysSerAspAlaGluAspIleAspCysArgLeuGluGluAsnLeuThr 849
Db 357 GTCCCATCATTTGTAGTGTGATGAGAGGACATTCAGCGCAGACTGGRGAGAGCTGRC 298
QY 850 LysLysTrpCysLeuGluTrpAspTrpAspTrpGluAsnGlyPheAlaIleGlyProGly 869
Db 297 GAAAATATTCCTAGATATATTAATGACTATGAATGAAATGGCTTTCGCAATTTGACCCAG 238
QY 870 GlyTrpGlyAlaAlaAsnArgLeuAspTrpSerTrpAspPheLeuAspThrValGln 889
Db 237 GCTGGGGTGCAGCTAATAGGCTGGATTTCTTACGATGACTTCTCGGACACTGTGCTA 178
QY 890 --GluThrAlaThrSerIleGlyAsnAlaLysSerSerArgIleLysArgSerAlaPro 909
Db 177 TAGAAACACGCAACAGCATCGGCAATGCCAGGCGTCAACGATTAAGAAAGAGTGCCTCAT 118
QY 909 euSerAspTrpLysIleLysLeuIlePheAsnIleThrAlaSerValProLeuProAspG 929
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Qy 2147 ygluProProSerIleMetAsnGlyTyrAlaSerGlySerAsnTyr----- 2162
Db 1434 AGGACGCTGAGCACTTGGGGTGTGTGATCTGAGCCCGCTTCCCGAGGTCTTACCC 1493
Qy 2163 -----SerPheGlyAlaMetValAl 2169
Db 1494 CAACAACCTAGACTGCACCTGGAGGATCTCATTTACCCATCGGCTATGTGTGCACATATCA 1553
Qy 2169 atyr-----SerCysAsnLysGlyPheTyr-----IleLysGlyGluLysGly 2183
Db 1554 GTTCTGAATTTTCTACCGAGCTAATCATGACTTCTTGAAATTCAAATGGACCTTA 1613
Qy 2183 sSerThrCysGluAlaThrGlyGlnTrpSerPro-----IlePr 2197
Db 1614 CCACACAGCCCACTGATGATGGACAAATTTAGCGGCACGGATCTCCCGCGGCCCTGCTGAG 1673
Qy 2197 oThrCysHisProVal----- 2202
Db 1674 CACAACGATGAACCCCTCACTCCATTTTATAGTGACCATTCGCMAAACCGGCAAGGATT 1733
Qy 2203 -----SerCysGlyGluProProLysValGluAs 2212
Db 1734 TAACTTGTCTTACCAAGCCTATGAATTACAGACTGTCCAGATCCACCCCAATTTTCAGAA 1793
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Qy 2232 nProGlyTyrLysSerValGlySerProValPheValCysGln-----AlaAsnArgHi 2250
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Qy 2308 lLysTrpAsnLysLysSerAsnProLysCysMetProAlaLysCysProGluProL 2328
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Qy 2367 ln-----GlnTrpAsn-----AspSerPhePro-ValCysLys 2377
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Qy 2462 aleuTyrThrCysLysProGlyPheGluLeuValGlyAsnThrThrThrLeu----- 2479
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Qy 2480 -----CysGlyGluAsnGlyHisTrp-----LeuGl 2488
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Qy 2581 rCysPheProGlyPheGlnValAlaGlyHisAlaMetGlnThrCysGluGluSer----- 2599
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Qy 2600 -----GlyTrpSerSerSerIleProThrCysMetProIleAspCysGlyLeuPr 2616
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Db 3003 A----- 3003
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Qy 2656 aValAlaLysThrTrpGluAsnThrLysGluSerProAlaThrHisSer-----Se 2673
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Qy 2693 yAsn-----ProValLeuIleCysGlnGluAspGlyThrTrpAsn-----GlySerAl 2709
Db 3096 CAGCCAGCAAGCAACAGCGGTGTTCAGAGATGGGTGTGGAGTAACAGGGGAAGCC 3155
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Db 3156 GCCCATGTGTAAGCGGTGCTTGGCCCGCAGCATTTGAAGTCTCAGCTCTCAGAACATGCTAT 3215
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3276	Db	TCCTGGTTACTACTTTAGAAGGCTCGAGGCTCTCTCGGTGCGAGCCCAATGGGACGTGGAA	3335
2764	Qy	x-----GlyAlaSerProArgCysGluAlaIleSerCysIysIysProAsnProValMe	2782
3336	Db	:CATAGGAGATGAGAGCCCAAGCTGTCCAGCTGGCCACTGGGTTCCTCCAGACCGGATTGT	3395
2782	Qy	tAsnGlySerIleIysGlySerAsnTrpThrTyrLeuSerThrLeuTyrTyrGluCysAs	2802
3396	Db	GAACGGTCACATTAGTCGAGATGCGTTCAGTTACAGACACACGGTGGTTATCCAGGTGCAA	3455
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3636	Db	CTATTTGTCGAGGCGGTCTCGAGCCAGTGTGGAGCAACGGCCAGTGGAGTAGCC	3695
2882	Qy	aThrProAspCysValProValArgCysAlaThrProProGlnLeuAlaAsnGlyValTh	2902
3696	Db	TCGTGCCACCGTGTGAGTGTGAACCTGTTCTGATCCAGGCTTTGTGGAAATGCCATTCG	3755
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3756	Db	TCACGGGCAACAGACTTCCTCGAGAGTTTGTGATGGATG-----AGTATCTGTGA	3809
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3990	Db	CAGAGGGAGCGAGAGCCTCATAGGCAACACAGCAGAGTGTGCGAGAGACACATCTACTG	4049
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4050	Db	GAGCGGGACACTGCCCCACTGCACAGAAATAATCTCTGGATTCTGTGTGTGATCCGGGAC	4109
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4230	Db	ATGCTCAGGACTCGACGCGGTGTGTGAGGCGGTGCTCTGTGGCAACACCTCGGCACAC	4289
3071	Qy	oAsnAlaPheIle-----SerGlnThrSerSerTrpIysGluAsnValIleThrTrpSe	3089
4290	Db	CAACGGAAATGTTTCAGTAGTATGCAATCTGTTCTCCAGCTCCGCTCATC---TATCC	4346
3089	Qy	rCysArgSerGlyTyrValIleGlnGlySerSerAspLeuIleCysThrGluIysGlyVa	3109

Db	4347	CTGCTGGGAAGGCTTACAAGACCTTCAGGGCTCATGACACGGCATTTGCACACCCCAATGGGAC	4406
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Db	4527	CCGAGGCTATGTTCATGAAGACAGTCACATCCGCCACTATTTCGTGTATCCAAAGACGGCAG	4586
Qy	3168	gtTpPheProGluArgIleSerCysSerProLysLysCysProLeuProGluAsnIleTh	3188
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Qy	3188	rHisLeuValHisGlyAspAspPheSerValAsnArgGlnValSerValSerCysAl	3208
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Qy	3208	aGluGlyTyThrPheGluGlyValAsnIleSerValCysGlnLeuAspGlyThrTrpGl	3228
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Db	4767	AGAGAGATC-----CCCCAGTGTCTCCCTGTGTCTTCGCGAGACCTCGGCATCCCCG	4820
Qy	3248	uHisGlyPheValGlySerIlySerTyThrPheGluSerThrIleIleTyrglnCysGl	3268
Db	4821	AGAAGGCGCACTTAGTGGGAAAAGTTTCACTATAAGTTCGAAGTCTTCTTCCAGTCAA	4880
Qy	3268	uProGlyTyrgluLeuGluGlyAsnArgGluArgValCysGlnGluAsnArgGlnTrpSe	3288
Db	4881	ATCTCCATTTNN	4940
Qy	3288	rGlyGlyValala-----	3292
Db	4941	NN	5000
Qy	3292	-----	3292
Db	5001	NN	5060
Qy	3292	-----	3292
Db	5061	NN	5120
Qy	3293	-----	3301
Db	5121	NN	5174
Qy	3301	rProLeuGluPheLeuAsnGlyLysAlaAsp-----lleGluAsnArgThrThrGl	3318
Db	5175	CCCC-----GCACACGGCATGTGAGAGCCATCATCTTCTTCTTCTTCTCGG	5219
Qy	3318	yProAsnValValTySerCysAsnArgGlyTySerLeuGluGlyProSerGluAlaHi	3338
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Qy	3338	s---CysThrGluAsnGlyThrTrpSerHisProValProLeuCysLys-----	3353
Db	5280	AACATGTAAAGCAGACATGAATGGACAGAAAGTCGCTGTGTGTGTGTGTGTGTGTGTGT	5339
Qy	3354	-----ProAsnProCysProValProPheVal	3362
Db	5340	GACAGAAGTAAATGAAACAGTTACTAAAACTCCAGTTCTCTCAGATGCTCTTTTCGTC	5397

LOCUS AY407075 5901 bp DNA linear GSS 15-DEC-2003
DEFINITION Mus musculus CSMD1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407075
VERSION AY407075.1 GI:39763046
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 5901)
AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 5901)
AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES location/Qualifiers
source 1..5901
gene /organism="Mus musculus"
gene /mol_type="genomic DNA"
gene /db_xref="taxon:10090"
gene <1..>5901
gene /gene="CSMD1"
ORIGIN /locus_tag="HCM2769"

Alignment Scores:
Pred. No.: 5, 83e-99 Length: 5901
Score: 1386.50 Matches: 527
Percent Similarity: 34.80% Conservatives: 231
Best Local Similarity: 24.20% Mismatches: 751
Query Match: 6.94% Indels: 675
DB: 29 Gaps: 91

US-09-977-053-4 (1-3571) x AY407075 (1-5901)

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Db	250	AAACTGGGCTCTACAGTTACCTATCAGTGTGACTCTGTGTACAGATTGTGGATCCCTCG	309
Qy	1727	ArgMetPheCysThrAspAsnGlySerTrpAsnGlyValSerProSerCysLeuAspVal	1746
Db	310	TCCATTGAGTGTGT-GACAGGGGCTGATGGAGCGCTC-----	347
Qy	1747	AspGluCysAlaValGlySerAspCysSerGluHisAlaSerCysLeuAsnValAspGly	1766
Db	347	-----	347
Qy	1767	SerTyrIleCysSerCysValProProTyrThrGlyAspGlyAsnCysAlaGluPro	1786
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Qy	1787	IleLeuCysLysAlaProGlyAsnProGluAanglyHisSerSerGlyGluIleTyrThr	1806
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2203 -----SerCysGlyGluProProLysVal 2210
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2249 ArgHisTrpHisSerGluSerProLeuMetCysValProLeuAspCysGlyLysProPro 2268
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1946 -----GATGAGTACCAATTTCTGAAGGACTGTCTGTGGCT----- 1980
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2414 uArgGlyAsnSerThrThrLeuCysGlnProAspGlyThrTrpSerSerProLeu----- 2432
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2499 euLysProLysGluIleLeuAsnGlyLysPheSerTyrThrAspLeu----- 2514
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2515 -----HisTyrGlyGlnThrValThrTyrSerCysAsnArgGlyPheArgLeuGlu 2532
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2673 --SerAsnPheLeuTyrGlyThrMetValSerTyrThrCysAsnProGlyTyrGluLeuL 2692
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Qy	2724	luAaNGlyPheLeuArgPheThrGluThrSerMet	-----GlySerAlaValGlnTr	2741
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RESULT 20
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 LOCUS 602553560F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4663335 5',
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ACCESSION BG534331
 VERSION BG534331.1 GI:13525871
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 769)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

Contact: Robert Strausberg, Ph. D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>

Plate: LLCM1465 row: g column: 16
 High quality sequence stop: 737.

Location/Qualifiers

source

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 SfiI (ggccctcgcc); Site 2: SfiI (ggccattggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGCGGCGGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 3.29e-100 Length: 769
 Score: 1382.00 Matches: 251
 Percent Similarity: 98.05% Conservative: 1
 Best Local Similarity: 97.67% Mismatches: 3
 Query Match: 6.92% Indels: 2
 DB: 12 Gaps: 0

US-09-977-053-4 (1-3571) x BG534331 (1-769)

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 301 ATTATTTATCAGTGTGAGCCTGCTATGAACCTAGAGGGGAAACAGGGAACGTGTGCGCAG 360
 QY 3283 GluAsnArgGlnTrrPheSerGlyValAlaIleCysLysGluThrArgCysGluThrPro 3302
 Db
 361 GAGAACACACAGTGGAGTGGAGGGGTGGCAATATATGCAAGAGACCCAGGTGTGAACTCCA 420
 QY 3303 LeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArgThrThrGlyProAsnValVal 3322
 Db
 421 CTTGAATTTCTCAATGGGGAAGCTGACATTTGAAACAGGACGACCTGGACCCCAACGTGGTA 480
 QY 3323 TyrSerCysAsnArgGlyTrrSerLeuGluGlyProSerGluAlaHisCysThrGluAsn 3342
 Db
 481 TATTCTCTCAACAGAGGCTACAGTCTTGAAGGGCCATCTGAGGGCACACATGTCACAGAAAT 540
 QY 3343 GlyThrTrrPheSerHisProValProLeuCysLysProAsnProCysProValProPheVal 3362
 Db
 541 GGAACCTGGAGCCGCCAGTCCCTCTCTGCAACCAATCCATGCCCTGTCTTTTGTG 600
 QY 3363 IleProGluAsnAlaLeuLeuSerGlyLysGluPheTrrValAspGlnAsnValSerIle 3382
 Db
 601 ATTTCCCGAGATGCTCTGCTGTCTGAAAAGAGGATTTTATGTTGATCAGAAATGTGTCATC 660
 QY 3383 LysCysArgGluGlyPheLeuGlnGlyHisGly-IleIleThrCys-AsnProAspG 3402
 Db
 661 AAATGTAGGGAAGGTTTTCTGCTGCGAGGGCCACGCGCCATCATTTACCTGCAAAACCCGACG 720
 QY 3402 LuThrTrrPheThrSerAlaLysCysGluLysIleSerCysGly 3417
 Db
 721 AGAAGTGGACACAGACAGGCGCCAAATGTGACAAATCTCATGTGT 767

RESULT 21
 CF407643 940 bp mRNA linear EST 02-SEP-2003
 LOCUS CF407643
 DEFINITION Canis familiaris cDNA clone CH3#049_F12 5', mRNA sequence.
 TITLE Canis familiaris cDNA Library in pBluescript
 EXPRESSED sequence tags from Canine heart
 UNPUBLISHED (2003)
 OTHER ESTs: CH3#049_F12T3
 CONTACT: George AL
 DIVISION of Genetic Medicine
 VANDERBILT University

ACCESSION CF407643
 VERSION CF407643.1 GI:34408733
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 940)
 Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.
 Expresed sequence tags from Canine heart
 Unpublished (2003)
 Other ESTs: CH3#049_F12T3
 Contact: George AL
 Division of Genetic Medicine
 Vanderbilt University

QY 1273 CysSerSerProCysLeuHsnGlyIleCysValAspGlyValAlaGlyTyrArg 1292
 Db 63 TGTAGCTCAGTCCCTGTTTAAATAGGAATCTGTGTGATGGTGTGGCTGCTATCGT 122

QY 1293 CysThrCysValGlyPheValGlyLeuHsnCysGluThrGluValAsnGluCysGln 1312
 Db 123 TGCACATGTGTGAAGGATTTGTAGCCCTGCATTTGTGAAGCAGATCCTNTGAATGCCAG 182

QY 1313 SerAsnProCysLeuAsnAlaValCysGluAspGlnValGlyGlyPheLeuCysLys 1332
 Db 183 TCAAAACCATGCTTAAATAATGAGTCTGTGAAGACCAAGTGTGGGGATTCCTGTGCATA 242

QY 1333 CysProGlyPheLeuGlyThrArgCysGlyLeuHsnValAspGluCysLeuSerGln 1352
 Db 243 TGCCCACTGGATTTTGGGTACCCGATGTGAAGAACGTGATGAGTGTCTCAGTCAG 302

QY 1353 ProCysLysAsnGlyAlaThrCysLysAspGlyAlaAsnSerPheArgCysLeuCysAla 1372
 Db 303 CCATGCAAAATGGAGCTACCTGTAAAGACGGTGGCCATAGCTTCAGATGCCCTGTGTGCA 362

QY 1373 AlaGlyPheThrGlySerHisCysGluLeuAsnLysLeuGluCysGlnSerAsnProCys 1392
 Db 363 GCTGGCTTCACAGGATCACCTGTGAATTTGAACATCAATGAATGTCAATCAATGT 422

QY 1393 ArgAsnGlnAlaThrCysValAspGluLeuAsnSerTyrSerCysLysCysGlnProGly 1412
 Db 423 AGAAATCAGGCCACATGTGTGAATTTGAATTTCAATGTTGTAAATGTTCAGCCAGA 482

QY 1413 PheSerGlyGlnArgCysGluThrGluGlnSerThrGlyPheAsnLeuAspPheGluVal 1432
 Db 483 TTTTCAGGCAAAAGGTGTGAACAGACAGTCTACAGGCTTTAACTGGATTTTGAAGTT 542

QY 1433 SerGlyIleTyrGlyTyrValMetLeuAspGlyMetLeuProSerLeuHisAlaLeuThr 1452
 Db 543 TCTGTATCTATGATATGTCTATGATGTGTGATGATGATGATGATGATGATGATGAT 602

QY 1453 CysThrPheTrpMetLysSerSerAspAspMetAsnTyrGlyThrProLeuSerTyrAla 1472
 Db 603 TGTACCTTCGTGATGAAATCCTCTGACGACATGAATATGGAACACCAATCTCTCTATGCA 662

QY 1473 ValAspAsnGlySerAspAsnThrLeuLeuLeuThrAspTyrAsnGlyTyrValLeuTyr 1492
 Db 663 GTTGATACGGCAGCAGACATACCTTCTCTCTGATGATGATGATGATGATGATGATGAT 722

QY 1493 ValAsnGlyArg 1496
 Db 723 GTGAATGGCAGG 734

RESULT 23
 CP409971 839 bp mRNA linear EST 02-SEP-2003
 LOCUS CH3#063_H05MF Canine heart normalized cDNA Library in pBluescript
 DEFINITION Canis familiaris cDNA clone CH3#063_H05 5', mRNA sequence.
 ACCESSION CP409971
 VERSION CP409971.1 GI:34411217
 KEYWORDS EST:
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 839)
 Y.Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
 TITLE Expressed sequence tags from Canine heart
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: CH3#063_H05MR
 Contact: George AL
 Division of Genetic Medicine
 Vanderbilt University
 529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
 Tel: 615 936 2660
 Fax: 615 936 2661
 Email: al.george@vanderbilt.edu
 Insert Length: 1614 Std Error: 0.00

Seq primer: MF: GTTTTCCAGTCACGACGTTG
 High quality sequence start: 83
 High quality sequence stop: 753.

FEATURES

source

1..839
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /clone="CH3#063_H05"
 /tissue_type="heart"
 /cell_type="heart"
 /dev_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"
 /clone_lib="Canine heart normalized cDNA Library in pBluescript"
 /note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dr primed"

ORIGIN

Alignment Scores:

Pred. No.: 4,51e-95 Length: 839
 Score: 1319.00 Matches: 229
 Percent Similarity: 90.19% Conservative: 10
 Best Local Similarity: 86.42% Mismatches: 24
 Query Match: 6.60% Indels: 2
 DB: 14 Gaps: 0

US-09-977-053-4 (1-3571) x CP409971 (1-839)

QY 3303 LeuGluPheLeuAsnGlyLysAlaAspIleGluAsnArgThrThrGlyProAsnValVal 3322
 Db 48 TTGGAGCTCCACCGCGGTGGCGCGCGCTCGAGCAGCAGCTGCTGGACTCAGGAGTG 107

QY 3323 TyrSerCysAsnArgGlyTyrSerLeuGluGlyProSerGluAlaHisCysThrGluAsn 3342
 Db 108 TATTCCTGCACAGAGGGTACAGCCTTGAAGAGGACACCTGAGATACATTCGCCGACAC 167

QY 3343 GlyThrTrpSerHisProValProLeuCysLysProAsnProCysProValProPheVal 3362
 Db 168 GGAGTTTGGAGCCACCCACATCTCTCTGCANACCAATCCATGCTCTCTTTTGTG 227

QY 3363 IleProGluAsnAlaLeuLeuSerGluLysGluPheTyrValAspGlnAsnValSerIle 3382
 Db 228 ATTCTCTGAGATGCTGTCTCTTCTGAAAAGGAGTTTATGTTGATCAGAACGTCCTATC 287

QY 3383 LysCysArgGluGlyPheLeuLeuGlnGlyHisGlyIleIleThrCysAsnProAspGlu 3402
 Db 288 AAGTGTAGAGAGGCTTCTCTCCAGGTTGGGGCATTCATCTGTAACCCGATGAG 347

QY 3403 ThrTrpThrGlnThrSerAlaLysCysGluLysIleSerCysGlyProProAlaHisVal 3422
 Db 348 ACATGACGGTGCACAAATGCCAAATGTGAATAATATCTGTGTCTCCACCACTCATGTA 407

QY 3423 GluAsnAlaIleAlaArgGlyValHisTyrGlnTyrGlyAspMetIleThrTyrSerCys 3442
 Db 408 GGAAATGGATGTCTGCGAGGCATACATTTATCATGTATGGGACATGATCATCTACTCTGT 467

QY 3443 TyrSerGlyTyrMetLeuGluGlyPheLeuArgSerValCysLeuGluAsnGlyThrTrp 3462
 Db 468 TACAGTGGATACATGTTGGAGGGCTCCCTTAAGAGATATTGTCTAGAGATATGGNACTGTG 527

QY 3463 ThrSerProProIleCysArgAlaValCysArgPheProCysGlnAsnGlyGlyIleCys 3482
 Db 528 ACATCACCTCTCTATTGTCAGAGCTGTCTGTGTGATCTCCATGTCAGATGGAGTATCTGC 587

QY 3483 GlnArgProAsnAlaCysSerCysProGluGlyTyrMetGlyArgLeuCysGluGluPro 3502
 Db 588 CAACGCCCAATGCTTGTCTCTGTCAGATGGCTGATGGGGCGCTCTGTGTGAAGACCA 647

http://image.llnl.gov

Plate: LLC1591 row: 1 column: 06

High quality sequence stop: 738.

Location/Qualifiers

FEATURES

source

1..756

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4732181"

/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 79"

/note="Organ: placenta; Vector: pDNR-LIB (Clontech);

Site_1: Sfil (ggcgctcgcc); Site_2: Sfil

(ggccatagggc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3'

and 3' adaptor sequence:

5'-ATTCTAGAGCGCGGCGGACATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.3

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH MGC Library."

ORIGIN

Alignment Scores:

Pred. NO.:	3.18e-93	Length:	756
Score:	1295.00	Matches:	250
Percent Similarity:	98.04%	Conservative:	0
Best Local Similarity:	98.04%	Mismatches:	1
Query Match:	6.48%	Indels:	5
DB:	12	Gaps:	0

US-09-977-053-4 (1-3571) x BG620159 (1-756)

Qy	476	AspLysLeuThrCysGlnGlyAsnSerGlnTrpAspGlyProGluProArgCysValGlu	495
Db	1	GATTAAGCTTACTTGTCAAGGAACAGCCAGCGGTGGGATGGCCAGAACCCCGGTGTGTGGAG	60
Qy	496	ArgHisCysSerThrPheGlnMetProLysAspValIleIleSerProHisAsnCysGly	515
Db	61	CGCCACTGTTCCACCTTTTCAGATGCCCAAGATGTTCATCATATCCCCCCACAACTGTGGC	120
Qy	516	LysGlnProAlaLysPheGlyThrIleCysTrpValSerCysArgGlnGlyPheIleLeu	535
Db	121	AAGCAGCCAGCCAAATTTGGACGATCTGCTATGTAAGTGGCCGCAAGGGTTCATTTTA	180
Qy	536	SerGlyValLysGluMetLeuArgCysThrThrSerGlyLysTrpAsnValGlyValGln	555
Db	181	TCTGGAGTCAAGGAATGCTCAGATGTACCACTTCTGGAAATGGAATGTGGAGTTCAG	240
Qy	556	AlaAlaValCysLysAspValGluAlaProGlnIleAsnCysProLysAspIleGluAla	575
Db	241	GCAGCTGTGTGTAAAGAGCTGGAGGCTCTCTCAAAATCAACTGTCTTAAGCAGATAGGCT	300
Qy	576	LysThrLeuGluGlnAspSerAlaAsnValThrTrpGlnIleProThrAlaLysAsp	595
Db	301	AAGACTCTGGAAACAGCAAGATTCTGCCAATGTTACTGTGGCAGATTCCAAACAGCTAAAGAC	360
Qy	596	AsnSerGlyGluLysValSerValHisValHisProAlaPheThrProProTrpLeuPhe	615
Db	361	AACCTCTGGTGAAGAGTGTCTAGTCCAGCTTCATCCAGCTTTTCCACCCACCTTACCTTTTC	420
Qy	616	ProIleGlyAspValAlaIleValTrpThrAlaThrAspLeuSerGlyAsnGlnAlaSer	635
Db	421	CCAATTGGAGATGTTGCTATCGTATACACGGCACTGACCTATCCGGCAACCCAGGCCAGC	480
Qy	636	CysIlePheHisIleLysValIleAspAlaGluProProValIleAspTrpCysArgSer	655
Db	481	TGCATTTTCCATATCAAGGTTATTGATGCAGAACCCCTCTGCTATAGACTGTGGCAGATCT	540
Qy	656	ProProValGlnValSerGluLysValHisAlaAlaSerTrpAspGluProGlnPhe	675
Db	541	CCACCTCCCGTCCAGGTTCTCGGAGAGAGGTACATGCCCGCAAGCTGGGATGAGCCTCAGTTC	600

Qy	676	SerAspAsnSerGlyAlaGluLeuValIleThrArgSerHisThrGlnGlyAspLeuPhe	695
Db	601	TCAGACAACTCAGGGGCTGAATTGGTTCATTACCAAGATCATACACAGGAGACCTTTTC	660
Qy	696	ProGln-GlyGluThrIleValGlnTrpThrAlaThrAspProSerGlyAsnAsnArgTh	715
Db	661	CCTCAAGGGGAGACTATAGTACAGTATACAGC-ACTGACCCCTCAGGCATATACAGGAC	719
Qy	715	r-CysAspIle-HisIleVal-IleLysGlySerPro	726
Db	720	CATGTGATATCCCATATTGTTCATATAAAGGTTCTCCG	756

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Job time : 27110.2 secs